

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:46 ; Search time 1191.56 Seconds
(without alignments)
9445.379 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_430

Perfect score: 176
Sequence: 1 acctgcaatccagctactgtc.....gagcgagaagtagactgct 176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	176	100.0	3505	2	ES4511	ES4511 UCP-2 promo
2	174.4	99.1	3270	5	AP306570	AP306570 Homo sapi
3	174.4	99.1	12177	5	DO087219	DO087219 Homo sapi
4	174.4	99.1	155668	12	AC024029	AC024029 Homo sapi
5	174.4	99.1	156370	5	AP003717	AP003717 Homo sapi
6	174.4	99.1	197031	12	AC019121	AC019121 Homo sapi
7	174.4	99.1	199384	5	AP003531	AP003531 Homo sapi
8	115	65.3	141252	5	AC146263	AC146263 Pan trogl
9	115	65.3	172959	12	AC119422	AC119422 Papio anu
10	114.2	64.9	162701	12	AC073317	AC073317 Homo sapi
11	114.2	64.9	183939	5	AC015684	AC015684 Homo sapi
12	114.2	64.9	206454	12	AC011227	AC011227 Homo sapi
13	114	64.8	401	7	BV190642	BV190642 scrm16786
14	114	64.8	132966	12	AP001277	AP001277 Homo sapi
15	114	64.8	136613	12	AC090379	AC090379 Homo sapi
16	114	64.8	149490	5	AL355344	AL355344 Human DNA
17	114	64.8	157138	12	AC144366	AC144366 Papio anu
18	114	64.8	162107	12	AP002423	AP002423 Homo sapi

C 19	114	64.8	166616	12	AC145761	AC145761 Papio anu
C 20	114	64.8	177748	12	AC016185	AC016185 Homo sapi
C 21	114	64.8	181041	12	AC087677	AC087677 Homo sapi
C 22	114	64.8	190225	5	AC023983	AC023983 Homo sapi
C 23	114	64.8	191161	12	AC016043	AC016043 Homo sapi
C 24	114	64.8	193779	12	AP001327	AP001327 Homo sapi
C 25	113.4	64.4	647	7	BV562782	BV562782 Gak3905
C 26	113.4	64.4	763	7	BV580787	BV580787 Gak3905
C 27	113.4	64.4	770	7	BV574328	BV574328 Gak3905
C 28	113.4	64.4	788	7	BV590640	BV590640 G591P6324
C 29	113.4	64.4	59133	5	AC004819	AC004819 Homo sapi
C 30	113.4	64.4	71371	5	AL356357	AL356357 Human DNA
C 31	113.4	64.4	119452	5	AC096552	AC096552 Homo sapi
C 32	113.4	64.4	142363	5	AC008167	AC008167 Homo sapi
C 33	113.4	64.4	160582	5	AC105429	AC105429 Homo sapi
C 34	113.4	64.4	163026	12	AC103883	AC103883 Homo sapi
C 35	113.4	64.4	172020	12	AC025873	AC025873 Homo sapi
C 36	113.4	64.4	175051	5	AC010531	AC010531 Homo sapi
C 37	113.4	64.4	182082	12	AC092842	AC092842 Homo sapi
C 38	113.4	64.4	191635	12	AC137760	AC137760 Homo sapi
C 39	113.4	64.4	220495	5	AP000886	AP000886 Homo sapi
C 40	113	64.2	164500	5	AC092418	AC092418 Homo sapi
C 41	112.6	64.0	185035	5	AC094770	AC094770 Homo sapi
C 42	112.6	64.0	185766	5	AP002754	AP002754 Homo sapi
C 43	112.6	64.0	188788	5	AP002380	AP002380 Homo sapi
C 44	112.6	64.0	190144	5	AL590080	AL590080 Human DNA
C 45	112.6	64.0	206860	12	AC025689	AC025689 Homo sapi

ALIGNMENTS

RESULT 1

LOCUS ES4511
DEFINITION UCP-2 promoter and use thereof.
ACCESSION ES4511
VERSION ES4511.1 GI:18629692
KEYWORDS JP 2000236886-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Toyota, Y., Kobayashi, M. and Igaki, S.
AUTHORS UCP-2 promoter and use thereof
TITLE Patent: JP 2000236886-A 1 05-SEP-2000;
JOURNAL TAKEDA CHEM IND LTD
COMMENT OS Homo sapiens (human)
PN JP 2000236886-A/1
PD 05-SEP-2000
PF 22-DEC-1999 JP 1999364724
PR

YUKIO TOYOTA, MAKOTO KOBAYASHI, SHIGERU IGAKI
PC C12N15/09, A61K45/00, A61P3/04, A61P3/06, A61P3/10, A61P9/12, PC
A61P9/00, C12N1/21.
PC C12N5/10, C12Q1/02, G01N33/15, G01N33/50, A61K31/11, A61K38/00,
PC A61K48/00,
PC (C12N15/09, C12R1:19), (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), (C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
PC C12R1:19),
PC (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)

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Location/Qualifiers
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ORIGIN


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QY	61	AAAGCAGCCTTGACAAACAGGAGACTGTCTACTCACTCAAAAGATAATTAATTAGCCAG	120
Db	113	AAAGCAGCCTTGACAAACATAGGAGACTGTCTACTCACTCAAAAGATAATTAATTAGCCAG	172
QY	121	GCTTAGTGCTCATCCCTGAGTCCAGACTAGGAGGACAGAGTACGCT	176
Db	173	GCTTAGTGCTCATCCCTGAGTCCAGACTAGGAGGACAGAGTACGCT	228

RESULT 4
AC024029/c 155668 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
DEFINITION
SEQUENCE, 15 unordered pieces.
AC024029
AC024029.3 GI:7230916
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 155668)
Waterston,R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 155668)
Waterston,R.H.
Direct Submission
Submitted (20-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7109555.
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0167N04
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer RT; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; sum-of-contigs
Quality coverage: 4.38 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
* 11378 14368: contig of 2991 bp in length
* 14369 14468: gap of unknown length
* 14469 20130: contig of 5662 bp in length
* 20131 20230: gap of unknown length
* 20231 25513: contig of 5283 bp in length
* 25514 25613: gap of unknown length
* 25614 30765: contig of 5152 bp in length
* 30766 30865: gap of unknown length
* 30866 37337: contig of 6472 bp in length
* 37338 37437: gap of unknown length
* 37438 45571: contig of 8134 bp in length
* 45572 45671: gap of unknown length

FEATURES
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*	38649	38748: gap of unknown length
*	38749	44925: contig of 6177 bp in length
*	44926	45025: gap of unknown length
*	45026	51784: contig of 6759 bp in length
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*	58956	68289: contig of 9334 bp in length
*	68290	68389: gap of unknown length
*	68390	77123: contig of 8734 bp in length
*	77124	77223: gap of unknown length
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*	87293	87392: gap of unknown length
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*	96130	104791: contig of 8662 bp in length
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*	143094	154361: contig of 11266 bp in length
*	154362	154461: gap of unknown length
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ORIGIN

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Matches 175; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	1	ACCGTATTTCCAGTACCTGTAGATCCGAGGTCAAGAGACCTGTGAGCCAGAGATTC	60
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QY	163418	AAGAGCAGCTTGACACACATAGGGAGACCTGTCACTCAACAAATTAATTAATTAGCCAG	163477
Db			

RESULT 7	AP003531	199384 bp	DNA	linear	PRI 27-APR-2002
LOCUS	AP003531/c				
DEFINITION	Homo sapiens genomic DNA, chromosome 11q clone:RP11-535C12, complete sequences.				
ACCESSION	AP003531				
VERSION	AP003531.2	GI:20334341			
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA Published Only in Database (2001)				
TITLE	2 (bases 1 to 199384)				
JOURNAL	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission Submitted (18-APR-2001) Maashira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22, Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) On Apr 26, 2002 this sequence version replaced gi:13699094.				
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Best Local Similarity	99.4%	Pred. No. 2e-48			
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QY	61 AAGACACGCTGGAGCAACACAGAGAGACCTGTGCATCAACAAAGATTAATTAATCAACCAG 120				
b	182355 AAGACACGCTGGAGCAACACAGAGAGACCTGTGTCTACCAAGATTAATTAATTAATCAACCAG 182296				
QY	121 GCTTAGTGCGTCATCCCTGTGTGCCAGCTACTAGAGGAGCAAGATAGGACTGCT 176				
Db	182295 GCTTAGTGCGTCATCCCTGTGTGTGCTCCAGCTACTAGAGGAGCAAGATAGGACTGCT 182240				
RESULT 8					
LOCUS	AC146263	141252 bp	DNA	linear	PRI 19-MAY-2004
DEFINITION	Pan troglodytes BAC clone R443-2801 from 7, complete sequence.				
ACCESSION	AC146263				
VERSION	AC146263.2	GI:47498252			
KEYWORDS	HTG.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pan.				
REFERENCE	1 (bases 1 to 141252)				

```

AUTHORS      Griffith, M., Bielicki, L. and Haakenson, W.
TITLE        The sequence of Pan troglodytes BAC clone RP43-2801
JOURNAL      Unpublished (2001)
REFERENCE    2 (bases 1 to 141252)
AUTHORS      Wilson, R.K.
TITLE        Direct Submission
JOURNAL      Submitted (01-NOV-2003) Genetics, Genome Sequencing Center, 4444
REFERENCE    Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS      3 (bases 1 to 141252)
TITLE        Wilson, R.K.
JOURNAL      Direct Submission
REFERENCE    Submitted (19-MAY-2004) Washington University School of Medicine,
AUTHORS      Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
TITLE        63108, USA
JOURNAL      On May 19, 2004 this sequence version replaced gi:3387216.
COMMENT      ----- Genome Center
              Center: Washington University Genome Sequencing Center
              Center code: WUGSC
              Web site: http://genome.wustl.edu
              Contact: submissions@wustl.wustl.edu
              ----- Summary Statistics
              Center project name: C_PR028001
              -----

NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:
The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, 'Clint', Yerkes #C0471; birthdate: 6-6-80). The
clone and detailed information can be obtained from ResGen
(http://www.resgen.com) or Pieter de Jong and co-workers at
http://www.bacpac.chori.org.

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
/map="7"
/clone="RP43-2801"
/clone_lib="RPCI-43"

ORIGIN
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Best Local Similarity 79.5%; Pred. No. 5,5e-28;
Matches 136; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

1  ACCGTGAATTCGAGTACTGTGAGAGTCCAGGTCAAGAGACGCTGTGAGCCAGAGATTC 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  76117  ACCGTGAATTCAGCACTTTGGAGGCTGAGGCAACGATTCGTGAGCCAGAGATTG 76058

61  AAGAGCAGCTGGAACAACAGGAGGAGACCTGTCACTACAAAGAAATTAATTAATGACGAG 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  76057  GAGAGCAGCTGGGCAATGTAGGAGAACTTGTCTCTACAAAATAATTAATTAATGACGAG 75998

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* 9791 9890: gap of unknown length
* 9891 13294: contig of 3404 bp in length
* 13295 13394: gap of unknown length
* 13395 16584: contig of 3190 bp in length
* 16585 16684: gap of unknown length
* 16685 20753: contig of 4069 bp in length
* 20754 20854: gap of unknown length
* 20854 24326: contig of 3473 bp in length
* 24327 24426: gap of unknown length
* 24427 28594: contig of 4168 bp in length
* 28595 28694: gap of unknown length
* 28695 32625: contig of 3931 bp in length
* 32626 32725: gap of unknown length
* 32726 39439: contig of 6714 bp in length
* 39440 39540: gap of unknown length
* 39540 44814: contig of 5275 bp in length
* 44815 44914: gap of unknown length
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* 52290 58734: contig of 6445 bp in length
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* 66885 66984: gap of unknown length
* 66985 74428: contig of 7844 bp in length
* 74429 74528: gap of unknown length
* 74529 84369: contig of 9841 bp in length
* 84370 84469: gap of unknown length
* 84470 91569: contig of 7100 bp in length
* 91570 91669: gap of unknown length
* 91670 101447: contig of 9778 bp in length
* 101448 101547: gap of unknown length
* 101548 119545: contig of 17998 bp in length
* 119546 119645: gap of unknown length
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* 137646 162701: contig of 24956 bp in length.
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FEATURES

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ORIGIN

Query Match 64.9%; Score 114.2; DB 12; length 162701;
Best Local Similarity 78.3%; Pred. No. 1.1e-27;
Matches 137; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGCTGAGAGAGCTGTTAGGCCAGAGATTCA 61
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DB 133766 CATATGTGGCAAAATGCTGTATATCCAGCTACTGCGAGGCTGAGGAGAACTGCT 133820

RESULT 11
AC015684 183939 bp DNA linear PRI 01-FEB-2002
LOCUS Homo sapiens chromosome 11, clone RP11-2C23, complete sequence.
AC015684
AC015684.11 GI:18129440
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 183939)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-2C23
2 (bases 1 to 183939)
Unpublished
1 (bases 1 to 183939)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Brown,A., Dearliano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,M., Forrest,C., Funke,R., Gage,D., Doyle,M.,
Galegani,J., Gardyna,S., Grant,G., Hages,B., Heatford,A., Klein,J.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Kataras,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,U., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testave,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 183939)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouhgalter,B.,
Brown,A., Camarata,J., Campiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cook,P., Dearliano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,M., Gage,D., Galegani,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hages,B., Horton,L., Hulme,W., Illie,I., Johnson,R., Jones,C.,
Kataras,A., Kataras,A., Kells,C., Lacroque,K., Lamazares,R.,
Lander,E., Lehoczky,J., Levine,R., Liu,G., Maclean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrum,J., Menau,L., Mhova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Niccol, R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunthang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Riebeck,M., Riley,R., Rhee,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,N.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Straus,N., Subramanian,A., Talamas,J., Testave,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 11, 2002 this sequence version replaced gi:1874886.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)

FEATURES
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1331
Center clone name: 2_C_23

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Query Match      64.9%; Score 114.2; DB 5; Length 183939;
Best Local Similarity 80.2%; Pred. No. 1,1e-27;
Matches 134; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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Db      79169 GCTGACACATGCTGTATATCCAGCTACTGAGGAGCTGAGGAGCA 79215

RESULT 12
AC011227
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
AUTHORS

2 (bases 1 to 206454)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cook,P., DeArrelano,K., Dewar,K., Domono,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hages,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tittrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 6, 2001 this sequence version replaced gi:13123322.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L3135
Center clone name: 11_A_11

----- Summary Statistics
Sequencing vector: MJ3; M77815; 7% of reads
Sequencing vector: Plasmid; n/a; 93% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 191082 bases at least Q40
Consensus quality: 18939 bases at least Q30
Consensus quality: 201696 bases at least Q20
Insert size: 17000; agarose-fp
Insert size: 202754; sum-of-ctnigs
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 9.0 in Q20 ba.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 38 contigs. The true order of the pieces
* is not known and their order in this sequence record is
```

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

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* 116623 116722: gap of 100 bp
* 116723 116775: contig of 953 bp in length
* 116776 117775: gap of 100 bp
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* 119567 120382: contig of 816 bp in length
* 120383 120482: gap of 100 bp
* 120483 121110: contig of 628 bp in length
* 121111 121210: gap of 100 bp
* 121211 121906: contig of 696 bp in length
* 121907 122006: gap of 100 bp
* 122007 122708: contig of 702 bp in length
* 122709 122808: gap of 100 bp
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* 123428 123527: gap of 100 bp
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* 140044 140143: gap of 100 bp
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* 151456 153113: contig of 1658 bp in length
* 153114 153213: gap of 100 bp
* 153214 154844: contig of 1631 bp in length
* 154845 154944: gap of 100 bp
* 154945 157033: contig of 2089 bp in length
* 157034 157133: gap of 100 bp
* 157134 206454: contig of 49321 bp in length.

FEATURES

source

1. 206454
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-11A11"
/clone_11b="RP11 Human Male BAC"
1. 114750
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
114751..114850
/estimated_length=100
114851..115820
/note="assembly_fragment"
115821..115920
/estimated_length=100
115921..116622
/note="assembly_fragment"
116623..116722
/estimated_length=100
116723..117675
/note="assembly_fragment"
117676..117775
/estimated_length=100
117776..118386
/note="assembly_fragment"
118387..118486
/estimated_length=100
118487..119466
/note="assembly_fragment"
119467..119566
/estimated_length=100
119567..120382
/note="assembly_fragment"
120383..120482
/estimated_length=100
120483..121110
/note="assembly_fragment"
121111..121210
/estimated_length=100
121211..121906
/note="assembly_fragment"
121907..122006
/estimated_length=100
122007..122708
/note="assembly_fragment"
122709..122808
/estimated_length=100
122809..123427
/note="assembly_fragment"
123428..123527
/estimated_length=100
123528..124282
/note="assembly_fragment"
124283..124382
/estimated_length=100
124383..125443
/note="assembly_fragment"
125444..125443

Query Match 64.2%; Score 114.2; DB 12; length 206454;

Best Local Similarity 80.2%; Pred. No. 1,1e-27;

Matches 134; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 5 GTATTTCAGTACTGTGAGAGTCCGAGGTCAGAGACTGCTTAGGCGCAGAGATTCAAGA 64

Db	54086	GTAATCCTAGACACTTTGGAGGCCGAGGTAGCGSAAATTGCTTAGAGACAGGAATTCAGA	54145
Oy	65	GCAGCCTTGACAACAACAGGAGACCTGTCACTAACAAAGATAAATAATTAGCCAGGCTT	124
Db	54146	CCAGCCCCAGCCAAACATGGCAAGACCTGTCTCTACTAAGAAATACATAATTAGCCAGGCAAT	54205
Oy	125	AGTGGCTCATCCCTGTGGTCCCAGCTACTAGGGAGGAGAGAAATAGAGA	171
Db	54206	GCTGGCACATGCTGTAAATCCAGCTACTTGGAGGCGTAGGAGCAGA	54252
<hr/>			
RESULT 13			
BVL90642			
LOCUS	BVL90642	401 bp	DNA linear STS 10-JUN-2004
DEFINITION	sgmml67865 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.		
ACCESSION	BVL90642		
VERSION	BVL90642.1	GI:48032193	
KEYWORDS	STS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases, 1 to 401) Nelson,R.M., Manneillo,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.		
TITLE	Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions		
JOURNAL	Genome Res. (2004) In press		
COMMENT	Contact: Andreas Braun Pharmaceuticals division Sequenom, Inc. 3565 John Hopkins Court, San Diego, CA 92121, USA Tel.: 18582028018 Fax: 18582029020 Email: abraun@sequenom.com Primer A: No primer sequence submitted Primer B: No primer sequence submitted STS size: 401.		
<hr/>			
FEATURES			
Source	Location/Qualifiers 1..401 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone_lib="Human DNA (Sequenom)" <1..>401		
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ORIGIN	STS		
Query Match	64.8%; Score 114; DB 7; Length 401;		
Best Local Similarity	79.4%; Pred. No. 6e-28;		
Matches 135; Conservative	0; Mismatches 35; Indels 0; Gaps 0;		
Oy	2	CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTACAGAGGACTGCTTAGGCCACAGACTTCA	61
Db	120	CCTTAATCCACAGACTTTTAGAGAGCGAGGTGGCGGATCATCTTGATCAGAGAGTTCA	179
Oy	62	AGAGACACCTTGAGACAACAGGAGAGACCTGTCACTAACAAAGATAAATAATTAGCCAGG	121
Db	180	AGACACACCTTGAGCCAAACATGGYGAACCCTCTCTTTAAAAATTAATTAAGCCAGG	239
Oy	122	CTTAGGGCTCATCCCTGTGGTCCAGCTACTAGGAGGAGCAGAAATAGAGA	171
Db	240	CTTAGTGGCCGACACTGTAGTCCCACTTAATTGGAGGCGTAGGCGAGAA	289
<hr/>			
RESULT 14			
AP001277		132966 bp	DNA linear HTG 30-MAY-2000
LOCUS	AP001277		
DEFINITION	Homo sapiens chromosome 18 clone RP11-886011 map 18q11.2, WORKING DRAFT SEQUENCE, 19 unordered pieces.		

ACCESSION	AP001277
VERSION	AP001277.2 GI:8117670
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
AUTHORS	1 (bases 1 to 132966)
TITLE	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
JOURNAL	Homo sapiens 132,966 genomic DNA of 19q11.2
REFERENCE	2 (bases 1 to 132966)
AUTHORS	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE	Direct Submision
JOURNAL	Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
COMMENT	On May 31, 2000 this sequence version replaced gi:7106155.
	----- Genome Center
	Center: RIKEN Genomic Sciences Center (GSC)
	Center code: RIKEN
	Web site: http://hgp.gsc.riken.go.jp/
	Contact: hattori@gsc.riken.go.jp
	----- Project Information
	Center project name: Humdrat18
	Center clone name: RP11-886011
	----- Summary Statistics
	Sequencing vector: PCR products; 100% of reads
	Assembly: Dye-terminator EP-amersham; 100% of reads
	Assembly program: Phrap; version 0.990329
	Consensus quality: 122160 bases at least Q40
	Consensus quality: 127107 bases at least Q30
	Consensus quality: 129558 bases at least Q20
	Insert size: 131166; sum-of-contigs
	Quality coverage: 5.73x in Q20 bases; sum-of-contigs

	NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

	1 18432 contig of 18432 bp in length
	18513 31839 contig of 13307 bp in length
	31940 46961 contig of 15022 bp in length
	47062 58376 contig of 11315 bp in length
	58477 68787 contig of 10311 bp in length
	68868 76179 contig of 7292 bp in length
	76280 82148 contig of 5869 bp in length
	82249 86877 contig of 4629 bp in length
	86978 94001 contig of 7024 bp in length
	94102 100574 contig of 6473 bp in length
	10675 106683 contig of 6009 bp in length
	106784 111994 contig of 5211 bp in length
	112095 117429 contig of 5335 bp in length
	117530 121564 contig of 4035 bp in length
	121665 125145 contig of 3481 bp in length
	125246 127181 contig of 2536 bp in length
	127882 129887 contig of 2006 bp in length
	129968 131384 contig of 1397 bp in length
	131485 132966 contig of 1482 bp in length

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 153.125 Seconds
(without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098A-1_COPY_255_430
Perfect score: 176

Sequence: 1 acctgtaattccagtactgt.....gagcagaagttagtactgt 176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
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Maximum Match	100%
Listing first	45 summaries

Database :

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1: N_Genseq_8:*
2: genseeqn1980s:*
3: genseeqn1990s:*
4: genseeqn2000s:*
5: genseeqn2001bs:*
6: genseeqn2002bs:*
7: genseeqn2002bs:*
8: genseeqn2003bs:*
9: genseeqn2003bs:*
10: genseeqn2003cs:*
11: genseeqn2003ds:*
12: genseeqn2004as:*
13: genseeqn2004bs:*
14: genseeqn2005s:*
15: genseeqn2006s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
c 1	176	100.0	3505	3	AAAG62932	AAAG62932	DNA contig
c 2	112.6	64.0	185035	6	ABR10147	ABT10147	Human bre
c 3	112.6	64.0	185035	8	ACA64951	ACA64951	Human PEN
c 4	112.6	64.0	185035	12	AQO20284	AdqQ20284	Human soD
c 5	112.4	63.9	3521	12	ADQ62296	AdqQ62296	Novel hum
c 6	112	63.6	2312	11	ADMO2195	AdmoI2195	Human CDN
c 7	112	63.6	2312	14	AEC85125	AEC85125	Human cDN
c 8	110.8	63.0	13001	4	AAK82979	Aak82979	Human imm
c 9	110.8	63.0	38653	12	ADH26544	Adh26544	Human hea
c 10	109.4	62.2	81099	11	ACH45018	Acth45018	Human ger
c 11	109.2	62.0	620	12	ADN12517	Adn12517	Human pte
c 12	109.2	62.0	31116	11	ACH44954	Acth44954	Human ger
c 13	109.2	62.0	31279	14	ADZ13355	Adz13355	Human can
c 14	109.2	62.0	58822	9	ADA02540	Ada02540	Human TCO
c 15	109.2	62.0	58822	9	ADA02540	Ada02540	Human TCO
c 16	109.2	62.0	58822	10	ADB72278	Adb72278	Human TCC
c 17	109.2	62.0	58822	10	ADB72278	Adb72278	Human TCC
c 18	109.2	62.0	58822	10	ADB95788	Adb95788	Human TCC

C	19	109.2	62.0	58822	10	AD595788	Human	TCO
C	19	108.2	61.5	310268	13	ABD32548	Human	can
C	21	108	61.4	135005	12	ADQ19501	Human	so5
C	22	107.8	61.2	1480	6	AA142843	Human	NP-
C	23	107.8	61.2	1890	6	AA142845	Human	NP-
C	24	107.6	61.1	2136	6	AAH18289	Human	GEN
C	25	107.6	61.1	285020	11	ACN44958	Human	cdn
C	26	107.6	61.1	322885	13	ADS93537	Human	MRC
C	27	107	60.8	201	13	ADS33303	Human	autc
C	28	107	60.8	39265	6	AB152838	Human	AD152838
C	29	107	60.8	57502	12	ADQ07092	Human	can
C	30	107	60.8	149671	6	ABK84797	Human	CDN
C	31	107	60.8	149671	9	ADB70361	Human	CDN
C	32	107	60.8	149671	12	ADJ37140	Human	mal
C	33	107	60.8	158417	13	ADS35461	Human	autc
C	34	106.8	60.7	312477	12	ADP65744	Human	ROO
C	35	106.2	60.3	832	4	AA188238	Human	pol
C	36	106.2	60.3	1793	4	AAH17207	Human	CDN
C	37	106.2	60.3	101961	14	AEH18616	Fibrotic	
C	38	106.2	60.3	114596	14	ADZ70595	Human	cdn
C	39	106.2	60.3	128117	14	AED18395	Fibrotic	
C	40	106.2	60.3	157230	14	AED18395	Human	brc
C	41	106.2	60.3	170508	14	AED89424	Human	brc
C	42	106.2	60.3	173115	14	AED89425	Human	brc
C	43	106.2	60.3	226475	9	AD58279	Human	tum
C	44	106	60.2	2575	4	AAK82973	Human	tum
C	45	106	60.2	2918	14	ADY15885	DNA	encod

ALIGNMENTS

	RESULT 1
AA62932	
ID	AAA62932 standard; DNA; 3505 BP.
AC	AAA62932;
XX	
DT	02-NOV-2000 (first entry)
XX	
DE	DNA containing human uncoupling protein-2 (UCP-2) promoter region.
XX	
KW	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;
KW	hypertension; hyperlipidaemia; anti-pyretic; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200039315-A1.
XX	
PD	06-JUL-2000.
XX	
PF	22-DEC-1999; 99WO-JF007198.
XX	
PR	24-DEC-1998; 98UP-00366719.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Toyoda Y, Kobayashi M, Igaki S;
DR	WPI; 2000-452407/39.
PT	
PT	DNA with promoter region containing regulator sequence of uncoupling
PT	protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,
PT	hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in
PT	therapy.
PS	
PS	Claim 4; Fig 1-6; 43bp; Japanese.
XX	
CC	This invention relates to DNA comprising a promoter region containing the
CC	regulatory sequences of human uncoupling protein-2 (UCP-2). Included in
CC	the invention are a recombinant vector containing the DNA sequence, cells
CC	transformed by the vector, and a method for screening for compounds or
CC	salts that can promote or inhibit the UCP-2 promoter activity using the

CC transformants. The DNA and cells transformed using it can be used to
CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidaemic
CC and anti-pyretic drugs. The present sequence represents DNA containing
CC the UCP-2 promoter sequences

XX
SQ Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 176; DB 3; Length 3505;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGACTGTGAGAGTCCGAGGCTCAGAGACTGCTTGAGGCCAGGAGTTTC 60
DB 255 ACCTGTAATTCAGACTGTGAGAGTCCGAGGCTCAGAGACTGCTTGAGGCCAGGAGTTTC 314
QY 61 AAGAGCAGCTGGACAACACAGGAGACCTGTCTACTCACTCAAAAGATTAATTAATTAAGCCAG 120
DB 315 AAGAGCAGCTGGACAACACAGGAGACCTGTCTACTCACTCAAAAGATTAATTAATTAAGCCAG 374
QY 121 GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAACTAGACTGCT 176
DB 375 GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAACTAGACTGCT 430

RESULT 2
ABT10147/c
ID ABT10147 standard; cDNA; 185035 BP.

XX ABT10147;

DT 04-DEC-2002 (first entry)

DE Human breast cancer associated coding sequence SEQ ID NO: 281.

KM Human; breast specific gene; breast cancer; differential expression;
KW cytostatic; gene therapy; gene; ss.

XX Homo sapiens.

OS MO200259271-A2.

PN 01-AUG-2002.

PF 25-JAN-2002; 2002MO-US002176.

PR 25-JAN-2001; 2001US-0263757P.

PR 25-APR-2001; 2001US-0286090P.

PR 23-MAY-2001; 2001US-0292517P.

XX (GENE-) GENE LOGIC INC.

PI Orr MS, Nation M, Digdians JC, Zeng W;

DR WPI; 2002-674803/72.

XX
PT Diagnosing breast cancer in a patient comprises detecting the level of
PT gene expression in cell or tissue samples, where a differential gene
PT expression is indicative of breast cancer.

XX
PS Claim 1; SEQ ID NO 281; 260pp + Sequence Listing; English.

XX
CC The present invention relates to methods of diagnosing breast cancer in a
CC patient, which comprise detecting the level of expression in a tissue
CC sample of two or more genes selected from those shown in ABT09867-
CC ABT1112, where a differential expression of the genes indicates breast
CC cancer. The methods are useful in diagnosing, treating, detecting the
CC progression, and in monitoring treatment of breast cancer in patients.
CC The methods are also useful as a screening tool for agents that modulate
CC the onset or progression of breast cancer. The breast cancer genes may be
CC used as diagnostic markers for the prediction or identification of the
CC malignant state of breast tissue, for confirming the type and progression
CC of cancer, and for drug screening and assays. The present sequence is a
CC coding sequence of the invention. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 185035 BP; 42256 A; 51727 C; 51210 G; 39842 T; 0 U; 0 Other;

Query Match 64.0%; Score 112.6; DB 6; Length 185035;
Best Local Similarity 82.5%; Pred. No. 2.1e-26;
Matches 141; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 2 CCTGTAAATTCAGACTGTGAGAGTCCGAGGCTCAGAGACTGCTTGAGGCCAGGAGTTTC 61
DB 150502 CCTGTAAATTCAGACTGTGAGAGTCCGAGGCTCAGAGACTGCTTGAGGCCAGGAGTTTC 150443
QY 62 AAGAGCAGCTGGACAACACAGGAGACCTGTCTACTCACTCAAAAGATTAATTAATTAAGCCAG 120
DB 150442 AAGAGCAGCTGGACAACACAGGAGACCTGTCTACTCACTCAAAAGATTAATTAAGCCAG 150383
QY 121 GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAACTAGAGA 171
DB 150382 GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAACTAGAGA 150332

RESULT 3
ACA64951/c
ID ACA64951 standard; DNA; 185035 BP.

XX ACA64951;

DT 27-JUN-2003 (first entry)

DE Human PEN1 DNA corresponding to AC004770.

KM Human; chronic inflammatory joint disease; infection; tumour;
KW anti-inflammatory; cytostatic; antirheumatic; antineumatic;
KW immunosuppressive; gene therapy; etiological pathogenicity; ds.

XX Homo sapiens.

OS DE10127572-A1.

PN 05-DEC-2002.

PF 30-MAY-2001; 2001DE-01027572.

PR 30-MAY-2001; 2001DE-01027572.

PR (PATR-) PATHOARRAY GMBH.

XX Haep1 T, Ungethuen U, Blaess S;

DR WPI; 2003-240797/24.

XX
PT Reagents for diagnosis, study and therapy of chronic inflammatory joint
PT and other diseases, comprises any of many specified genes or derived
PT proteins.

XX
PS Claim 1; Page; 12pp; German.

XX
CC This invention describes a novel reagent for diagnosis, molecular
CC definition and therapy of chronic inflammatory joint diseases, and other
CC inflammatory disorders, infective or tumour diseases in humans. The
CC products of the invention have anti-inflammatory, cytostatic,
CC antirheumatic, antineumatic and immunosuppressive activity and can be
CC used for gene therapy. The reagent of the invention and any proteins and
CC antibodies derived from it, are used (i) for analysing tissue and blood
CC samples for medical diagnosis; (ii) for diagnosis and characterisation of
CC chronic joint diseases, on the basis of molecular characterisation, and
CC determining the etiological pathogenicity principle of as yet
CC uncharacterised inflammatory diseases, also monitoring progression and/or
CC treatment of disease, and optimisation of therapy and (iii) for
CC developing treatments for inflammatory diseases, particularly of joints,
CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides

CC used in the method of the invention
XX Sequence 185035 BP; 42256 A; 51727 C; 51210 G; 39842 T; 0 U; 0 Other;
SQ

Query Match 64.0%; Score 112.6; DB 8; Length 185035;
Best Local Similarity 82.5%; Pred. No. 2.1e-26;
Matches 141; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 2 CCTGTATTCCAGTACTGTGAGAGTCCGAGGTCCAGAGCTCTTGAGGCCAGAGTTCA 61
DB 150502 CCTGCAATCCAGACACTTTGGAGGCCGAGGTGGAGATTGCTTGAGGCCAGAGTTTG 150443

QY 62 AGAGCAGCTCTGAGCAACACAGGAGGA-CTGTCACTCAAAAGATAATTAATTAAGCCAG 120
DB 150442 AGACACAGCTCTGGGCAACATAGTGAGACCTGTCTCTCAAAAAAATAATTAAGCCAA 150383

QY 121 GCTTAGTGCTCATCTCCCTGTGTGCTCCAGCTACTAGGAGCAGAGATAGGA 171
DB 150382 GCATGTGTGGACATAGTGTGAGACCCAGCTACTTGGAGGCTGAGTAGGA 150332

RESULT 4
ADQ20284/C
ID ADQ20284 standard; DNA; 185035 BP.
XX
AC ADQ20284;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3104.
XX
KM soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human;
XX
KM Homo sapiens.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnick A;
XX
PI WPI; 2004-441208/41.
XX
DR
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 3104; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytoskeletal applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 185035 BP; 42256 A; 51727 C; 51210 G; 39842 T; 0 U; 0 Other;

Query Match 64.0%; Score 112.6; DB 12; Length 185035;
Best Local Similarity 82.5%; Pred. No. 2.1e-26;
Matches 141; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 2 CCTGTATTCCAGTACTGTGAGAGTCCGAGGTCCAGAGCTCTTGAGGCCAGAGTTCA 61
DB 150502 CCTGCAATCCAGACACTTTGGAGGCCGAGGTGGAGATTGCTTGAGGCCAGAGTTTG 150443

QY 62 AGAGCAGCTCTGAGCAACACAGGAGGA-CTGTCACTCAAAAGATAATTAATTAAGCCAG 120
DB 150442 AGACACAGCTCTGGGCAACATAGTGAGACCTGTCTCTCAAAAAAATAATTAAGCCAA 150383

QY 121 GCTTAGTGCTCATCTCCCTGTGTGCTCCAGCTACTAGGAGCAGAGATAGGA 171
DB 150382 GCATGTGTGGACATAGTGTGAGACCCAGCTACTTGGAGGCTGAGTAGGA 150332

RESULT 5
ADQ62996/C
ID ADQ62996 standard; cDNA; 3521 BP.
XX
AC ADQ62996;
XX
DT 07-OCT-2004 (first entry)
XX
DE Novel human cDNA sequence #157.
XX
KM ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KM cytoskeletal; gene therapy; diagnostic marker; morbid state; osteoporosis;
KM neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KM cancer.
XX
XX
OS Homo sapiens.
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX
PR 21-JAN-2003; 2003JP-00102206.
XX
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isegaki T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
PI WPI; 2004-535376/52.
XX
DR P-PADB; ADQ65184.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 157; 249pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX
SQ Sequence 3521 BP; 727 A; 1051 C; 919 G; 824 T; 0 U; 0 Other;

Query Match 63.9%; Score 112.4; DB 12; Length 3521;
Best Local Similarity 78.8%; Pred. No. 6e-27;
Matches 134; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 2 CCTGTATTCCAGTACTGTGAGAGTCCGAGGTCCAGAGCTCTTGAGGCCAGAGTTCA 61

```
Db 910 CCTGTAATCCCAACACTTTGGAGGCTGAGGAGGAGGATTTGCTTAAGGCGCAGAGTTCA 851
Oy 62 AGAGCAGCCTTGACAACAACAGGAGACTGTCTACTACTAAAGATTAATTAATTAAGCCAG 121
Db 850 AAGACAGCCTTGAGCAACATAGAGAGCCCTGTCTCTCAAAAATTTTAAATTAAGCTGG 791
Oy 122 CTTAGTGCTCATCCTGTGTGTCCAGCTTACTAGGAGGCGAAGTAGGA 171
Db 790 CGTGATGGCGCATGCTGTAGTTCCAGCTACTTGGGAAACAGAGTGGGA 741

RESULT 6
ADM02195
ID ADM02195 standard; cDNA; 2312 BP.
XX
XX
AC ADM02195;
XX
DT 20-MAY-2004 (first entry)
XX
XX Human cDNA of the invention SEQ ID NO:880.
XX
XX ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
XX Homo sapiens.
XX
XX EP1347046-A1.
XX
XX 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y,
XX
XX WPI: 2003-723558/69.
XX
XX P-PSDB; ADM04638.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
XX PT developing a diagnostic marker or medicines for regulating their
XX PT expression and activity, or as a target of gene therapy.
XX
XX PS Claim 1; SEQ ID NO 880; 305bp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
XX CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful
XX CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
XX CC as a primer for synthesizing the polynucleotide or as a probe for
XX CC detecting the polynucleotide. The polynucleotides ADM03316-ADM03758 are
XX CC useful in gene therapy, for developing a diagnostic marker or medicines
XX CC for regulating their expression and activity, or as a target of gene
XX CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
XX CC are useful as pharmaceutical agents. The present sequence represents a
XX CC cDNA sequence of the invention.
XX
XX Sequence 2312 BP; 609 A; 493 C; 563 G; 647 T; 0 U; 0 Other;
SQ

Query Match 63.6%; Score 112; DB 11; Length 2312;
Best Local Similarity 82.0%; Pred. No. 7e-27;
Matches 141; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Oy 1 ACCTGTAATTCAGTACTGTGAGATCCGAGTCAAGGACTGTTGAGGCCAGGAGTTC 60
Db 1142 ACCTGTAATCCCGGCACTTTGGAGGCTGAGTGGAGGACTGCTTGAATCCAGGAGTTC 1201
Oy 61 AAGAGCAGCCTTGACAACAACAGGAGAC-CTGTCACTACAAAGATTAATTAATTAAGCA 119
Db 1202 AAGACAGCCTTGAGCAACATAGTAGACTTTGCTTCAAAAATTTAATTAAGCTG 1261

RESULT 7
ADM05125
ID ADM05125 standard; cDNA; 2312 BP.
XX
XX
AC ADM05125;
XX
DT 01-DEC-2005 (first entry)
XX
XX Human cDNA clone FEBRA20093520, SEQ ID 880.
XX
XX Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;
XX KM Antulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;
XX KM stomach ulcer; gastrointestinal ulcer; gene; ss.
XX
XX Homo sapiens.
XX
XX EP1580263-A1.
XX
XX 28-SEP-2005.
XX
XX 12-APR-2002; 2004EP-00027348.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y,
XX
XX WPI: 2005-667421/69.
XX
XX P-PSDB; AEC87568.
XX
XX New full-length cDNA sequences, useful for treating diseases, e.g.
XX PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.
XX
XX PS Example 3; SEQ ID NO 880; 296bp; English.
XX
XX The present invention relates to novel human cDNAs (AEC84246-AEC86688)
XX CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing
XX CC the functions of the proteins, and for developing medicines for diseases
XX CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal
XX CC ulcer. Note: The sequence data for this patent did not form part of the
XX CC printed specification but was obtained in electronic format directly from
XX CC BPO.
XX
XX Sequence 2312 BP; 609 A; 493 C; 563 G; 647 T; 0 U; 0 Other;
SQ

Query Match 63.6%; Score 112; DB 14; Length 2312;
Best Local Similarity 82.0%; Pred. No. 7e-27;
Matches 141; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Oy 1 ACCTGTAATTCAGTACTGTGAGATCCGAGTCAAGGACTGCTTGAAGGCCAGGAGTTC 60
Db 1142 ACCTGTAATCCCGGCACTTTGGAGGCTGAGTGGAGGACTGCTTGAATCCAGGAGTTC 1201
Oy 61 AAGAGCAGCCTTGACAACAACAGGAGAC-CTGTCACTACAAAGATTAATTAATTAAGCA 119
Db 1202 AAGACAGCCTTGAGCAACATAGTAGACTTTGCTTCAAAAATTTAATTAAGCTG 1261
Oy 120 GGGTATAGTGCATCCTGTGTGTCCAGCTTACTAGGAGGCGAAGTAGGA 171
Db 1262 GGCATGATGGCATATGCTGTGTCTCCAGCTACTTGGAGGCCAAGGACAGGA 1313

RESULT 8
```


AAK82979/c
ID AAK82979 standard; DNA; 13001 BP.
XX
AC AAK82979;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37791.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
OS Cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234986P.
PR 26-SEP-2000; 2000US-0235464P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236337P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239345P.
PR 13-OCT-2000; 2000US-0239347P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.

PF	03-AUG-2001; 2001US-00922445.
XX	
PR	03-AUG-2001; 2001US-00922445.
XX	
PA	(SEQU-) SEQUENOM GEMINI LTD.
XX	
PI	Andersson MK, Berglund LGT, Reneland RH, Adam GIR,
XX	
DR	WPI; 2004-086115/09.
XX	
PT	Diagnosing predisposition to left ventricular diastolic heart failure in
PR	a human comprises detecting the presence or absence of an allelic variant
XX	
PS	at position 24941 of hUNC93B1 gene.
XX	
CC	Claim 1; SEQ ID NO 1; 53pp; English.
XX	
CC	The invention relates to diagnosing predisposition to left ventricular
CC	diastolic heart failure in a human comprising detecting the presence or
CC	absence of an allelic variant at position 24941 of the heart failure
CC	associated gene appearing as ADH26544(hUNC93B1), encoding a possible 12
CC	transmembrane receptor protein) in the sample, where the presence or
CC	absence of the allelic variant is indicative of a predisposition to left
CC	ventricular diastolic heart failure in the human. The method further
CC	comprises determining the genotype of the human at position 24941 of
CC	ADH26544. The method is useful for diagnosing predisposition to left
CC	ventricular diastolic and systolic heart failure. The hUNC93B1 gene is
CC	located on chromosome 11q13. The present sequence is the human heart
XX	failure associated gene hUNC93B1.
SQ	Sequence 38653 BP; 7944 A; 10836 C; 11667 G; 8201 T; 0 U; 5 Other;
	Query Match 63.0%; Score 110.8; DB 12; Length 38653;
	Best local Similarity 78.2%; Pred. No. 4,9e-26;
	Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
OY	2 CCTGTAATTCACGACTGTGAGAGTCCGAGGTCACTGCTGAGGCCAGGAGTTCA 61
DB	37583 CCTGTAATCCCACAACCTTTGGAGGCTGAAGGCAGAGAGATTGCTTAGCGCAGGAACTTCA 37642
OY	62 AGACGAGCGTTGACACACAGGAGAGCCTGTCACTACAAAGAATAAATTATGACCAG 121
DB	37643 AGACGAGCGTTGGGACACATGAGAGAACCTGTCTCTACAAAATAATTAAAAAATAGCTGG 37702
OY	122 CTATGAGGCTCATCCCTGTGTGTCACACTGACCTAGGAGGACGAAGTAGGA 171
DB	37703 CGTAGTGCGGTGTGCTGTGATTCCAGCTACTTGGGAGACTGAAGTGGGA 37752
RESULT 10	
ACN45018/C	
ID ACN45018 standard; DNA; 81099 BP.	
XX	
AC	ACN45018;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Human genomic sequence hCG17395.
XX	
KM	Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
OS	Homo sapiens.
PX	
PN	WO2003073826-A2.
XX	
PD	12-SEP-2003.
XX	
PF	28-FEB-2003; 2003WO-US006235.
XX	
PR	01-MAR-2002; 2002US-00087192.
XX	
PA	(SAGR-) SAGRES DISCOVERY.
XX	
PI	Morris DW;

XX	XX	WT1; 2003-328604/31.
DR	XX	Recombinant nucleic acid sequence for diagnosis and treatment of carcinoma
XX	XX	comprises a nucleotide sequence.
PT	XX	
XX	XX	Claim 1; SEQ ID NO 1756; Opp; English.
PS	XX	
XX	XX	The present invention relates to novel DNA and protein sequences which
CC	CC	are associated with carcinomas. The sequences are useful for: (i) for
CC	CC	screening drug candidates; (ii) for screening of bioactive agent capable
CC	CC	of binding to CarcinoMa Associated Protein (CAP); (iii) for screening of
CC	CC	a bioactive agent capable of modulating the activity of CAP; (iv) for
CC	CC	evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC	CC	carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC	CC	carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC	CC	(x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC	CC	determining CarcinoMa Associated (CA) gene copy number. In addition, the
CC	CC	CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC	CC	carcinoma including lymphoma. The present sequence is one such CA coding
CC	CC	sequence. Note: This patent is an equivalent to basic patent
CC	CC	US2002182586m1, for which no sequence data was published
XX	XX	
XX	XX	Sequence 81099 BP; 20015 A; 18716 C; 19786 G; 22439 T; 0 U; 143 Other;
XX	XX	
XX	XX	Query Match 62.2%; Score 109.4; DB 11; Length 81099;
XX	XX	Best Local Similarity 76.6%; Pred. No. 1.9e-25;
XX	XX	Matches 134; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
XX	XX	
XX	XX	2 CCTGTATTCCAGTACTGTGAGAGTCCGAGGTCCAGAGGCAAGAGTTCA 61
XX	XX	Db 18811 CCTGAATATCCACGACTTGTGGAGGCCAAGGCAAGGAGCTGTTAGCCAGAGGTTCC 18752
XX	XX	62 AGAGCAGCCTGTGACAAACACAGGAGAGCTGTCTACTCAATGAATTAATTAATTAAGCCAGG 121
XX	XX	Db 18751 AGACCGACCTGTGGGCAACATAGAAAGACCTCATCTTCAAAAAATTAATTAAGCCAGG 18692
XX	XX	122 CTTATGTTGCTCATTCCTGTGTGTTCCACGCTTACTATGAGGAGCAGAGTGAAGTGGTCT 176
XX	XX	Db 18691 CGTGTGTCTCTACGCGCTGTGTAGTCCAGCTACTCAGAGAGGCTGAAGTGGAGGAGCT 18637
XX	XX	
XX	XX	RESULT 11
XX	XX	ADN12517
XX	XX	ID ADN12517 standard; cDNA; 620 BP.
XX	XX	AC ADN12517;
XX	XX	DT 29-JUL-2004 (first entry)
XX	XX	DE Human prostate/colon/lung/breast cancer-related cDNA 32, SEQ:32.
XX	XX	Human; cancer; tumour; prostate cancer; colon cancer; lung cancer;
XX	XX	breast cancer; drug screening; diagnosis; prognosis; prevention;
XX	XX	gene mapping; tissue typing; tissue profiling; cytostatic; gene therapy;
XX	XX	ss.
XX	XX	Homo sapiens.
XX	XX	WO2004039943-A2.
XX	XX	13-MAY-2004.
XX	XX	16-MAY-2003; 2003WO-US015465.
XX	XX	17-MAY-2002; 2002US-038153P.
XX	XX	04-FEB-2003; 2003US-0445222P.
XX	XX	(CHIR) CHIRON CORP.
XX	XX	Scott EM, Lamson G, Kassam A, Zhang G, Sakamoto D, Garcia PD;
XX	XX	WT1; 2004-376173/35.
XX	XX	

XX New isolated polynucleotides, useful for gene mapping or tissue typing or
PT profiling, as diagnostic reagents, and for preventing or treating cancer,
XX e.g. prostate, colon, or breast cancer.

PS Claim 2; SEQ ID NO 32; 190pp; English.

XX The invention relates to nucleic acids (ADN12486-ADN13970) isolated from
CC human prostate, colon, lung and breast cancer cDNA libraries, and to 57
CC proteins (ADN13971-ADN14027) encoded by a subset of these cDNA sequences
CC (ADN13914-ADN13970). The invention also relates to vectors and host cells
CC comprising a nucleic acid of the invention; a method for the recombinant
CC production of a protein of the invention; an antibody specific for a
CC protein of the invention; a polynucleotide library comprising at least
CC one nucleic acid sequence of the invention; a method for detecting a
CC cancerous cell by PCR or probe hybridization; inhibiting a cancerous
CC phenotype (particularly aberrant proliferation) of a cell; a method of
CC identifying an agent that modulates the biological activity of a gene
CC product differentially expressed in a cancerous cell compared with a
CC normal cell; and a method of treating a cancer patient using the agent
CC identified. The nucleic acids and polypeptides can be used to diagnose,
CC prognose, treat or prevent cancers such as prostate, colon, lung or
CC breast cancer, and can also be used to screen for drugs for the treatment
CC of cancer. The nucleic acids can also be used for gene mapping, tissue
CC typing and tissue profiling. The present sequence represents a
CC specifically claimed cancer-related cDNA of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 620 BP; 177 A; 139 C; 162 G; 142 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 109.2; DB 12; Length 620;
Best Local Similarity 77.6%; Pred. No. 3.8e-26;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGCTCAGAGAGCTGTTGAGCCAGAGTTCA 61

DB 290 CCTGTAAATTCAGTACTGTGAGAGTCCGAGCTCAGAGAGCTGTTGAGCCAGAGTTCA 349

QY 62 AGAGCAGCCTGGGCAACACAGGAGAGCTGTCTCACTCAAGAAATAAATTAATTAAGCCAGG 121

DB 350 AGAGCAGCCTGGGCAACACAGGAGAGCTGTCTCACTCAAGAAATAAATTAATTAAGCCAGG 409

QY 122 CTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGGAGAGTAGGA 171

DB 410 TGTGTGTGCGACGTGCTGTAAATCCAGCTACTGCGGAGGCTGAAGCAGA 459

RESULT 12

ACN44954
ID ACN44954 standard; DNA; 31116 BP.

AC ACN44954;

DT 18-NOV-2004 (first entry)

XX Human genomic sequence hCG38622.

KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

OS Homo sapiens.

PN WO2003073826-A2.

PD 12-SEP-2003.

PF 28-FEB-2003; 2003WO-US006235.

PR 01-MAR-2002; 2002US-00087192.

PA (SAGR-) SAGRES DISCOVERY.

PI Morris DW;

DR WPI; 2003-328604/31.

XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma

PT comprises a nucleotide sequence.

PS Claim 1; SEQ ID NO 1660; 0pp; English.

XX The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for treating
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) as a biochip;
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US200212556A1, for which no sequence data was published

XX Sequence 31116 BP; 7214 A; 8217 C; 7722 G; 7963 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 109.2; DB 11; Length 31116;
Best Local Similarity 77.6%; Pred. No. 1.5e-25;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGCTCAGAGAGCTGTTGAGCCAGAGTTCA 61

DB 24557 CCTGTAAATTCAGTACTGTGAGAGTCCGAGCTCAGAGAGCTGTTGAGCCAGAGTTCA 24616

QY 62 AGAGCAGCCTGGGCAACACAGGAGAGCTGTCTCACTCAAGAAATAAATTAATTAAGCCAGG 121

DB 24617 AGAGCAGCCTGGGCAACACAGGAGAGCTGTCTCACTCAAGAAATAAATTAATTAAGCCAGG 24676

QY 122 CTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGGAGAGTAGGA 171

DB 24677 GATGTGTGTGACAGCTGTGTGCTCCAGCTATTGCGGAGCTGAAGCAGA 24726

RESULT 13

ADZ13255
ID ADZ13255 standard; DNA; 31279 BP.

AC ADZ13255;

DT 16-JUN-2005 (first entry)

XX Human cancer-associated genomic DNA #63.

KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;

KW cytostatic; gene; ds.

OS Homo sapiens.

PN WO2005031001-A2.

PD 07-APR-2005.

PF 23-SEP-2004; 2004WO-US031617.

PR 23-SEP-2003; 2003US-00669920.

PA (CHIR) CHIRON CORP.

PI Morris DW, Malandro MS;

DR WPI; 2005-273395/28.
XX Nucleic acid array useful for detecting cancer associated nucleic acid,

PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 775; 198bp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer,
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acid. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated genomic DNA of
CC the invention.
XX
SQ Sequence 31279 BP; 7246 A; 8268 C; 7755 G; 8010 T; 0 U; 0 Other;
Query Match 62.0%; Score 109.2; DB 14; Length 31279;
Best Local Similarity 77.6%; Pred. No. 1.5e-25;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAGAGACTGTTGAGCCAGAGTTCA 61
DB 24713 CTTGCATATCCAGACATTTGGGAGCTGAGGCGGGTGATGCTTAAGCCAGAGTTCA 24772
QY 62 AGAGCAGCTGGACAAACACAGGAGACCTGTCTACTCAAAAGATAATTAATTAGCCAGG 121
DB 24773 AGACCACTCTGGGCAACATAGTGTAGACCTGTCTTACAAAATAATTAATTAGCTGGG 24832
QY 122 CTTAGTGCTCATCTCTGTGGTCCAGCTACTAGAGGAGCAAGTAGGA 171
DB 24833 GATGTGTGTGACCCCTGTGTGTCCAGCTATTGTGGGGGCTGAAGCAAGA 24882
RESULT 14
ADA02540
ID ADA02540 standard; DNA; 58822 BP.
XX
AC ADA02540;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human TCOF1 carcinoma associated gene, SEQ ID NO:1058.
XX
KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057146-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041414.
XX
PR 26-DEC-2001; 2001US-00035832.
XX
PA (SAGR-) SAGRES DISCOVERY.

XX
PI Morris DW;
XX
DR WPI; 2003-587068/55.
XX
PT New recombinant nucleic acid encoding carcinoma associated protein,
XX useful for preparing compositions for treating carcinomas.
PS Claim 1; SEQ ID NO 1058; 245pp; English.
XX
CC The invention relates to recombinant carcinoma associated (CA) nucleic
CC acid sequences from mouse and human (ADA01482-ADA03094), and to
CC recombinant carcinoma associated proteins (CAP) encoded by them. The
CC invention also encompasses expression vectors and host cells comprising a
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 58822 BP; 14199 A; 14875 C; 15625 G; 13656 T; 0 U; 467 Other;
Query Match 62.0%; Score 109.2; DB 9; Length 58822;
Best Local Similarity 77.6%; Pred. No. 1.9e-25;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAGAGACTGTTGAGCCAGAGTTCA 61
DB 740 CTTGTAAATTCAGACATTTGAGGGGCTGAGGGTGGTGATCATTCTGAGCCAGAGTTCA 799
QY 62 AGAGCAGCTGGACAAACACAGGAGACCTGTCTACTCAAAAGATAATTAATTAGCCAGG 121
DB 800 AGACCACTCTGGGCAACATAGTGTAGAACCTCTCTTACAAAATAATTAATTAGCTGGG 859
QY 122 CTTAGTGCTCATCTCTGTGGTCCAGCTACTAGAGGAGCAAGTAGGA 171
DB 860 CATGTGTGACATGCTGTAGTCCAGCTACTCGGAGGCTGAGGACAGGA 909
RESULT 15
ADA02540/c
ID ADA02540 standard; DNA; 58822 BP.
XX
AC ADA02540;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human TCOF1 carcinoma associated gene, SEQ ID NO:1058.
XX
KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057146-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041414.

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 ; Search time 1218.72 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_430

Perfect score: 176
Sequence: 1 acctgcatccagctactgt.....gagcagaagtagactgct 176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113.4	64.4	1209	3	BU182693
2	112.2	63.0	881	14	BU798537
3	110.8	63.0	282	1	AI244764
4	110.6	62.8	465	11	AQ713218
5	109.2	62.0	447	1	AA699702
6	109.2	62.0	541	1	AA225358
7	109.2	62.0	554	11	AQ784105
8	108.6	61.7	388	1	AA228270
9	108.6	61.7	494	1	AA228270
10	108.6	61.7	578	11	AI354333
11	108.2	61.5	754	5	CD652416
12	107.8	61.2	749	8	CN417549
13	107.6	61.1	826	11	AQ747017
14	107.2	60.9	536	11	AQ314458
15	107.2	60.8	434	14	B42135
16	107.2	60.8	689	11	AG088851
17	107.2	60.8	787	4	CB988735
18	107.2	60.8	808	4	CD109864
19	107.2	60.8	939	4	CB990645

20	106.6	60.6	296	10	H81788
21	106.6	60.6	705	14	AG013775
22	106.2	60.3	270	4	CA774055
23	106.2	60.3	271	1	AA366936
24	106.2	60.3	314	1	AA484256
25	106.2	60.3	459	1	AI917132
26	106.2	60.3	617	14	AG070727
27	106.2	60.3	968	7	BF345228
28	106.2	60.2	348	8	CN269051
29	106.2	60.2	361	11	AQ194840
30	106.2	60.2	412	11	AY760888
31	106.2	60.2	450	9	DB360062
32	106.2	60.2	521	1	AA837027
33	106.2	60.2	552	9	DB302779
34	106.2	60.2	652	8	CN271031
35	106.2	60.2	669	1	AF075373
36	106.2	60.2	669	1	AI110874
37	106.2	60.2	707	1	AV713579
38	106.2	60.2	807	5	CD644267
39	106.2	60.2	893	1	AL521749
40	106.2	60.2	954	2	BG723587
41	105.4	59.9	2412	6	CR859663
42	105.4	59.9	352	1	AA736557
43	105.4	59.9	400	1	AA728939
44	105.4	59.9	428	1	AI000825
45	105.4	59.9	549	9	DB326947

ALIGNMENTS

RESULT 1
BU182693 1209 bp mRNA linear EST 04-SEP-2002
AGENCOURT_7931720 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6150589
LOCUS
DEFINITION
5', mRNA sequence.

ACCESSION
BU182693
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)

REFERENCE
1 (bases 1 to 1209)
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCMP
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13485 row: h column: 14
High quality sequence stop: 330.

FEATURES

source

1. 1209
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6150589"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match	64.4%	Score 113.4;	DB 3;	Length 1209;
Best Local Similarity	78.9%;	Pred. No. 2.4e-17;		
Matches 135; Conservative	0;	Mismatches 36;	Indels 0;	Gaps 0;

Oy 1 ACCGTAAATCCAGTACTGTGAGAGTCCAGGTCAGAGACTGCTTGAGGCCAGAGATTC 60
 Db 303 ACCTCGCAATCCACACTTTGAGAGGCCAAGGTGGAGGAAATGAAATGAGCCCAAGATAC 244

6' AAGAGCAGCCTGGACACACACGGGAGACCTGTCACTCAACAAAGAATAAATAATTAATTCAG 120
243 AAGACCGAGCCTGGGCAACATAGTGAGACCCCGTCACCTACAAACAAACACGAAAAATTTAACAG 184

```

oy      121 GCTTAGTGGCTCATCCCTGTGTCCAGCTACTAGGGAGGCAGAAGTAGGA 171
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
db      183 GCATGTTGGACACGCGCTTAGTCCAGCTACTAGGGAGGCTGAGGCAGGA 133

```

RESULT 2	LOCUS	DEFINITION
DUT98537/c	881 bp	DNA linear GSS 12-DEC-2005
DUT98537	foamy virus vector	integration junctions in
fov1_fp001q130		

ACCESSION	DU798537
VERSION	DU798537.1
KEYWORDS	GI:83580028
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE	
AUTHORS	Trobridge, G.D., Miller, D.G., Jacobs, M.A., Allen, J.M., Kiem, H.P., Kall, R., and Russell, D.W.
TITLE	Poamy virus receptor integration sites in normal human cells
JOURNAL	Proc Natl Acad Sci U S A. (2006) In press
COMMENT	Contact: Trobridge GD

Division of Clinical Research
Fried Hutchinson Cancer Research Center
Mailbox D1-100, 1100 Fairview Ave N., Seattle, WA 98109-1024, USA
Tel.: 206 667 6653
Fax: 206 667 6124
Email: jgfrb@dfhcrc.org
Empty vector: chromosome junction sequences in fibroblasts rescued
as plasmids in bacteria. The plate number (65: fp001) indicates
rescue enzyme. fp001, fp002, fp003 = Nsil. fp004, fp005 = NdeI
Seq primer: AAACCGACTTGATTCGAGAAC
Class: viral tagged.

FEATURES	Location/Qualifiers
source	1. .881

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/sex="male"
/cell_type="Human Primary Fibroblast"
/cell_line="GM05387, Coriell Institute for Medical
Research, Camden, NJ"
/clone_id="Foamy virus vector integration junctions in
fibroblasts"
/note="Vector: pDeltaPhiPmcNO; Vector provirus
LTR:chromosome junctions were rescued as plasmids in
bacteria."

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Query Match	63.6%;	Score 112;	DB 14;	Length 881;
Best Local Similarity	82.0%;	Pred. No. 5.4e-17;		
Matches 141;	Conservative	0;	Mismatches 30;	Indels

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QY      1  ACCTGTAATTCAGTACTGTGAGAGTCGAGGTCAGAGGACTGCTTAGAGGCCAGAGATTC 60
Db      625 ACCTGTAATCCAGTACTTTGGGAGGCCAAGGTGGAGAGATTCTTAGCTCAGGAGATT 566

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Oy	61	AAGACAGCCTGGACAACACAGGAGA - CCGTCACTTCGAAGAATAAATTAATACC	119
Dd	565	AAGACCAAGCCTGGCAACATAGTAGAATCTGTCTTAAATATAAATTACCCA	506
Oy	120	GCGTTAGTGCCATCCCTGATGATCCCAACTAGAGGAGGACAGAAGTACGA	171
Dd	505	GGCATGTGGACATCTCTTCAGATCCCACTACTGGGAGGCTGAATGGGA	454

LOCUS	282 bp	EST 28-JAN-1999
DEFINITION	q937b07.x1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1867453 3'	
	similar to confins Alu repetitive element, contains element MER22	
	repetitive element ;, mRNA sequence.	

ACCESSION	AI244764
VERSION	AI244764.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

REFERENCE

Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 282)

AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CCAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strusberg, Ph.D.
strusberg@nci.nih.gov

Email: cgapbio-remail.lln.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CGNA Library Preparation: M. Bento Soares, Ph.D.
CGNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: www-bio.llnll.gov/bbrp/image/image.html
Insert length: 2237 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence: stop: 242.

FEATURES	Location/Qualifiers
source	1. .282

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1867453"
/lab_host="DH10B"
/clone_1lb="NCT_COAP_Kid3"
/notes="Organ: kidney; Vector: pT73D-PacI; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptor (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldi."

```

ORIGIN

Query Match	63.0%	Score 110.8	DB 1	Length 282
Best Local Similarity	78.2%	Pred. No. 1.2e-16		
Matches 133	0	Mismatches 37	Indels 0	Gaps 0

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Oy      2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTAGAGGACTGCTTGAAGGCCAGAGATTCA 61
        |||||
Db      83 CCTGTAATGCAGTACTTTGGGAGGCTGAGGCCAGGGGAGTGTCTGAGTCCAGAGTTGG 14

```

```

OY      62 AGAGCAGCTTGGACAA CACAGGGAAGCTGTCACTACAAAAGATTAATTAGCCAGG 122
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB     143 AGACCAGCTGGACAACATGGCGAAGCTGTCTTCAAAAAAATTACAAAAATCAGTCAGG 202

```

122 CTTAGTGGCTCATCCCTGTGTGTCACAGCTACTAGGGAGGACAGAACTAGA 171

AA225358 541 bp mRNA linear EST 20-AUG-1997
LOCUS
DEFINITION nc24d02.s1 NCI CGAP Pr1 Homo sapiens cDNA clone IMAGE:1009059
similar to contains Alu repetitive element; contains element PFR5
repetitive element ;, mRNA sequence.
ACCESSION AA225358
VERSION AA225358.1 GI:1846696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 541)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb@remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquí,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNLT at:
www.bio.linn.gov/db/ftp/image/image.html
Insert Length: 467 Std Error: 0.00
Seq primer: -41m13 fwd. RT from Amerisham
High quality sequence stop: 434.
Location/Qualifiers
1. 541
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1009059"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr1"
/note="Vector: PAMPI0; Site_1: Not; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into PAMPI0 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

ORIGIN
Query Match 62.0%; Score 109.2; DB 1; Length 541;
Best Local Similarity 77.6%; Pred. No. 2,7e-16;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTATTCAGTCTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
DB 100 CCTGTATTCAGTCTGTGAGAGTCAAGAGACTGCTTGAGGCCAGAGTTGG 159
QY 62 AGAGCAGCCTGGAACAACAGGAGAGACTGTCTCACTAACAAGATAAATTAATGACGAG 121
DB 160 AGACAGCAGCCTGGAACAACAGTGTCTCTACTAATAAATAATTAATGAGCTGG 219
QY 122 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGAGCAAGTAAGA 171
DB 220 CGTGTGTGGACACCTGTATTCACAGCTACTCGGAGGCTGAGGACGGA 269

RESULT 7
AQ784105

LOCUS AQ784105 554 bp DNA linear GSS 03-AUG-1999
DEFINITION HS_3250_A2_H10_T7C CTT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3250 Col=20 Row=O, genomic survey
sequence.
ACCESSION AQ784105
VERSION AQ784105.1 GI:5691729
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 554)
Mahairas,G.G., Wallace,J.C., Sutch,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3867
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htec.washington.edu>
Plate: 3250 row: O column: 20
Seq primer: T7
Class: BAC ends
High quality sequence stop: 554.
Location/Qualifiers
1. 554
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/clone="Plate=3250 Col=20 Row=O"
/sex="male"
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 62.0%; Score 109.2; DB 1; Length 554;
Best Local Similarity 77.6%; Pred. No. 2,7e-16;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTATTCAGTCTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
DB 140 CCTGTATTCAGTCTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTCA 199
QY 62 AGAGCAGCCTGGAACAACAGGAGAGCTGTCTCACTAACAAGATAAATTAATGACGAG 121
DB 200 AGACAGCAGCCTGGAACAACAGTGTCTCTACTAATAAATAATTAATGAGCTGG 259
QY 122 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGAGCAAGTAAGA 171
DB 260 TGTGTGTGGACACCTGTATTCACAGCTACTCAGAGGCTGAGGACGGA 309

RESULT 8
AA228270 388 bp mRNA linear EST 21-AUG-1997
LOCUS
DEFINITION nc38b02.r1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:1010379
similar to contains Alu repetitive element; mRNA sequence.
ACCESSION AA228270
VERSION AA228270.1 GI:1849841
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Carnarhini;
TITLE Homnidae; Homo.
1 (baes 1 to 388)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL COMMENT
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 rstraus@u.washington.edu

Contact: Robert Strausberg, Ph.D.
Email: cgaabs@emall.nih.gov
Tissue procurement: W. Marston Linehan, M.D., Rodrigo Chuagui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Kitzman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
www-bio.1nl.gov/bdip/image/image.html
Insert length: 551 Std Error: 0.00
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 378.

FEATURES	Location/Qualifiers
source	1. .388

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/clone="IMAGE:1010379"
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/dev stage="45 years old"
/lab host="DH10B"
/clone_id="NCI CGAP Pr2"
/notes="Vector: pAMP10; Site 1: NotI, Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-created, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic interepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

```

ORIGIN	Query Match	Score	DB 1	Length
	61.7%	108.6	DB 1	368

Best Local Similarity 77.2%; Pred. No. 3.9e-16;
Matches 132; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Oy 1 ACCGTAAATCCAGTACTGTAGAGATCCAGGTCAGAGCTTGTAGGCGCAGAGTTC 60
 127 ACCCTTAATCCAGCACTTTGGGAGGCTGAGCCAGGAGGATTCCTTAGCTTAGAGATTC 186
 Db

61 AAGAGCAGCCTGACACACACAGGGAGACCTGTCACTACAAAGATAATAATTAGCCAG 120

18 AAGACCGGCTGGGCAACATGGTGAATCCCTGCTCTTACCAAAAAATACAAAAATATGCGAG 248
121 GCTTAGTGGCTCATCCCTGTGGTCCCACTACTAGGAGGCGAAGTAGGA 171

Db 247 GTGTGGGGGCGCCCTATGTGTCGCCAGCTACTGGGGAGGCTGAGATGGGA 297

RESULT 9					
AI354333/c	AI354333	494 bp	mRNA	linear	EST 15-FEB-1999
LOCUS	qt78Bell.x1	NCI_CGAP Esoc2	Homo sapiens	cDNA clone IMAGE:1961420	3'
DEFINITION	similar to contains Alu repetitive element;; mRNA sequence.				
ACCION					

ACCESSION	AI159433
VERSION	AI159433.1
KEYWORDS	GI:4094486
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE	AUTHORS	TITLE
1	(bases 1 to 494)	Hominiidae; Homo.
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgabds-remail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: www.bio.llnl.gov/bbrp/imagenet/imagenet.html
Insert length: 1028 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 411.

FEATURES	Location/Qualifiers
source	1. .494

```

/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1961420"
/tissue_type="squamous cell carcinoma"
/lab_host="RDH108"
/clone_id="NCT_CGAP_Eso2"
/notes="organ: esophagus; Vector: pCMV-SPORT6; Site_1:
Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dir. Average insert size 1.1 Kb. Life Technologies
catalog #: 11502-010"

```

ORIGIN

Query Match	61.78; Score 108.6; DB 1; Length 494;
-------------	---------------------------------------

Best Local Similarity 77.25; Pred. No. 3.8e-16;
Matches 132; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

DQ 2 CCGTATATTCCAGTACTGTGAGAGTCGCCAGTCCAGAGGCTGGACGAGCATTTCA 61
||||||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db 280 CCGTATATCCAGCACTTTGGAGGGCAGAAGCGAGTGATCACTGAGGTCAAGAGTTTCG 22

62 AGAGCAGCCTGGACACACAGGGAGACCTGTCACTTACAAAGAAATAAATTAAATTCACCG 121

D0 AGCACGACCGC196 CAGCAATGGTAAAGGCC197 CTCTCATCTAATTAAGGAAGAATA198
D122 CTTAGTGCCGTACTCCCTGTCGTGCCAGCTACTAGGAGGCAGAGTAGGAC172
Db 160 CATTGGTGCGCATGCTCTGTAATCCAGCTACTTGGGAGGCTGAGGACGAGAC110

RESULT 10

AQ315010/C				
LOCUS	AQ315010	578 bp	DNA	linear
DEFINITION	PPCt11-9d04	TV PPCt-11	Homo sapiens genomic clone	PPCt-11-9d04.
				GSS 04-MAY-1999

genomic survey sequence.

ACCESSION	AQ315010
VERSION	AQ315010.1
KEYWORDS	GI:4046473
	GSS.

SOURCE	ORGANISM	Homo sapiens	Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 578)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Ramsay, J., Gussard, S., et al. 2013. The 1000 Invertebrate Genomes
Project. *Genome Biology* 14:R111. doi:10.1186/gb-2013-14-r111

TITLE	Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Contact: Shaying Zhao, William Niernan, Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Email: jwallace@eu.washington.edu

Clones are derived from the human BAC library RPci-11. For BAC library availability, please contact Pieter de Jong (piet@eu.jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 1114 row: A column: 4

Seq primer: T7

Class: BAC ends

High quality sequence stop: 826.

Location/Qualifiers

1. 826

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=1114 Col=4 Row=A"

/sex="male"

/clone_id="RPci-11 Human Male BAC library"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 61.1%; Score 107.6; DB 11; Length 826;

Best Local Similarity 77.1%; Pred. No. 6,4e-16;

Matches 131; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Dy 2 CCTGTATTTCAGACTCTGTGAGTCCGAGAGTCAAGAGACTCCTTGAGCCAGAGTTCA 61
|||||
Dd 300 CCGTAATTCACAGACACTGTGGAGCCGAGAGGAGCATCACCTTGAGCCAGAGTTCC 241
|||||
Dy 62 AGAGCACCCTGGACAACACAGGAGGACCTGTCACTAACAAAGATAATTAATTAGCCAG 121
|||||
Dd 240 AGACCAACCTGGACAACATGTGAACCCGCTCTAATTAATAATCAAAAATTAGCCAG 181
|||||
Dy 122 CTTAGTGCTCATCCCTGTGGTCCAGCTACTAGGAGGAGAAGTAGGA 171
|||||
Dd 180 CATGTGGCGGATGCTGTATATCCACACTTCTGGAGGCTGAGGACAGA 131
|||||

RESULT 14

AQ314458/c

LOCUS

DEFINITION

RPci11-104P13.TV RPci-11 Homo sapiens genomic clone RPci-11-104P13,

Accession

AQ314458

VERSION

AQ314458.1 GI:4045921

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 536)

Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Sub,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Other GSSES: RPci11-104P13.TV

Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208 Email: hb@tigr.org

Clones are derived from the human BAC library RPci-11. For BAC library availability, please contact Pieter de Jong (piet@eu.jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from

Research Genetics (info@oxygen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers	Source
1. .536	

```

/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="GDB:7539924"
/db_xref="taxon:9606"
/clone="RPC1-11-104Pl3"
/sex="Male"
/cell_type="Lymphocytes"
/clone_1fb="RPC1-11"
/notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
ppc11 Human Male BAC Library"

```

ORIGIN

Query Match	60.9%	Score 107.2;	DB 11,	Length 536;
Best Local Similarity	77.4%	Pred. No. 8.4e-16;		
Matches 130; Conservative	0;	Mismatches 38;	Indels 0;	Gaps 0;

QY 4 TGTAAATTCAGTAAGTGTGAGAGCTGCAGGTCAGAGCAAGAGTTCAG 63
Db 396 TGTAAATTCAGCACTCTGGAGAGGCCAAAGGAGGAGAGCTGTGAGGCCAGGAATTCATG 337
QY 64 AGCAAGCTGTGACAAACAGGAGAGCTGTGCATCAAAAAGATTAATTAATTAACCAAGGCT 123
Db 336 ACCAGAGCTGGGCAAAAAGAGCAAGCAAGCTGTCTGTCAAAAATTAATTAATTAACCAAGGCA 277
QY 124 TAGTGGCTATCCTCTGTGTCCCAAGTACTAGGAGAGGAGAAATGAGA 171
Db 276 TAGTGGTGACACTGTGTAGTCTTAGGTACTGTGGAGAGCTGAGGAAAGA 229

RESULT 15

LOCUS	B42135	434 bp	DNA	linear	GSS 18-OCT-1997
DEFINITION	HS-1055-A2-E08-MF-V0001.abl C17 Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=16 Row=1, genomic survey sequence.				

ACCESSION	B42135
VERSION	B42135.1
KEYWORDS	GI:2546387
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 434)	Mahair, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.	Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence

JOURNAL COMMENT	Unpublished (1997)
Contact: Mahairas GG, Zackrone KD, Hood L	

University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301

FEATURES

TURES	Location/Qualifiers
Source	1. .434

```
/organism="Homo sapiens"  
/mol_type="genomic DNA"  
/db_xref="taxon:9606"  
/clone=Plate=CT 777 Col=16 Row=1  
/sex="M"
```

```

/clone_11b="CIT Human Genomic Sperm Library C"
/notes="Organ: sperm; Vector: pBelBAC11; BAC Clones in
B-Coli DH10B"

```

ORIGIN

Query Match	60.8%	Score 107	DB 11	length 434
Best Local Similarity	76.6%	Pred. No. 9.5e-16		
Matches 131; Conservative	0	Mismatches 40	Indels 0	Gaps 0

QY 1 ACCTGTAATTCAGAGTACGTGAGAGTCCGAGGTCCAGAGACATCGTTGAGGCCAGAGATTC 60

Db 66 ACCTGTAATTCAGAGTACGTGAGAGTCCGAGGTCCAGAGATCACTTGAGGTCCAGAGATTC 125

QY 61 AAGGCAACCTGGACAACAACAGGAGACCTGTCATACACAGAATAATTAATTAATACCAAG 120

Db 126 GAGACCAACCTGGACAACATGATGTAATTAATCTCTCTACGAAAAATACAAAGAAATTAACCG 185

QY 121 GCTTAGTGGCTATCTCCCTGTGGTCCCAAGCTACTAGGAGAGCGAAGATAGGA 171

Db 186 GCATGATGTGTGATCCTGTAAATCCCAAGCTACTACAGAAAGCTGAGGACAGGA 236

Search completed: June 6, 2006, 00:08:43
Job time : 1223.72 secs


```

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14689
; LENGTH: 39754
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(39754)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689

```

```

Query Match          99.1%; Score 174.4; DB 3; Length 39754;
Best Local Similarity 99.4%; Pred. No. 5.5e-51;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGGACTGCTTGAAGCCAGAGTTTC 60
    |||||||
DB 27938 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGGACTGCTTGAAGCCAGAGTTTC 27997
    |||||||
QY 61 AAGAGCAGCTGAGCAACACAGAGAGACTGTCTCACTCAAAAGATATAATTAATTAAGCCAG 120
    |||||||
DB 27998 AAGAGCAGCTGAGCAACACAGAGAGACTGTCTCACTCAAAAGATATAATTAATTAAGCCAG 28057
    |||||||
QY 121 GCTTAGTGCTCATCCCTGTGTCCAGCTACTAGGAGGACAGAGTGAAGTGAAGTCTT 176
    |||||||
DB 28058 GCTTAGTGCTCATCCCTGTGTGTCCAGCTACTAGGAGGACAGAGTGAAGTGAAGTCTT 28113
    |||||||

```

```

RESULT 3
US-09-949-016-17686
; Sequence 17686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17686
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17686

```

```

Query Match          65.3%; Score 115; DB 3; Length 601;
Best Local Similarity 79.5%; Pred. No. 9.4e-31;
Matches 136; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```

```

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGGACTGCTTGAAGCCAGAGTTTC 60
    |||||||

```

```

DB 14 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGGACTGCTTGAAGCCAGAGTTTC 73
    |||||||
QY 61 AAGAGCAGCTGAGCAACACAGAGAGACTGTCTCACTCAAAAGATATAATTAATTAAGCCAG 120
    |||||||
DB 74 GAGACAGCTGGGCAACGTAAGGAGACTGTCTCAACAAAAATATAATTAATTAAGCCAG 133
    |||||||
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCAGCTACTAGGAGGACAGAGTGAAGTGAAGTCTT 171
    |||||||
DB 134 GTGTGTAGCAGACGCTGTGTGTCCAGCTACTTGGAGTGTGACATGAGGA 184
    |||||||

```

```

RESULT 4
US-09-949-016-12860
; Sequence 12860, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12860
; LENGTH: 148609
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12860

```

```

Query Match          65.3%; Score 115; DB 3; Length 148609;
Best Local Similarity 79.5%; Pred. No. 9.6e-30;
Matches 136; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```

```

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGGACTGCTTGAAGCCAGAGTTTC 60
    |||||||
DB 30046 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGGACTGCTTGAAGCCAGAGTTTC 30105
    |||||||
QY 61 AAGAGCAGCTGAGCAACACAGAGAGACTGTCTCACTCAAAAGATATAATTAATTAAGCCAG 120
    |||||||
DB 30106 GAGACAGCTGGGCAACGTAAGGAGACTGTCTCAACAAAAATATAATTAATTAAGCCAG 30165
    |||||||
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCAGCTACTAGGAGGACAGAGTGAAGTGAAGTCTT 171
    |||||||
DB 30166 GTGTGTAGCAGACGCTGTGTGTCCAGCTACTTGGAGTGTGACATGAGGA 30216
    |||||||

```

```

RESULT 5
US-09-949-016-16787
; Sequence 16787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16787

```



```

; LENGTH: 148609
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16787

```

Query Match	65.3%;	Score 115;	DB 3;	Length 148605;
Best Local Similarity	79.5%;	Pred. No. 9.6e-30;		
Matches 136;	Conservative	0;	Mismatches 35;	Indels 0;

OY 1 ACCGTAATTTCCAGTACTGTGAGAGTCCGAGGTCAGAGACGCTTGAGGCGCAGAGATTG 60
 Db 30046 ACCGTATATCAGACACTTTGGAGGCGTGAGGCAAGACGATTGCTTGAGCCCGAGAGTTG 30105

QY	Db
61	30106
AAAGGACAGCTGACAAACACAGGAGACCTGTCATCTCAAAAGATTAATTAATTGACAG	GAGACCAAGCTGGCAACGTAAGGAGACTGTCTCTACAAAATAATAAAATTGACAG
120	30165

Qy 121 GCTTAGTGGCTCATCCCTGTGTTGCCAGCTACTAGGGAGGCAGAATGGA 171
 | | | | |
Db 30166 GTGTGGTAGCACACGCCCTGTGCTCCCACTTAATTGGGATGCTGACAATGGGA 30216

RESULT 6
US-09-949-016-17080/C
; Sequence 17080, Application US/09949016

Query Match	63.9%	Score 112.4;	DB 3;	Length 49401;
Best Local Similarity	78.8%	Pred. No. 5e-29;		
Matches 134; Conservative	0;	Mismatches 36;	Indels 0;	Gaps 0;

0y 2CCGTAATTTCCAGTACTGTGAGAGTCCGAGGTCAGAGGACCTGCTTAGGCCAGAGATTCA 61
 40664 CCGTCACTCCAGACATTTGGAGGCTGAGGACAGAGAGACCTGCTTAGGCCAGAGATTCC 40605
 Db

62 AGAGCAGCCTGACAAACAAGGAGACTGTCACTCAAAAGAAATAATAATTAGCAG 121
 40604 AGACCACTTGGGCAACAAAGGAGACTGTCTTCAAAAACCTTTAAAAATTAGCCGG 40555

Qy 122 CTTAGTGGCTCATCCCTGTGTCGCCAGCTACTAGGAGGCAGAAGTAGCA 171
|||
Db 40544 TTGTGTGTGCATGCGCTGTCACTCAGCTACTTGGAAGGCTGAGGTGGAA 40495

```

: RESULT 7
: US-09-949-016-11844/c
: Sequence 11844, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307

```

```

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ. ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11844
LENGTH: 119981
TYPE: DNA
ORGANISM: Human
US-03-949-016-11844

```

Query Match	63.1%;	Score 111;	DB 3;	Length 119981;
Best Local Similarity	81.9%;	Pred. No. 2.3e-28;		
Matches 140;	Conservative 0;	Mismatches 30;	Indels 1;	Gaps 1;

Accession	Sequence	Position
QY	2 CCTGTATTCAGTACTGTGTGAGAGTCGAGTCCAGTCCAGGACAGTGTCTTGAGGCCAGAGTTCA	61
Db	26713 CCTGTATCCAGCACTTTGGGAGGGGTGAGTGGGAGGATTCCTTGAGGCCAGAGTTCA	26654

OY	62	AGAGCAGGCTGTGCACACACAGGGAGAGCT-GTCACTACAAAGAATTAATAATTAGCCAG	120
Db	26653	AGACCAGGCTGGGCAACATAGTAGAGACTCTCTATATAAAAAAATTTAAAATTAGCCTG	26594

Qy	121	GCTTAGTGGTCATCCCTGTCGTCCAGCTACTAAGGAGGCAGAAGTACGA	171
Db	26593	GCATGTGGCAATGCGCTGTGTTCCCAAGCTAGTTGGAGGAGCAGAAGCAGGA	26543

```

1      RESULT 8
2      US-09-949-016-13606/c
3      Sequence 13606, Application US/03949016
4      Patent No. 6812339
5      GENERAL INFORMATION:
6      APPLICANT: VENTER, J. Craig et al.
7      TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
8      WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
9      FILE REFERENCE: C0001307
10     CURRENT APPLICATION NUMBER: US/09/949,016
11     CURRENT FILING DATE: 2000-04-14
12     PRIOR APPLICATION NUMBER: 60/241,755
13     PRIOR FILING DATE: 2000-10-20
14     PRIOR APPLICATION NUMBER: 60/237,768
15     PRIOR FILING DATE: 2000-10-03
16     PRIOR APPLICATION NUMBER: 60/231,438
17     PRIOR FILING DATE: 2000-09-08
18     NUMBER OF SEQ ID NOS: 207012
19     SOFTWARE: FastSeq for Windows Version 4.0
20     SEQ ID NO 13606
21     LENGTH: 119982
22     TYPE: DNA
23     ORGANISM: Human
24     US-09-949-016-13606

```

Query Match	63.1%	Score 111;	DB 3;	Length 119982;
Best Local Similarity	81.9%	Pred. No. 2.3e-28;		
Matches 140;	Conservative 0;	Mismatches 30;	Indels 1;	Gaps 1;

Oy 2 CCTGTATTTCAGTACTGTGTAGAGTCCAGAGTCAAGAGGACTGCTGTAGGCCAGAGATTCA 61
 Db 26713 CCTGTATTCCAGCACTTTGGAGAGGTGAGTGGAGAGATTGCTCTGAGGCCAGAGATTCA 26654

62 GGAGCAGCCTGACACACAGGGAACT -GTCACTACAAAGATTAATTTAGCCAG 120
26653 AGACCAAGCTGGCAACATCTGTGAGACCTGCTCTATATATAAAATTTAAATTTAGCCCTG 26594

Oy 121 GCTTAGTGGTCATCCCTGTGTTGCCAGCTACTAAGGAGGCAGAAGTAAGA 171
| | | | |
db 26593 GCATTGTGGCATATGCTGTGTGTTCCACGCTAGTTGGGAGGCAGAAACAAGA 26543

```
RESULT 9
US-09-922-445-1
Sequence 1, Application US/09922445
Patent No. 6528268
GENERAL INFORMATION:
APPLICANT: Andersson, Maria K.
APPLICANT: Berglund, Lars G. T.
APPLICANT: Reneland, Rickard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
FILE REFERENCE: G3126US
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 38653
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)..(26156)
OTHER INFORMATION:
NAME/KEY: misc.feature
LOCATION: (24801)..(24801)
OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can be
NAME/KEY: misc.feature
LOCATION: (24941)..(24941)
OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can be
NAME/KEY: exon
LOCATION: (26157)..(26252)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (26253)..(26401)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (26402)..(26543)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (26544)..(27024)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (27025)..(27178)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (27179)..(30519)
OTHER INFORMATION:
NAME/KEY: misc.feature
LOCATION: (27645)..(27645)
OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
NAME/KEY: exon
LOCATION: (30520)..(30681)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (30682)..(30894)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (30895)..(31027)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (31028)..(31747)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (31748)..(31841)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (31842)..(32400)
OTHER INFORMATION:
```

```
NAME/KEY: misc.feature
LOCATION: (32163)..(32163)
OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
NAME/KEY: A or C
LOCATION: (32401)..(32528)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (32529)..(33414)
OTHER INFORMATION:
NAME/KEY: misc.feature
LOCATION: (32614)..(32614)
OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
NAME/KEY: A or G
LOCATION: (33415)..(33597)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (33598)..(34314)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (34315)..(34588)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (34589)..(35404)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (35405)..(35523)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (35524)..(38341)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (38342)..(38653)
OTHER INFORMATION:
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/AC004923
DATABASE ENTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1)..(38653)
US-09-922-445-1
Query Match 63.0%; Score 110.8; DB 3; Length 38653;
Best Local Similarity 78.2%; Pred. No. 1,7e-28;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 2 CCTGTATTCAGTACTGTGAGAGTCCAGGTGAGAGCACTGTTAGGCCAGAGTTCA 61
DB 37583 CCTGTATTCAGTACTGTGAGAGTCCAGGTGAGAGCACTGTTAGGCCAGAGTTCA 37642
QY 62 AGAGCAGCTGAGCAACACAGGAGAGCTGTCTACTACAAAGTAATAATTAGCCAGG 121
DB 37643 AGACGAGCTGGGCAACATAGAGAGACCTGTCTCTCAAAAAATTAAAAATAGCTGGG 37702
QY 122 CTTAGTGGCTACTCCTGTGTGTCCTCCAGCTACTATAGGAGGACCAAGTAGGA 171
DB 37703 CGTAGTGGGCTGTGCTGTGTATTCAGCTTAGTTGGAGAGTAGGGA 37752
RESULT 10
US-09-949-016-150302
Sequence 150302, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
```

```

? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO: 150302
? LENGTH: 601
? TYPE: DNA
? ORGANISM: Human
? OS=949-016-150302

```

Query Match	62.4%	Score 109.8	DB 3	Length 601
Best Local Similarity	78.1%	Pred. No. 6.5e-29		
Matches 132; Conservative	0	Mismatches 37	Indels 0	Gaps 0

```

QY      3 CTGTATTTCCAGTACTGTGAGAGTCCGAGGTACAGAGACTGCTTGAGGCCACGAGATTCAA 62
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
db      82 CTGTATCCGAGCACTTTGGGAGGCCAAGGTGGGTGCAATCGCTTTGAGGTCAGAGAGTTTGA 141

```

Qy GAGCAGCTTGGACCAACAAGGAGACTGTCTACTAACGAATTAATTGCGCCAGGC 122
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db GACCAGCTTGGCCAACAAGGTGAACCATCTCTAAATAACAATAATTAGCCAGAC 201
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 123 TTAGTGGCTATCCCTGTGTCCTCAGACTACTAGGGAGGCAGAGTAGGA 171
| | | | | | | | | | | | | | | | | |
Db 202 ATGTGGCAGTGCTCTGTATCCCACTACTTGGAGGCGACAGGGAGGA 250

RESULT 11
US-09-949-016-15968/c
; Sequence 15968, Application US/09949016

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH ATTENTION DEFICIT/HYPERACTIVITY DISORDER AND WITH

; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; CURRENT APPLICATION NUMBER: 00/041,755

; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231 498

```

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0.0
; SEQ ID NO 1596A

```

```

; TYPE: DNA
; ORGANISM: Human
FEATURE:
;
```

```

; LOCATION: (1) .. (17607)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15968

```

Query Match	62.4%;	Score 109.8;	DB 3;	Length 17607;
Best Local Similarity	78.1%;	Pred. No. 2.7e-28;		
Matches 132; Conservative	0;	Mismatches 37;	Indels 0;	

OY 3 CTGTAATTCACGACTACTGTGAGAGTCCGAGGTACAGAGCACTGCTTGAGGCCACGAGATTCAA 62
 Db 13804 CTGTAATTCACGACTACTGTGAGAGTCCGAGGTACAGAGCACTGCTTGAGGCCACGAGATTCAA 13745

QY	63	GAGCAGCCTTGGACACACACAGGGAGCCTGTCTACTACCAAGATTAATTAATTTAGCCAGGC	122
Db	13744	GACCAGCCTGGCCCAACAAAGGTGAAACCATCTCTACTAAAAATACAAAAATTTAGCCAGAC	13685

Oy 123 TTAAGTGGCTATCCCTGTGTTGCCACTACGAGGCGAGAATTAGCA 171
| | | | | | | | | | | | | | | | | |
Db 13684 ATGCTGGCAGCTGCCTGTAAATCCAGCTACTTGGAAGCAGAGGAGCA 13636

RESULT 12
US-09-949-016-43162
; Sequence 43162, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307

;
; CURRENT FILING DATE: 2000-04-14
;
; PRIOR APPLICATION NUMBER: 60/241,755
;
; PRIOR FILING DATE: 2000-10-20
;

;
; PRIOR FILING DATE: 2000-10-03
;
; PRIOR APPLICATION NUMBER: 60/231,498
;
; PRIOR FILING DATE: 2000-09-08
;

```

; SOFTWARE: FABRSEQ FOR WINDOWS VERSION 3.0
; SEQ ID NO 43162
; LENGTH: 601

```

US-09-949-016-43162

Matches 131; Co

Db 117 CCTGTGATCCAGCAGCTTTGGGAGGCCGAGGCAATGCGATCCTGTAGGTCAGAGATTGG 176

Db 177 AGACCAGCCTAGCCACATGTTGAAACCCGCTCTACTAAAAATACAAAAATCAGCCAGG 230

Db 237 CATGTGGGACATCCCTGCAATCCGACTACTCGGGAGGCTGAAGCAGGA 286

RESULT 13
US-09-949-016-43164
; Sequence 43164, Application US/09949016
; Patent No 6812310

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

```
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 43164
```

ORGANISM: Human
US-09-949-016-43164

Best Local Simila
Matches 131; Co

2 CCGTAATTCGAGTACTGTGAGAGTCCGAGGTCAGAGGACTGCTGAGGCCAGAGTTCAC 61

[illegible]

RESULT 2
US-10-301-480-688929
; Sequence 688929, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688929
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-688929

Query Match 65.6%; Score 115.4; DB 12; Length 463;
Best Local Similarity 80.2%; Pred. No. 3,4e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 64
DB 21 GTAATCTTAGCACTTTCCGAGGCCGAGGTAGCGGATGCTTAAAGATATCATTAATTAAGCCAGGCAAT 80
QY 65 GCAGCTTGACAAACACAGGAGAGCTGTCTACTAATAAATAAATAATTAATTAAGCCAGGCTT 124
DB 81 CCAGCCCAAGCAACATGCGAAGACCTGTCTTAAAGATATCATTAATTAAGCCAGGCAAT 140
QY 125 AGTGGCTCATCTCTGTGTCCTCCAGCTACTAGGAGGAGCAAGTAGAGA 171
DB 141 GGTGGCAATGCTGTATTCCTCCAGCTACTTGGAGGCTGAGGAGGA 187

RESULT 3
US-10-027-632-235356
; Sequence 235356, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: US/10/027,632
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235356
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235356

Query Match 65.6%; Score 115.4; DB 6; Length 494;
Best Local Similarity 80.2%; Pred. No. 3,4e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;
QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 64
DB 52 GTAATCTTAGCACTTTCCGAGGCCGAGGTAGCGGATGCTTAAAGATATCATTAATTAAGCCAGGCAAT 111
QY 65 GCAGCTTGACAAACACAGGAGAGCTGTCTACTAATAAATAAATAATTAATTAAGCCAGGCTT 124
DB 112 CCAGCCCAAGCAACATGCGAAGACCTGTCTTAAAGATATCATTAATTAAGCCAGGCAAT 171
QY 125 AGTGGCTCATCTCTGTGTCCTCCAGCTACTAGGAGGAGCAAGTAGAGA 171
DB 172 GGTGGCAATGCTGTATTCCTCCAGCTACTTGGAGGCTGAGGAGGA 218

RESULT 4
US-10-027-632-235356
; Sequence 235356, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: US/10/027,632
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235356
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235356

Query Match 65.6%; Score 115.4; DB 7; Length 494;
Best Local Similarity 80.2%; Pred. No. 3,4e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 64
DB 52 GTAATCTTAGCACTTTCCGAGGCCGAGGTAGCGGATGCTTAAAGATATCATTAATTAAGCCAGGCAAT 111
QY 65 GCAGCTTGACAAACACAGGAGAGCTGTCTACTAATAAATAAATAATTAATTAAGCCAGGCTT 124
DB 112 CCAGCCCAAGCAACATGCGAAGACCTGTCTTAAAGATATCATTAATTAAGCCAGGCAAT 171
QY 125 AGTGGCTCATCTCTGTGTCCTCCAGCTACTAGGAGGAGCAAGTAGAGA 171
DB 172 GGTGGCAATGCTGTATTCCTCCAGCTACTTGGAGGCTGAGGAGGA 218

RESULT 5
US-10-027-632-235357
; Sequence 235357, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
US-10-027-632-235356

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235357
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235357
```

```

Query Match      65.6%; Score 115.4; DB 6; Length 1092;
Best Local Similarity 80.2%; Pred. No. 4.3e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;
```

```

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGAGTCTTGAGGCCAGAGTTCAAGA 64
   |||||
DB 52 GTATTCCTACACTTTTGGAGGCCGAGGTGAGCGGATTTGCTTGAGGACAGGAGTTCAAGA 111
   |||||
QY 65 GCAGCCTGGAACAACACAGGAGACCTGTCACTACCAAGAAATAAATTATAGCCAGCTT 124
   |||||
DB 112 CCAGCCGACCAACATGGAAGACCTGTCTCTACTAAGAAATACATAAATTATAGCCAGCAT 171
   |||||
QY 125 AGTGGCTATCCTGTGTGTCCTCCAGCTACTAGGAGGAGCAAGTAAGA 171
   |||||
DB 172 GGTGGCAGATGCTGTATCCAGCTACTTGGAGGCTGAGGACAGGA 218
   |||||
```

```

RESULT 6
US-10-027-632-235357
; Sequence 235357, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235357
; LENGTH: 1092
```

```

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235357
```

```

Query Match      65.6%; Score 115.4; DB 7; Length 1092;
Best Local Similarity 80.2%; Pred. No. 4.3e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;
```

```

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGAGTCTTGAGGCCAGAGTTCAAGA 64
   |||||
DB 52 GTATTCCTACACTTTTGGAGGCCGAGGTGAGCGGATTTGCTTGAGGACAGGAGTTCAAGA 111
   |||||
QY 65 GCAGCCTGGAACAACACAGGAGACCTGTCACTACCAAGAAATAAATTATAGCCAGCTT 124
   |||||
DB 112 CCAGCCGACCAACATGGAAGACCTGTCTCTACTAAGAAATACATAAATTATAGCCAGCAT 171
   |||||
QY 125 AGTGGCTATCCTGTGTGTCCTCCAGCTACTAGGAGGAGCAAGTAAGA 171
   |||||
DB 172 GGTGGCAGATGCTGTATCCAGCTACTTGGAGGCTGAGGACAGGA 218
   |||||
```

```

RESULT 7
US-09-925-065A-48526
; Sequence 48526, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48526
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-48526
```

```

Query Match      65.1%; Score 114.6; DB 4; Length 1333;
Best Local Similarity 78.9%; Pred. No. 8.7e-29;
Matches 135; Conservative 1; Mismatches 35; Indels 0; Gaps 0;
```

```

QY 1 ACCTGTAATTCAGTACTGTGAGTCCGAGGTGAGAGACTGTTGAGGCCAGAGTTTC 60
   |||||
DB 184 ACCTGTAATTCAGTACTGTGAGTCCGAGGTGAGAGACTGTTGAGGCCAGAGTTTC 243
   |||||
QY 61 AAGAGCAGCTGGAACAACACAGGAGACTGTGCTACTCAAAAGAAATAAATTATAGCCAG 120
   |||||
DB 244 GAGAGCAGCTGGAACAACAGTGAAGAGACTGTGCTCAAAAATAAATAAATTATAGCCAG 303
   |||||
QY 121 GCTTAGTGGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGAGCAAGTAAGA 171
   |||||
DB 304 GTGTGTGAGCAGCAGCTGTGTGTCCTCCAGCTACTAGGAGGAGCAAGTAAGA 354
   |||||
```

```

RESULT 8
US-09-925-065A-48526
; Sequence 48526, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
;; CURRENT APPLICATION NUMBER: US/09/925,065A
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 48526
;; LENGTH: 1333
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-48526

Query Match 65.1%; Score 114.6; DB 5; Length 1333;
Best Local Similarity 78.9%; Pred. No. 8.7e-29;
Matches 135; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGATTC 60
DB 184 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGATTC 243
QY 61 AAGAGCAGCTGTGACACACAGGAGAGCCTGTGACTACCAAAAGATAATTAATTAGCCAG 120
DB 244 GAGACAGCCTGTGAGCAACGTAAGGAGAGCTTGTCTCTCAAAAATAATTAATTAGCCAG 303
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGACAGAGTAGA 171
DB 304 GTGTGTAGACACAGCCTGTGTGTCCTCAGCTACTAGGAGGATCTGACATGGGA 354

RESULT 9
US-10-301-480-149764
; Sequence 149764, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: In the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 149764
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-149764

Query Match 65.1%; Score 114.6; DB 12; Length 1333;
Best Local Similarity 78.9%; Pred. No. 8.7e-29;
Matches 135; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGATTC 60
DB 184 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGATTC 243
QY 61 AAGAGCAGCTGTGACACACAGGAGAGCCTGTGACTACCAAAAGATAATTAATTAGCCAG 120

DB 244 GAGACAGCCTGTGAGCAACGTAGGAGACTTGTCTCTACAAAATAATTAATAGCCAG 303
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGACAGAGTAGA 171
DB 304 GTGTGTAGACACAGCCTGTGTGTCCTCAGCTACTAGGAGGATCTGACATGGGA 354

RESULT 10
US-10-301-480-763173
; Sequence 763173, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: In the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 763173
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-763173

Query Match 65.1%; Score 114.6; DB 12; Length 1333;
Best Local Similarity 78.9%; Pred. No. 8.7e-29;
Matches 135; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGATTC 60
DB 184 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGATTC 243
QY 61 AAGAGCAGCTGTGACACACAGGAGAGCCTGTGACTACCAAAAGATAATTAATTAGCCAG 120
DB 244 GAGACAGCCTGTGAGCAACGTAAGGAGAGCTTGTCTCTCAAAAATAATTAATTAGCCAG 303
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGACAGAGTAGA 171
DB 304 GTGTGTAGACACAGCCTGTGTGTCCTCAGCTACTAGGAGGATCTGACATGGGA 354

RESULT 11
US-10-301-480-75521
; Sequence 75521, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: In the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 75521
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-75521

Query Match 64.9%; Score 114.2; DB 12; Length 463;
Best Local Similarity 80.2%; Pred. No. 8.7e-29;
Matches 134; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Oy 5 GTAATATCCAGTACTGTGAGAGTCCAGAGTCAGAGACTGTGAGGCCAGAGATTCAAGA 64
 Db 21 GTAATCTTACGACTTTTCGAGGCCAGAGTGAAGCGAATTGCTTGAGACAGAGATTCAAGA 80
 Oy 65 GCAGCTTGACAACACAGAGGAGACTGTCTACTACAAGAAATTAATTAATTGACAGGCTT 124
 Db 81 CCAAGCCACAGCAACATGGCAAGACTGTCTCTACTAAGAAATTAATTAATTGACCAAGGAT 140
 Oy 125 AGTGGCTCATCCCTGTGGTCCAGACTACTAGGAGGACAGAAATGAGA 171
 Db 141 GGTGGACAATGCTCTTAATCCAGACTCTTGGAGAGGCTGAGGACAGGA 187

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RESULT 12
US-10-301-480-688930
; Sequence 688930, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688930
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-688930

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	Query Match	Similarity	Score	DB 12	Length	463
Best Local	Similarity	80.2%	Pred. No.	8.7e-29		
Matches	134	Conservative	0	Mismatches	33	Indels 0; Gaps 0
QY	5	GTAATTCAGTACTGTGAGAGTCCAGGTCAGAGGACGCTTGAGAGCCAGAGTTCAAG	64			
DB	21	GTAATCCTAGACCTTTCGAGGCCAGGTGAGCGGATTGCTTGAGAGCAGAGTTCAAG	80			
QY	65	GCAGCTTGACAACACAGGAGACCTGTGCCTCAACAAGATTAAATTAGCCAGCTT	124			
DB	81	CCAGCCACAGCAACATGCGCAAGACTGTCCTCACTAATAAATACTAAATTAGCCAGCAT	140			
QY	125	AGTGGCTATCCCTGTGGTCCAGCTACTAGGAGAGCAAGATTAGA	171			
DB	141	GCTGGACATGCTGTAAATCCAGCTACTTGGAGAGCTGAGGCCAGA	187			

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RESULT 13
US-09-925-065A-48525
: Sequence 48525, Application US/09925065A
: Publication No. US20040181048A1
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single
: TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.115
: CURRENT APPLICATION NUMBER: US/09/925.065A
: CURRENT FILING DATE: 2001-08-08
: PRIOR APPLICATION NUMBER: US 60/243,036
: PRIOR FILING DATE: 2000-10-24
: PRIOR APPLICATION NUMBER: US 60/252,147
: PRIOR FILING DATE: 2000-11-20
: PRIOR APPLICATION NUMBER: US 60/250,092
: PRIOR FILING DATE: 2000-11-10
: PRIOR APPLICATION NUMBER: US 60/261,766
: PRIOR FILING DATE: 2001-01-16

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? PRIOR APPLICATION NUMBER: US 607,289,846
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO: 48525
? LENGTH: 1333
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-925-065A-48525

```

Query Match	64.4%	Score 113.4	DB 4	Length 1333
Best Local Similarity	78.9%	Pred. No. 2,3e-28		
Matches 135, Conservative	0	Mismatches 36	Indels 0	Gaps 0

QY 1 ACCTTAATTCAGATACGTGTAGATATCCAGAGGTTCAGAGGACCTGTGAGGCCAGAGATTTC 60

Db 184 ACCTTAATTCAGACGACTTTGGGAGGCTTAGGCGAMAGCATTTGCTTGAGGCCAGGAGTTG 243

QY 61 AAGACAGCCTTGACAMACAGGAGAGCCTGTCACTACACAGAAATTAATTAATTAACCGAG 120

Db 244 GAGACCACTTGGGAGACGTAGGAGACCTTGTCTACAAAAAATTAATAATTAACCGAG 303

QY 121 GCTTAGTGCTTATCCCTGTGTGTCCAGCTACTAGGAGGCGAAGTAGGAA 171

Db 304 GTGTGTAGACACAGCCTGTGTGTCCCACTTACTTGGGAGATGCTGACATGTGGA 354

```

RESULT 14
US-09-925-065A-48527
; Sequence 48527, Application US/09925065A
; Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT FILING DATE: US/09/925, 065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48527
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-48527

```

Query Match	64.4%	Score 113.4	DB 4	Length 1333
Best Local Similarity	78.9%	Pred. No. 2.3e-28		
Matches	135	Conservative	0	Mismatches 36; Indels 0; Gaps 0
QY	1	ACCTGTAATTCACGACTCTGTGAGAGTCGAGAGCTGCTTGGAGCCAGAGTTC	60	
DB	184	ACCTGTATATCACAAGCATTTTGGAGGCTGAGCAAGAAGATTGCTTGGAGCCAGAGATTG	243	
QY	61	AAGAGCAGCTCTGGACACACAGGGAGACTGTCACTACAAAGATAAATAATTATTCGCG	120	
DB	244	GAGACCAAGCCCTGGGCAACGTGAGGAGACTTGTCTCTCAAAAAATAAAAAAATTAGCCAG	303	
QY	121	GCTTAGTGGCTCATCCCTGTGTGTCGCCAGCTACTAGGGGAGCAGAGTAGTA	171	
DB	304	GTTGTGTAGCACACAGCCTGTGTGTCCCACTATTGGGATGCTGACATGGGA	354	

```

RESULT 15
US-09-925-065A-48528
; Sequence 48528, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.15
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48528
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-48528

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Query Match	64.4%	Score	113.4	DB	4	Length	1333
Best Local Similarity	78.9%	Pred. No.	2.3e-28				
Matches 135, Conservative	0	Mismatches	36			Indels	0
						Gaps	0

QY 1 ACCTGTAATTCAGTCTCTGTGAGAGTCCAGGTCACAGACCTGCTTGAGGCCAGAGATTG 60

DB 184 ACCTGTAATCACAGCACTTTGGGAGGCTGAGGCAGACGATTTCTTGAGGCCAGAGATTG 243

QY 61 AAGACCAAGCTGACACACACAGGGAGAACCTGTGCATCACAAAGATTAATTAATTAAGCCAG 120

DB 244 GAGACCAAGCTGGGACACAGTGGAGAACCTTGTCTTACAAAATAATTAATTAATTAAGCCAG 303

QY 121 GCTTAGTGAGTATCTCCCTGTGTGCTCCAGCTACTAGGAGGAGCAGAGTAAGAGA 171

DB 304 GTGTGTATGACACAGCGCTGTGTGCTCCCACTACTATTTGGATGTGTGACACTGGGA 354

Search completed: June 6, 2006, 00:20:56
Job time : 352.008 secs

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:44:48 ; Search time 5.13032 Seconds
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Title: US-09-869-098a-1_COPY_255_430

Perfect score: 176

Sequence: 1 acctgatactcagctactgt.....gagcagaagtagactgt 176

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	112	63.6	2312	US-11-293-697-880	Sequence 880, App
2	103	58.5	3550	US-11-293-697-509	Sequence 509, App
3	103	58.5	5515	US-10-524-021-1	Sequence 1, Appl
4	101.4	57.6	1947	US-11-293-697-1980	Sequence 1980, App
5	99.8	56.7	2218	US-11-293-697-2254	Sequence 2254, App
6	99.6	56.6	3178	US-10-505-928-277	Sequence 277, App
7	98.2	55.8	138941	US-10-489-730-10	GENERAL INFORMATI
8	98	55.7	2561	US-11-293-697-1616	Sequence 1616, App
9	98	55.7	2789	US-11-293-697-2050	Sequence 2050, App
10	97.6	55.5	1935	US-11-293-697-2208	Sequence 2208, App
11	97.6	55.5	2374	US-11-293-697-441	Sequence 441, App
12	96.6	54.9	2849	US-11-293-697-1604	Sequence 1604, App
13	96.4	54.8	2143	US-11-293-697-1407	Sequence 1407, App
14	96.4	54.8	2252	US-11-293-697-1292	Sequence 1292, App
15	96.4	54.8	2389	US-11-293-697-2013	Sequence 2013, App
16	96	54.5	2387	US-11-293-697-1487	Sequence 1487, App
17	95.8	54.4	3564	US-11-293-697-639	Sequence 639, App
18	95.8	54.4	128361	US-10-505-928-151	Sequence 151, App
19	95.2	54.1	2915	US-11-293-697-59	Sequence 59, Appl
20	95	54.0	2017	US-11-293-697-2207	Sequence 2207, App
21	95	54.0	2460	US-11-293-697-595	Sequence 595, App
22	95	54.0	2800	US-11-293-697-23	Sequence 23, Appl
23	95	54.0	4086	US-11-301-554-1801	Sequence 1801, App
24	95	54.0	54550	US-11-318-813-42	Sequence 42, Appl
25	95	54.0	394191	US-10-506-549-3	Sequence 3, Appl

C 26	94.8	53.9	2909	US-11-293-697-1113	Sequence 1113, App
C 27	94.8	53.9	128361	US-10-505-928-151	Sequence 151, Appl
C 28	94.4	53.6	2836	US-11-293-697-30	Sequence 30, Appl
C 29	94.2	53.5	138941	US-10-489-730-10	GENERAL INFORMATI
C 30	93.6	53.2	2607	US-11-293-697-608	Sequence 608, App
C 31	93.4	53.1	1977	US-11-293-697-2303	Sequence 2303, App
C 32	93.4	53.1	2140	US-11-293-697-513	Sequence 513, App
C 33	93.4	53.1	2342	US-11-293-697-1268	Sequence 1268, App
C 34	93.4	53.1	2682	US-11-293-697-1324	Sequence 1324, App
C 35	93.4	53.1	2731	US-11-293-697-1412	Sequence 1412, App
C 36	93.4	53.1	1783	US-11-293-697-1729	Sequence 1729, App
C 37	92.8	52.7	1733	US-11-293-697-1577	Sequence 1577, App
C 38	92.6	52.6	2237	US-11-293-697-1855	Sequence 1855, App
C 39	92.6	52.6	2856	US-11-293-697-1116	Sequence 1116, App
C 40	92.4	52.5	2462	US-11-293-697-2214	Sequence 2214, App
C 41	91.8	52.2	391	US-10-511-937-583	Sequence 583, App
C 42	91.8	52.2	1177	US-10-196-749-381	Sequence 381, App
C 43	91.8	52.2	1177	US-11-101-316-129	Sequence 129, App
C 44	91.8	52.2	1981	US-11-293-697-443	Sequence 443, App
C 45	91.8	52.2	2067	US-11-293-697-2313	Sequence 2313, App

ALIGNMENTS

RESULT 1
US-11-293-697-880
; Sequence 880, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 880
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-880

Query Match 63.6%; Score 112; DB 7; Length 2312;
Best Local Similarity 82.0%; Pred. No. 3.1e-24;
Matches 141; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 1 ACCTGTAATCCAGTACTGTGAGATCCGAGTCAAGACTGCTGAGCCAGAGATTG 60
DB 1142 ACCTGTAATCCAGTACTGTGAGATCCGAGTCAAGACTGCTGAGCCAGAGATTG 1201

QY 61 AAGAGCAGCTTGAGCAACACAGGAGAC-CTGTCACTACAAAGATTAATTAGCCA 119
DB 1202 AAGACGAGCTTGAGCAACATAGTAGACTTGTGCTTACAAATATTAATTAATTA 1261

QY 120 GCGTTAGTGGCTATCCCTGTGTGCTCCAGCTACTAGGAGGCAAGATTAGCA 171
DB 1262 GCGATGTGACATGCTGTGTGCTCCAGCTACTAGGAGGCAAGATTAGCA 1313

RESULT 2
US-11-293-697-509/C
; Sequence 509, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260

;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 509
;; LENGTH: 3550
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-293-697-509

Query Match 58.5%; Score 103; DB 7; Length 3550;
Best Local Similarity 78.9%; Pred. No. 1.4e-21;
Matches 135; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCGAGGTCAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 1837 CCTGTAATCCAGTACTTTGGAGGCCGAGCGGGTGTGATCACTTGAGGTCAAGAGTTCA 1778
QY 62 AGAGCAGCCTGGACAACACAGG-AGACTGTCTACTCAAAAGATAATTAATTAGCCAG 120
DB 1777 AGACCAAGCCTGGCAACATGGGGAAGCCCTGTCTCTACTAAATAACAAAATTAGCCAG 1718
QY 121 GCTTAGTGCTCATCCCTGTGTGTCAGACTAGGAGGAGAGTAAGA 171
DB 1717 GCGTGTGGCGGGTGCCTGTAATCCAGCTACTCAGAGGCTGAGGAGGA 1667

* RESULT 3

US-10-524-021-1
;; Sequence 1, Application US/10524021
;; Publication No. US2006009590A1
;; GENERAL INFORMATION:
;; APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
;; APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
;; APPLICANT: YAMADA, Yoshiiji
;; APPLICANT: YOKOTA, Mitsuhiro
;; TITLE OF INVENTION: Method for diagnosing a risk of restenosis after percutaneous cor
;; TITLE OF INVENTION: Intervention
;; FILE REFERENCE: C0200501
;; CURRENT APPLICATION NUMBER: US/10/524,021
;; CURRENT FILING DATE: 2005-02-09
;; PRIOR APPLICATION NUMBER: JP P2002-233041
;; PRIOR FILING DATE: 2002-08-09
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 5515
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-524-021-1

Query Match 58.5%; Score 103; DB 6; Length 5515;
Best Local Similarity 78.9%; Pred. No. 1.6e-21;
Matches 135; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCGAGGTCAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 2581 CCTGTAATCCAGACTTTGGAGGCCAAGGTGGAGATCACTTGAGGCCAGAGTTCA 2640
QY 62 AGAGCAGCCTGGACAACACAGG-AGACTGTCTACTCAAAAGATAATTAATTAGCCAG 120
DB 2641 AGACCAAGCCTGGCAACATGTGTGAGCCCTGTCTCTACTAAATAACAAAATTAGCCAG 2700
QY 121 GCTTAGTGCTCATCCCTGTGTGTCAGACTAGGAGGAGAGTAAGA 171
DB 2701 GCATGTGCCACACACACTGTGTCTCAGCTACTCAGAGGCTGAGGAGGA 2751

RESULT 4

US-11-293-697-1980
;; Sequence 1980, Application US/11293697
;; Publication No. US20060105376A1
;; GENERAL INFORMATION:
;; APPLICANT: HELIX RESEARCH INSTITUTE

;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: H1-A0106
;; CURRENT APPLICATION NUMBER: US/11/293,697
;; CURRENT FILING DATE: 2005-12-05
;; PRIOR APPLICATION NUMBER: US/10/108,260
;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1980
;; LENGTH: 1947
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-293-697-1980

Query Match 57.6%; Score 101.4; DB 7; Length 1947;
Best Local Similarity 75.4%; Pred. No. 3.6e-21;
Matches 126; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCGAGGTCAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 1679 CCTGTAATCCAGACTTTGGAGGTCGAGGTGGAGGATCACTTGAGGCCAGAGTTCA 1738
QY 62 AGAGCAGCCTGGACAACACAGGAGACTGTCTACTCAAAAGATAATTAATTAGCCAG 121
DB 1739 AGACCAAGCCTGGCAACATGTGTGAACCCATCTATACAAAATAATTAGCCAG 1798
QY 122 CTTAGTGCTCATCCCTGTGTGTCAGACTACTAGGAGGAGTAAGA 168
DB 1799 TGTGTGTAGTGCACACCTGTATATCCAGCTACTCGGAGGCTGAGGCA 1845

RESULT 5

US-11-293-697-2254
;; Sequence 2254, Application US/11293697
;; Publication No. US20060105376A1
;; GENERAL INFORMATION:
;; APPLICANT: HELIX RESEARCH INSTITUTE
;; APPLICANT: Novel full length cDNA
;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: H1-A0106
;; CURRENT APPLICATION NUMBER: US/11/293,697
;; CURRENT FILING DATE: 2005-12-05
;; PRIOR APPLICATION NUMBER: US/10/108,260
;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2254
;; LENGTH: 2218
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-293-697-2254

Query Match 56.7%; Score 99.8; DB 7; Length 2218;
Best Local Similarity 77.8%; Pred. No. 1.1e-20;
Matches 133; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCGAGGTCAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 1014 CCTGTAATCCAGACTTTGGAGGCCAAGGTGGCGGATCACTTGAGGCCAGAGTTCC 1073
QY 62 AGAGCAGCCTGGACAACACAG-AGAGACTGTCTACTCAAAAGATAATTAATTAGCCAG 120
DB 1074 AGACCAAGCCTGGCAACATGTGTGAACCCCTGTCTCTACTAAATAACAAAATTAGCCAG 1133
QY 121 GCTTAGTGCTCATCCCTGTGTGTCAGACTACTAGGAGGAGAGTAAGA 171
DB 1134 GCTGGGTGGACATGCTGTATGTCAGCTACTCGGAGGCTGAGGAGGA 1184

RESULT 6

US-10-505-928-277/C
;; Sequence 277, Application US/10505928
;; Publication No. US20060088532A1
;; GENERAL INFORMATION:

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1  APPLICANT: Ludwig Institute for Cancer Research et al
2
3  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
4
5  FILE REFERENCE: 28967/33178
6
7  CURRENT APPLICATION NUMBER: US/10/505,928
8
9  CURRENT FILING DATE: 2004-08-27
10
11 PRIOR APPLICATION NUMBER: US 60/363, 019
12
13 PRIOR FILING DATE: 2002-03-07
14
15 NUMBER OF SEQ ID NOS: 866
16
17 SOFTWARE: PatentIn 3.2
18
19 SEQ ID NO 277
20
21 LENGTH: 3178
22
23 TYPE: DNA
24
25 ORGANISM: Homo sapiens
26
27 US-10-505-928-277

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Query Match	56.6%	Score 99.6	DB 6	Length 3178
Best Local Similarity	74.1%	Pred. No. 1.4e-20		
Matches 126	Conservative 0	Mismatches 44	Indels 0	Gaps 0

[illegible]

RESULT 7
US-10-489-730-10/c

1 APPLICANT: Melino, Gianro
 2 APPLICANT: Hayes, Ian
 3 APPLICANT: de Laurentzi, Vincenzo
 4 APPLICANT: Barcaroli, Daniela
 5 APPLICANT: Candi, Eleonora
 6 APPLICANT: Bernasola, Francesca
 7 APPLICANT: Tobler, Andreas
 8 APPLICANT: Novak, Urban
 9 TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
 10 FILE REFERENCE: 19319_002
 11 CURRENT APPLICATION NUMBER: US/10/489,730
 12 PRIOR FILING DATE: 2004-03-16
 13 PRIOR APPLICATION NUMBER: PCT/GB02/04238
 14 PRIOR FILING DATE: 2002-09-17
 15 PRIOR APPLICATION NUMBER: US 60/322,436
 16 PRIOR FILING DATE: 2001-09-17
 17 NUMBER OF SEQ ID NOS: 39
 18 OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank #
 19 US-10-489-730-10

Query Match	Score	DB	Length
55.8%	98.2	6	138941

Best Local Similarity // .45; Pred. NO. 9e-20;
Matches 132; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

2 CCTGTATTCCAGTACTGTGAGAGTCCGAGTCAGAGACTGCTTGGAGCCAGAGATTCA 61

b
133671 CCTGTATCCGAGCACTTTGGGAGGCCGAGCTGGCAGATCACTTGAACAAGAGTTCA 133612

62 AGAGCAGCCTGGACAAACAAGGGAGA-CCTGTCACTACAAAGAATTAATTAATTAGCCAG 120

b 133611 AGAGCAGTCTGGGCACACCGTGAACCCCATCTACAAAGAATACAAAATT

121 GCTTAGTGGCTATCCCTGCTGTCCAGCTACTAGGAGCAGAACTAGCA 171
133551 GCGTGGTGGCATGCTTGTGGTCCAGCTACTTGGAGGCTGAGGTAGCA 133501

RESULT 8

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US-11-293-697-1616
; Sequence 1616, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1616
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1616

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Best Local Similarity	-73.5%;	Pred. No. 3.8e-20;		
Matches 125;	Conservative 0;	Mismatches 45;	Indels 0;	Gaps 0;

Qy	Db
2	2302
CCGTAATTCAGACTGAGAGTCCAGAGTCAGAGACTGCTTGAGGTCAGAGTTCA	CGTATATCCAGACATTGGATGCCAGAGTGGCAGATTCATTGAGGTCAGAGTTCA
61	2365

62 AGAGCAGCCTGGACAAACACAGGGAGACCTGTCACTACAAGAAATTAATTAATTTAGCCAGG 121

Db 2362 AGACCAGCTGGCCACATGTGTAACCCGGCTCTACTAAATACAAATTAAGCTGGG 2422

QY	122	CTTAGGCTC	ATCCCTC	GTGTC	CCAGCTA	CTAGGAGG	CAGAGT	AGA	171
Db	2422	TGCTGGACAT	CTCTGAT	CCAGCTA	CTCAGAGG	CTGAGG	CA	GA	2471

RESULT 9
US-11-29

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1  Sequence: 2050, Application US/11293697
2  Publication No. US20060105376A1
3  GENERAL INFORMATION:
4  APPLICANT: HELIX RESEARCH INSTITUTE
5  TITLE OF INVENTION: Novel full length cDNA
6  FILE REFERENCE: H1-A0106
7  CURRENT APPLICATION NUMBER: US/11/293,697
8  CURRENT FILING DATE: 2005-12-05
9  PRIOR APPLICATION NUMBER: 2002-10/108,260
10 PRIOR FILING DATE: 2002-03-28
11 NUMBER OF SEQ ID NOS: 5458
12 SOFTWARE: PatentIn Ver. 2.1
13 SEQ ID NO 2050
14 LENGTH: 2799
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 US-11-293-697-2050

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Query Match	55.7%	Score 98	DB 7	Length 2799
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Best Local Similarity 73.5%; Pred. NO. 3.9e-20;
Matches 125; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

2 CCTGTAATTCAGTACTGTGAGTCCAGGTACAGAGACTGTTGAGCCAGAGTTCA 6

Db 2540 CCTGTAATCCAGCAGCTTTGGGAGGCGTAGGCGAGCTGGATCACTGGAGGTCAGGAGTTTG 2599

62 AGAGCAGCCTGGCAACACAGGGAGACCTGTCTACTACAAAGATTAATTAATTAGCCAGS 121

Db 2600 AGACCAGCCTGGCCAACTGTTGTAACCTGTTCTACTAAAAATACAAAATTA

QY 122 CTTAGTGGCTCATCCCTGTGGTCCAGCTACTAGGAGGCAGAAGTAGGA 171

Db 2660 CGTGTGGCGGGTGCTGTATCTTAGTACTCAGGAGACTGAGGCAGGA 2709

RESULT 14

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US-11-293-697-1292
; Sequence 1292, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1292
; LENGTH: 2252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1292
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Query Match          54.8%; Score 96.4; DB 7; Length 2252;
Best Local Similarity 72.9%; Pred. No. 1,1e-19;
Matches 124; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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QY      2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      1891 CCTGTAAATCCAGCACTTTGGAGTGGAGGTGGCGGATCACTTGAGGTCAAGAGTTCA 1950
QY      62 AGAGCAGCCTGGAACAACAGGAGAGACCTGTCACTACAAGAAATTAATTAATTAGCCAGG 121
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      1951 AGACGAGCCTGGCCACATGTGTAAACCGTCTCTACTAACAATACAAAGATTAGCTCGG 2010
QY      122 CTTAGTGGCTCATTCCTGTGTCCTCCAGCTACTAGGAGGCGAAGTAGGA 171
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      2011 TGTGTGGCACGCGGCTGTATCGACGCCCTTGGAAGGCCAAGGCAGGA 2060
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RESULT 15

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US-11-293-697-2013
; Sequence 2013, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2013
; LENGTH: 2389
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2013
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Query Match          54.8%; Score 96.4; DB 7; Length 2389;
Best Local Similarity 72.9%; Pred. No. 1,1e-19;
Matches 124; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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QY      2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
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DB      2116 CCTGTAAATCCAGCACTTTGGAGGCGAGGCGAGATCACCTAAGTCAAGAGTTCA 2175
QY      62 AGAGCAGCCTGGAACAACAGGAGAGACCTGTCACTACAAGAAATTAATTAATTAGCCAGG 121
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      2176 AGACGAGCCTGGCCACATGTGTAAACCGTCTCTACTAACAATACAAAGATTAGCCAGG 2235
QY      122 CTTAGTGGCTCATTCCTGTGTCCTCCAGCTACTAGGAGGCGAAGTAGGA 171
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DB 2236 TGAAGTGGCAGGTGCTGTAAATCCAGCTACTCAAGAGGCTGAAGGCAGGA 2285

Search completed: June 6, 2006, 00:22:28
Job time : 7.13032 secs

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Query Match 100.0%; Score 463; DB 2; Length 3505;
Best Local Similarity 100.0%; Pred. No. 2,2e-113;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 255 ACCGTGAATTCAGACTGTGAGAGTCCAGAGTCCAGAGTCTGTGAGCCAGAGTTTC 314
QY 61 AAGAGAGCTGTGAGCAACACAGGAGAGCTGTGACTCAACAAAGATTAATTAATTAAGCCAG 120
DB 315 AAGAGAGCTGTGAGCAACACAGGAGAGCTGTGACTCAACAAAGATTAATTAATTAAGCCAG 374
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGAGGAGGAGAAATAGAGACTGTGTTC 180
DB 375 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGAGGAGGAGAAATAGAGACTGTGTTC 434
QY 181 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCAGCTGCAATTCAGCTGGCAAC 240
DB 435 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCAGCTGCAATTCAGCTGGCAAC 494
QY 241 AAAAAAGAGCCCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAATTAATTAATTAAC 300
DB 495 AAAAAAGAGCCCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAATTAATTAATTAAC 554
QY 301 CCTAAACACATCTCTTTTCAAGAGAGCTTCTTAAGAGCTTCATGCTGCGTCTGTG 360
DB 555 CCTAAACACATCTCTTTTCAAGAGAGCTTCTTAAGAGCTTCATGCTGCGTCTGTG 614
QY 361 ATCTCCACTCTCTTTTCAAGAGCTCAACCTTTTAAACAGTCTCTTTTGGCAAGATTAATA 420
DB 615 ATCTCCACTCTCTTTTCAAGAGCTCAACCTTTTAAACAGTCTCTTTTGGCAAGATTAATA 674
QY 421 AGTATATAGTTCTGGAATCCAGATTCTCCCTGTTTGACAG 463
DB 675 AGTATATAGTTCTGGAATCCAGATTCTCCCTGTTTGACAG 717

RESULT 2
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LOCUS AF306570
DEFINITION Homo sapiens uncoupling protein 2 gene, promoter region and exon 1;
ACCESSION AF306570
VERSION AF306570.1 GI:11037742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 3270)
Schneitzler, C., Oberkofler, H., Esterbauer, H. and Patsch, W.
TITLE UCP2 promoter region and exon 1
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 3270)
Schneitzler, C., Oberkofler, H., Esterbauer, H. and Patsch, W.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) Laboratory Medicine, Landeskliniken
Salzburg, Mellner Hauptstr. 48, Salzburg A-5020, Austria
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Best Local Similarity 99.8%; Pred. No. 6e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCGTGAATTCAGACTGTGAGAGTCCAGAGTCCAGAGTCTGTGAGCCAGAGTTTC 60
DB 1170 ACCGTGAATTCAGACTGTGAGAGTCCAGAGTCCAGAGTCTGTGAGCCAGAGTTTC 1229
QY 61 AAGAGAGCTGTGAGCAACACAGGAGAGCTGTGACTCAACAAAGATTAATTAATTAAGCCAG 120
DB 1230 AAGAGAGCTGTGAGCAACACAGGAGAGCTGTGACTCAACAAAGATTAATTAATTAAGCCAG 1289
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGAGGAGGAGAAATAGAGACTGTGTTC 180
DB 1290 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGAGGAGGAGAAATAGAGACTGTGTTC 1349
QY 181 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCAGCTGCAATTCAGCTGGCAAC 240
DB 1350 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCAGCTGCAATTCAGCTGGCAAC 1409
QY 241 AAAAAAGAGCCCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAATTAATTAATTAAC 300
DB 1410 AAAAAAGAGCCCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAATTAATTAATTAAC 1469
QY 301 CCTAAACACATCTCTTTTCAAGAGAGCTTCTTAAGAGCTTCATGCTGCGTCTGTG 360
DB 1470 CCTAAACACATCTCTTTTCAAGAGAGCTTCTTAAGAGCTTCATGCTGCGTCTGTG 1529
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DB 1530 ATCTCCACTCTCTTTTCAAGAGCTCAACCTTTTAAACAGTCTCTTTTGGCAAGATTAATA 1589
QY 421 AGTATATAGTTCTGGAATCCAGATTCTCCCTGTTTGACAG 463
DB 1590 AGTATATAGTTCTGGAATCCAGATTCTCCCTGTTTGACAG 1632

RESULT 3
DQ087219 12177 bp DNA linear PRI 18-JUN-2005
LOCUS DQ087219
DEFINITION Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier)
ACCESSION DQ087219
VERSION DQ087219.1 GI:67515418
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 12177)
Livingston, R.V., Rieder, M.J., Shaffer, T., Bertucci, C., Baier, C.N.,
Rajkumar, N., Wills, H.T., Daniels, M., Downing, T.K., Stanaway, T.B.,
Nguyen, C.P., Gilderleeve, H., Cassidy, C.M., Johnson, E.J.,
Swanson, J.E., McFarland, I., Yool, B., Park, C. and Nickerson, D.A.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2005) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: <http://egp.gs.washington.edu>).
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Query Match 99.7%; Score 461.4; DB 5; Length 12177;
Best Local Similarity 99.8%; Pred. No. 4.5e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 53 ACCTGTAATTCAGTACTGTGAGTCCGAGTCCAGAGACTGCTTGAGGCCAGAGTTTC 112
   |||||

QY 61 AAGAGCAGCTTGACACACAGAGAGACTGCTGACCTGACCTGACCTGACCTGACCTGAC 120
   |||||
Db 113 AAGAGCAGCTTGACACACATAGAGAGACTGCTGACCTGACCTGACCTGACCTGAC 172
   |||||

QY 121 GCTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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Db 173 GCTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 232
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QY 181 CCAGAGAGTCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 240
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Db 233 CCAGAGAGTCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 292
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QY 241 AAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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Db 293 AAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352
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QY 301 CCTAAACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
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Db 353 CCTAAACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 412
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QY 361 ATCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
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Db 413 ATCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 472
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QY 421 AGTATATAGTTTCTGGAATCCAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 463
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Db 473 AGTATATAGTTTCTGGAATCCAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 515
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RESULT 4
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DEFINITION Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
SEQUENCE 15 unordered pieces.
AC024029.3 GI:7230916
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
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REFERENCE 1 (bases 1 to 155668)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 155668)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2000) Genome Sequencing Center, Washington
          University School of Medicine, 4444 Forest Park Parkway, St. Louis,
          MO 63108, USA
COMMENT On Mar 13, 2000 this sequence version replaced gi:7109555.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NH0167N04
----- Summary Statistics -----
Sequencing vector: M13, 10%
Sequencing vector: plasmid, 0%
Chemistry: Dye-terminator Big Dye, 0% of reads
Chemistry: Dye-terminator Big Dye, 0% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 154268; sum-of-coverage
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.38 in Q20 bases; sum-of-coverage
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1907 4798: gap of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11378: gap of unknown length
* 11378 14368: contig of 2991 bp in length
* 14369 14469: gap of unknown length
* 14469 20130: contig of 5662 bp in length
* 20131 20230: gap of unknown length
* 20231 25513: contig of 5283 bp in length
* 25514 25614: gap of unknown length
* 25614 30765: gap of 5152 bp in length
* 30766 30865: gap of unknown length
* 30866 37337: contig of 6472 bp in length
* 37338 37437: gap of unknown length
* 37438 45571: contig of 8134 bp in length
* 45572 45672: gap of unknown length
* 45672 60199: contig of 14588 bp in length
* 60200 60299: gap of unknown length
* 60300 71424: contig of 11125 bp in length
* 71425 71525: gap of unknown length
* 71526 86218: contig of 14694 bp in length
* 86219 86319: gap of unknown length
* 86320 104104: contig of 17786 bp in length
* 104105 104204: gap of unknown length
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Location/Qualifiers
1. 155668
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/mol_type="genomic DNA"
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/chromosome="11"
/clone="RP11-167N4"
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vector_side:left"
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misc_feature 37438..45571
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gap 45572..45671
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misc_feature 45672..60199
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ORIGIN

Query Match 99.7%; Score 461.4; DB 12; Length 155668;
Best Local Similarity 99.8%; Pred. No. 2.6e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 70159 ACCTGAATTCAGTACTGTGAGAGTCGAGGTCAGAGGACTGCTTGAGCCAGGAGTTTC 70100
QY 61 AAGAGGAGCTTGAGACACAGAGGAGACTGCTGACTACAAAGATAATAATTAATGACGAC 120
Db 70099 AAGAGGAGCTTGAGACACAGAGGAGACTGCTGACTACAAAGATAATAATTAATGACGAC 70040
QY 121 GCTTAAGTGGCTCATCCCTGTGTGTCCAGCTTACTAGAGGAGCAGAGTGAAGCTTGTGC 180
Db 70039 GCTTAAGTGGCTCATCCCTGTGTGTCCAGCTTACTAGAGGAGCAGAGTGAAGCTTGTGC 69980
QY 181 CCGAGAGGTAAACATGCGACTGAGCCAGCCAGCCAGCCAGCTGATTCACCTGGGAGAC 240
Db 69979 CCGAGAGGTAAACATGCGACTGAGCCAGCCAGCCAGCTGATTCACCTGGGAGAC 69920
QY 241 AAAAAGAGACCTGTCTCAAAAAATAGTTAAATTAATAATAATAATAGTTTAAAC 300
Db 69919 AAAAAGAGACCTGTCTCAAAAAATAGTTAAATTAATAATAATAATAGTTTAAAC 69860
QY 301 CCTAAACACATCTCTCTTTTCAAGAGACTTCTTAAGACTTCATGCTGCTGTGTG 360
Db 69859 CCTAAACACATCTCTCTTTTCAAGAGACTTCTTAAGACTTCATGCTGCTGTGTG 69800
QY 361 ATCTCCACTTCCTTTTTCAGGCTCCACACTTTTAACAGTCTTTTGGCCAGATATA 420
Db 69799 ATCTCCACTTCCTTTTTCAGGCTCCACACTTTTAACAGTCTTTTGGCCAGATATA 69740
QY 421 AGTATATAGTTTCTGGAATCCAGATTCTTCCCTGTTGACAG 463
Db 69739 AGTATATAGTTTCTGGAATCCAGATTCTTCCCTGTTGACAG 69697
RESULT 5
AP003717/c 156370 bp DNA linear PRI 27-APR-2002
LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-167N4, complete
DEFINITION
ACCESSION AP003717
VERSION AP003717.3 GI:20334343
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totsuki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 156370)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totsuki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submision
JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenhiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel:81-45-503-9111, Fax:81-45-503-9170
On Apr 26, 2002 this sequence version replaced gi:16904692.
COMMENT
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
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ORIGIN

Query Match 99.7%; Score 461.4; DB 5; Length 156370;
Best Local Similarity 99.8%; Pred. No. 2.6e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCTGTAATCCGATCTGTGAGAGTCCGAGTCCAGAGCTGCTTGAGGCCAGAGTTTC 60
Db 44873 ACCCTGTAATCCGATCTGTGAGAGTCCGAGTCCAGAGCTGCTTGAGGCCAGAGTTTC 44814
QY 61 AAGAGAGCCTGGAACAACAGGAGACCTGTGACTGACAAAGAAATAATTAATAGCCAG 120
Db 44813 AAGAGAGCCTGGAACAACAGGAGACCTGTGACTGACAAAGAAATAATTAATAGCCAG 44754
QY 121 GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAGTAGAGCTCTTGTTC 180
Db 44753 GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAGTAGAGCTCTTGTTC 44694
QY 181 CCAGAGGCTCAACATGCACTGAGTACGTCGAGCCCACTGCAATTCAGCTGGGCAAC 240
Db 44693 CCAGAGGCTCAACATGCACTGAGTACGTCGAGCCCACTGCAATTCAGCTGGGCAAC 44634
QY 241 AAAAAGAGACCCGTGTCAAAAAATAAGTAAATAATAATAATAATAATAATAATAA 300
Db 44633 AAAAAGAGACCCGTGTCAAAAAATAAGTAAATAATAATAATAATAATAATAA 44574
QY 301 CCTAAACACATCTCTCTTTTCAAGAGACCTCTTAAGACCTCATGCTGCTGTTG 360
Db 44573 CCTAAACACATCTCTCTTTTCAAGAGACCTCTTAAGACCTCATGCTGCTGTTG 44514
QY 361 ATCTCCACTCTCTCTTTTTCAGCGCTCCACACTTTTAAACAGTCTCTTTGCCAAGATATA 420
Db 44513 ATCTCCACTCTCTCTTTTTCAGCGCTCCACACTTTTAAACAGTCTCTTTGCCAAGATATA 44454
QY 421 AGTATATAGTTTCTGGAATCAGATTCTTCCCTGTTTGACAG 463
Db 44453 AGTATATAGTTTCTGGAATCAGATTCTTCCCTGTTTGACAG 44411

RESULT 6
AC019121 197031 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT
DEFINITION
SEQUENCE, 23 unordered pieces.
AC019121
AC019121.3 GI:8440022
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 197031)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 197031)
Waterston, R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 10, 2000 this sequence version replaced gi:7105573.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Project Information -----
Center project name: H NH0535C12
----- Summary Statistics -----
Sequencing vector: M13, 55%
Sequencing vector: plasmid, 45%
Chemistry: Dye-primer ET, 55% of reads
Chemistry: Dye-terminator Big Dye, 45% of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 182418 bases at least Q40
Consensus quality: 187565 bases at least Q30
Consensus quality: 190012 bases at least Q20

Insert size: 190000; agarose-fp
Insert size: 194831; sum-of-contigs
Quality coverage: 4.10 in Q20 bases; agarose-fp
Quality coverage: 4.05 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
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5865 5858: gap of unknown length
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12866 12965: gap of unknown length
12966 18581: contig of 5616 bp in length
18582 18681: gap of unknown length
18682 23851: contig of 5170 bp in length
23852 23951: gap of unknown length
23952 28414: contig of 4463 bp in length
28415 28514: gap of unknown length
28515 33195: contig of 4681 bp in length
33196 33295: gap of unknown length
33296 33396: contig of 5353 bp in length
33396 38748: gap of unknown length
38749 38749: gap of unknown length
38749 44925: contig of 6177 bp in length
44926 45025: gap of unknown length
45026 51784: contig of 6759 bp in length
51785 51884: gap of unknown length
51885 58855: contig of 6971 bp in length
58856 58955: gap of unknown length
58956 68289: contig of 9334 bp in length
68290 68390: gap of unknown length
68390 77123: contig of 8734 bp in length
77124 77223: gap of unknown length
77224 87292: contig of 10069 bp in length
87293 87392: gap of unknown length
87393 96029: contig of 8637 bp in length
96030 96129: gap of unknown length
96130 104791: gap of 8662 bp in length
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116913 117012: gap of unknown length
117013 131368: contig of 14356 bp in length
131369 131468: gap of unknown length
131469 142993: contig of 11525 bp in length
142994 143093: gap of unknown length
143094 154361: contig of 11268 bp in length
154362 154461: gap of unknown length
154462 173802: contig of 19341 bp in length
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FEATURES
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Best Local Similarity 99.8%; Pred.No.2.5e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db       163418  AAGAGCAGCCTGACCAACATAGGGAGACTGTCTACTACAAAGAATTAATTAATTAAGCCAG 163477
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QY      121  GCTTAGTGGCTCATCCCTGTGGTCCCGACTACATAGGAGGACAGAGTAGAGCTGCTGTG 180
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Db       163478  GCTTAGTGGCTCATCCCTGTGGTCCCGACTACATAGGAGGACAGAGTAGAGCTGCTGTG 163537
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Db       163598  AAAAAAGACCTGTCTCAAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 163657
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QY      301  CCTAAACACATCTTCTTTTCAAAAGAGACTTCTTAAGACTTCATCTGCTGCTGTG 360
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Db       163658  CCTAAACACATCTTCTTTTCAAAAGAGACTTCTTAAGACTTCATCTGCTGCTGTG 163717
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QY      361  ATCTCCACTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAGAGATAATA 420
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Db       163718  ATCTCCACTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAGAGATAATA 163777
          |||
QY      421  AGTATATAGTTTCTGGAATCCAGATTCTTCCTGTGTGACAG 463
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RESULT 7
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LOCUS          Homo sapiens genomic DNA, chromosome 11q clone:RP11-535c12,
DEFINITION     complete sequences.
ACCESSION      AP003531
VERSION        AP003531.2   GI:20334341
KEYWORDS       HTG.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE      1
AUTHORS       Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Torok,Y., Watanabe,H. and Sakaki,Y.
TITLE         Published Only in Database (2001)
JOURNAL       2 (bases 1 to 199384)
REFERENCE     Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Torok,Y., Watanabe,H. and Sakaki,Y.
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TITLE Direct Submission
JOURNAL Submitted (18-APR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shuhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://bgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2002 this sequence version replaced gi:1369094.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
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/clone="RP11-535C12"

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Best Local Similarity 99.8%; Pred. No.2:5e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGCTTGAGGCCAGAGTTC 60
DB 182415 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGCTTGAGGCCAGAGTTC 182356
QY 61 AAGAGCAGCTGAGCAACACAGAGGAGACTGTCTCACTCAAAAGTAATTAATTAGCCAG 120
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QY 121 GCTTATGCTGCTATCCCTGAGTCCGAGTCACTAAGAGGAGCAAGTATGAGCTGTGTC 180
DB 182295 GCTTATGCTGCTATCCCTGAGTCCGAGTCACTAAGAGGAGCAAGTATGAGCTGTGTC 182236
QY 181 CCAGAGAGTCAAGACTGAGTCACTGAGAGCCAGCCAGTCTGAGCTGAGGCAAC 240
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DB 182055 ATCTCCACTTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAGATATA 181996
QY 421 AGTATATAGTTTCTGAATCCAGATTCTTCCCTGTTTGAACAG 463
DB 181995 AGTATATAGTTTCTGAATCCAGATTCTTCCCTGTTTGAACAG 181953

RESULT 8
AF208500 3301 bp DNA linear PRI 09-JAN-2000
LOCUS Homo sapiens uncoupling protein 2 (UCP2) gene, promoter and exon 1.
DEFINITION AF208500
ACCESSION AF208500.1 GI:6684000
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
1 (bases 1 to 3301)
Tu,N., Chen,H., Winkler,U., Reinert,I., Marmann,G., Pirke,K.M. and Lentes,K.U.
Molecular cloning and functional characterization of the promoter region of the human uncoupling protein-2 gene
Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)
JOURNAL PUBMED 10558866

REFERENCE 2 (bases 1 to 3301)
AUTHORS Tu,N., Chen,H., Winkler,U., Reinert,I., Pirke,K.M. and Lentes,K.U.
TITLE Functional characterization of the 5'-flanking and promoter regions of the human UCP2 gene
JOURNAL Biochem. Biophys. Res. Commun. (2000) In press
REFERENCE 3 (bases 1 to 3301)
AUTHORS Lentes,K.-U., Tu,N. and Chen,H.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics, Center for Psychobiological and Psychosomatic Research, University of Trier, Friedrich-Wilhelm-Strasse 23, Trier D-54290, Germany
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/note="5' flanking region and promoter"
3298..3301
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3298..3301
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ORIGIN
Query Match 70.8%; Score 327.8; DB 5; Length 3301;
Best Local Similarity 92.3%; Pred. No.3:6e-77;
Matches 431; Conservative 0; Mismatches 26; Indels 10; Gaps 8;

QY 5 GTTAATTCAGTACTGTGAGAGT--CCAGGTCAGAGAGTCTTGAGGCCAGAGAGTTCAA 62
DB 1320 GTTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGAGTCTTGAGGCCAGAGAGTTCAA 1379
QY 63 GAGCAGCTGAGCAACACAGAGGAGACTGTCTCACTCAAAAGTAATTAATTAATTAAGCCAG 121
DB 1380 GAGCAGCTGAGCAACACTAGAGAGAGTGTCTCACTCAAAAGTAATTAATTAATTAAGCCAG 1438
QY 122 CTT--AGTGGCTCATCCCTGTGCTCCAGCTACTAAGGAGGAGAGAGTACTGCTTGT 179
DB 1439 CTTTATGAGTTCATCCCTGTGCTCCAGCTACTAAGGAGGAGAGTACTGCTTGT 1497
QY 180 CCAGAGAGTCAAGACTGAGTCACTGAGAGCCAG--CCAGCTGAGCTTCCAGCTGAGCA 238
DB 1498 CCAGAGAGTCAAGACTGAGTCACTGAGAGCCAGCCAGCTGAGCTTCCAGCTGAGCA 1557
QY 239 ACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 298
DB 1558 ACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1617
QY 299 ACCCTAAACACATCTCTTTTCAAGAGAGACTTTTAAGAGCTTCATGCTGCTGCTGT 358
DB 1618 ACCCTAAACACATCTCTTTTCAAGAGAGACTTTTAAGAGCTTCATGCTGCTGCTGCTGT 1677
QY 359 TGATCTCAGTCTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTTTC--CCAGAGATA 417
DB 1678 TGATCTCAGTCTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTTTC--CCAGAGATA 1737
QY 418 ATAAGTATATAGTTTCTGAATCCAGATTCTT--CCCTGTTTGAACAG 463
DB 1738 ATAAGTATATAGTTTCTGAATCCAGATTCTTTCCTGTTTGAACAG 1784

RESULT 9
AC136431 168721 bp DNA linear PRI 21-DEC-2002
LOCUS Homo sapiens chromosome 16 clone RP11-148M17, complete sequence.
DEFINITION

ACCESSION AC136431
VERSION AC136431.3 GI:27356680
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 168721)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE
AUTHORS Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
TITLE 3 (bases 1 to 168721)
JOURNAL DOE Joint Genome Institute.
REFERENCE
AUTHORS Submitted (09-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
TITLE Direct Submission
JOURNAL Submitted (21-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 21, 2002 this sequence version replaced gi:24819747.
Draft Sequence Produced By DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.2.
FEATURES
source
1..168721
location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-148M17"
ORIGIN
Query Match 34.2%; Score 158.4; DB 5; Length 168721;
Best Local Similarity 73.9%; Pred. No. 3.6e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
QY 2 CCTGTAATTCAGTGTGAGAGTCCGAGGTGAGAGGCTTGAGGCGAGATTCA 61
DB 18726 CCTGTAATTCAGTGTGAGAGTCCGAGGTGAGAGGCTTGAGGCGAGATTG 18785
QY 62 AGAGCAGCTGGAACACAGGAGGAGCTGTCACTAAGAAATTAATTAATGACGAG 121
DB 18786 AGAGCAGCTGGAACACAGGAGGAGCTGTCACTAAGAAATTAATTAATGACGAG 18845
QY 122 CTTAGTGGCTATCCCTGTGTGCTCCAGCTACTAGGAGGCAAGTGA---CTGCTT 177
DB 18846 CTTAGTGGCTATCCCTGTGTGCTCCAGCTACTAGGAGGCTGAGTGGGAGATGCGTTG 18905
QY 178 GTCCAGAGAGTCAAGCTGAGTGAAGTGAAGCCAGCCAGCTTCAGCTGAGG 237
DB 18906 AGCCCAAGAGTGAAGTGAAGTGAAGCCAGCCAGCTTCAGCTGAGG 18964
QY 238 AACAAAAAGAGCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 297
DB 18965 GACAGAGCAAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 19024
QY 298 AACCTTAAC 307
DB 19025 ATCCCTAGAC 19034

RESULT 10
AC138962/c
LOCUS AC138962
DEFINITION Homo sapiens chromosome 16 clone RP11-906M12, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC138962
VERSION AC138962.1 GI:27805374
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 173113)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
COMMENT Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1642708
Center clone name: RPC1-11_906M12

Summary Statistics
Consensus quality: 171480 bases at least Q40
Consensus quality: 171615 bases at least Q30
Consensus quality: 171780 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 172913; sum-of-ctnigs estimation
Quality coverage: 15.53 in Q20 bases; agarose-fp estimation
Quality coverage: 16.17 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1119: contig of 1119 bp in length
* 1120 1219: gap of unknown length
* 1220 70508: contig of 69289 bp in length
* 70509 70608: gap of unknown length
* 70609 173113: contig of 102505 bp in length.
location/Qualifiers
1..173113
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-906M12"
/clone_1ib="RPC1 human BAC library 11"
1120..1219
gap
/estimated_length=unknown
70509..70608
gap
/estimated_length=unknown
ORIGIN
Query Match 34.2%; Score 158.4; DB 12; Length 173113;
Best Local Similarity 73.9%; Pred. No. 3.6e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
QY 2 CCTGTAATTCAGTGTGAGAGTCCGAGGTGAGAGGCTTGAGGCGAGATTCA 61

DEFINITION Homo sapiens chromosome 16 clone RP11-482B16, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC138897
VERSION AC138897.1 GI:27805309
KEYWORDS HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 175785)
DOE Joint Genome Institute.
AUTHORS Sequencing of Human Chromosome 16
TITLE Unpublished
JOURNAL 2 (bases 1 to 175785)
REFERENCE DOE Joint Genome Institute.
AUTHORS Direct Submission
TITLE Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 591493
Center clone name: RP11_482B16

Summary Statistics
Consensus quality: 175156 bases at least Q40
Consensus quality: 175239 bases at least Q30
Consensus quality: 175390 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 175585; sum-of-contigs estimation
Quality coverage: 16.07 in Q20 bases; agarose-fp estimation
Quality coverage: 16.47 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 47298: contig of 47298 bp in length
* 47299 47398: gap of unknown length
* 47399 106534: contig of 59136 bp in length
* 106535 106634: gap of unknown length
* 106635 175785: contig of 69151 bp in length.
Location/Qualifiers
1.175785
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-482B16"
/clone_lib="RP11 human BAC library 11"
47299..47398
gap
/estimated_length=unknown
106535..106634
gap
/estimated_length=unknown
ORIGIN
Query Match 34.2%; Score 158.4; DB 12; Length 175785;
Best Local Similarity 73.9%; Pred. No. 3.6e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
2 CCTGTAATTCAGACTGTGAGCTCGAGGTGAGAGCTGTTGAGGCGAGGTTCA 61
Db 108733 CCTGTAATTCAGACTGTGAGCTCGAGGTGAGAGCTGTTGAGGCGAGGTTTG 108674
QY 62 AGAGCAGCTGAGCAACAGGAGGAGCTGCTACTACAAAGATTAATTAATGACGAG 121
|||||

Db 108673 AGACCAAGCTGGGCAATGAGAGACTATCTCTACAAAAAATCAAAAATTAAGTACG 108614
QY 122 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGAGAGGAGAGTAGA-----CTGCTT 177
Db 108613 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGAGAGGAGAGTAGAGGAGTGG 108554
QY 178 GTCCAGAGGTCAAGACTGAGTACAGTACCCAGCCACTGCTGCTTCAGCTTGCGC 237
Db 108553 AGCCCAAGAGGTGAGAGATCAGTGAAGCCAGATTGACCA-CTGCACTCCAGCTGCGT 108495
QY 238 AACAAAAGAGACCCCTCTCAAAAAAATAGTTAAATTAATTAATTAATTAATTAAT 297
Db 108494 GACAGCAAGACCCCTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAAT 108435
QY 298 AACCTTAAC 307
Db 108434 ATCCCTGAC 108425
RESULT 13
AC136434
LOCUS 189911 bp DNA linear HTG 01-NOV-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-261B14, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
ACCESSION AC136434
VERSION AC136434.1 GI:24462324
KEYWORDS HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 189911)
DOE Joint Genome Institute.
AUTHORS Sequencing of Human Chromosome 16
TITLE Unpublished
JOURNAL 2 (bases 1 to 189911)
REFERENCE DOE Joint Genome Institute.
AUTHORS Direct Submission
TITLE Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 506699
Center clone name: RP11_261B14

Summary Statistics
Consensus quality: 187721 bases at least Q40
Consensus quality: 188330 bases at least Q30
Consensus quality: 188586 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 189611; sum-of-contigs estimation
Quality coverage: 9.23 in Q20 bases; agarose-fp estimation
Quality coverage: 7.79 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1304: contig of 1304 bp in length
* 1305 1404: gap of unknown length
* 1405 3583: contig of 2179 bp in length
* 3584 3684: gap of unknown length
* 3684 51653: contig of 47970 bp in length
* 51654 51754: gap of unknown length
* 51754 189911: contig of 138158 bp in length.

FEATURES
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Location/Qualifiers
1. .189911
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-261B14"
/clone_1ib="RP1 human BAC library 11"
1305. .1404
/estimated_length=unknown
3584. .3563
/estimated_length=unknown
51654. .51753
/estimated_length=unknown
gap
gap
gap
ORIGIN
Query Match 34.2%; Score 158.4; DB 12; Length 189911;
Best Local Similarity 73.9%; Pred. No. 3.5e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
QY 2 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGACTGCTTGAGGCCAGAGTTCA 61
188348 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGACTGCTTGAGGCCAGAGTTTG 188407
QY 62 AGAGCAGCTTGACAAACAGAGGAGACTGTCTCACTACAAAGATTAAATTATTAAGCCAGG 121
188408 AGAGCAGCTTGAGCAACATGAGAGACTCATCTCTCAAAAAATTATTAAGCTAGG 188467
QY 122 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGGAGGAGAGTATGGA----CTGCTT 177
188468 CTTGTGTGGACATGCTGTGTATGTCTCCAGCTACTAGGGAGGCTGTGAGGAGATGGCTTG 188527
QY 178 GTCCAGAGGTCAAGACTGCACTGAGTGAAGCCAGCCACTGATTCAGCTGGGC 237
188528 AGCCCAAGAGGTGAGAGATGCACTGAGCCGAGATGACCA-CTGACCTCAGCTGGGT 188586
DB 238 AACAAAAAGAGACCTGTCTCAAAAAATAATTAAATAATAATAATAATAATTAGTTTA 237
QY 188587 GACAGAGCAAGACCTGTCTCAAAAAATAATAATAATAATAATAATAATAATAAAGCAG 188646
DB 298 AACCTTAAC 307
QY 188647 ATCCCTAGAC 188656
DB
RESULT 14
AC126760 211419 bp DNA linear PRI 01-DEC-2002
LOCUS Homo sapiens chromosome 16 clone RP11-1307B12, complete sequence.
AC126760
AC126760.4 GI:25989066
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 211419)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 211419)

AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 1, 2002 this sequence version replaced gi:24431616.
www.jgi.doe.gov
Draft Sequence Produced by DOE Joint Genome Institute
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
FEATURES
source
Location/Qualifiers
1. .211419
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1307B12"
ORIGIN
Query Match 34.2%; Score 158.4; DB 5; Length 211419;
Best Local Similarity 73.9%; Pred. No. 3.5e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
QY 2 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGACTGCTTGAGGCCAGAGTTCA 61
81719 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGACTGCTTGAGGCCAGAGTTTG 81778
QY 62 AGAGCAGCTTGACAAACAGAGGAGACTGTCTCACTACAAAGATTAAATTATTAAGCCAGG 121
81779 AGAGCAGCTTGAGCAACATGAGAGACTCATCTCTCAAAAAATTATTAAGCTAGG 81838
QY 122 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGGAGGAGAGTATGGA----CTGCTT 177
81839 CTTGTGTGGACATGCTGTGTATGTCTCCAGCTACTAGGGAGGCTGTGAGGAGATGGCTTG 81898
QY 178 GTCCAGAGGTCAAGACTGCACTGAGTGAAGCCAGCCACTGATTCAGCTGGGC 237
81899 AGCCCAAGAGGTGAGAGATGCACTGAGCCGAGATGACCA-CTGACCTCAGCTGGGT 81957
DB 238 AACAAAAAGAGACCTGTCTCAAAAAATAATTAAATAATAATAATAATAATAATTAGTTTA 237
QY 81958 GACAGAGCAAGACCTGTCTCAAAAAATAATAATAATAATAATAATAATAAAGCAG 82017
DB 298 AACCTTAAC 307
QY 82018 ATCCCTAGAC 82027
DB
RESULT 15
AC140522 235330 bp DNA linear HTG 25-FEB-2003
LOCUS Homo sapiens chromosome 16 clone RP11-826F21, WORKING DRAFT
AC140522
AC140522.5 unsorted pieces.
VERSION SBQUENCE
AC140522.1 GI:28557856
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1611829
Center clone name: RPCI-11_826F21

Summary Statistics

Consensus quality: 233805 bases at least Q40
Consensus quality: 234198 bases at least Q30
Consensus quality: 234471 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 234930; sum-of-configs estimation
Quality coverage: 13.22 in Q20 bases; agarose-fp estimation
Quality coverage: 9.85 in Q20 bases; sum-of-configs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 20830: contig of 20830 bp in length
* 20831 20930: gap of unknown length
* 20931 42777: contig of 21847 bp in length
* 42778 42877: gap of unknown length
* 42878 78821: contig of 35944 bp in length
* 78822 78921: gap of unknown length
* 78922 131770: contig of 52849 bp in length
* 131771 131870: gap of unknown length
* 131871 235330: contig of 103460 bp in length.

FEATURES

source

1. 235330
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-826F21"
/clone_1ib="RPCI human BAC library 11"
20831..20930
/estimated_length=unknown
42778..42877
/estimated_length=unknown
78822..78921
/estimated_length=unknown
131771..131870
/estimated_length=unknown

ORIGIN

Query Match 34.2%; Score 158.4; DB 12; Length 235330;
Best Local Similarity 73.9%; Pred. No. 3.4e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

QY 2 CCGTGAATTCACACTGTCGAGAGTCCGAGGTGAGAGGACTGCTGAGAGCCAGAGTTCA 61
DB 2105 CCGTGAATTCACACTGTCGAGAGTCCGAGGTGAGAGGACTGCTGAGAGCCAGAGTTG 2046
QY 62 AGAGCAGCCTGAGCAACACAGGAGACTGTCTACTACCAAGAATAAATAATTAGCCAGG 121
DB 2045 AGACGAGCCTGAGCAACACAGGAGACTGTCTACTACCAAGAATAAATAATTAGCCAGG 1986
QY 122 CTTAGTGGCTCATTCCTGTGTGCTCCAGCTACTAGGAGGCGAAGTAGGA----CTGCTT 177
DB 1985 CGTGTGGGCAATGCTGTGTGCTCCAGCTACTAGGAGGCGTGAATGGGAGATGGCTTG 1926
QY 178 GTCCAGGAGGTGAGCTGAGCTGAGAGCCAGCACTGCACTTCAGCTGGGC 237
DB 1925 AGCCAGAGAGGTGAGAGTCAAGTGAAGCCAGAGTTGACCA-CTGCACTCAGCTGGGT 1867
QY 238 AACAAAAAGAGCCCTGTCTCAAAAAATAAGTTAAATAAATAAATAAATAAGTTTA 297

DB 1866 GACAGAGCAAGACCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAGCAG 1807
QY 298 AACCTTAAC 307
DB 1806 ATCCCTAGAC 1797

Search completed: June 5, 2006, 22:27:29
Job time : 3138.62 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 402.823 Seconds
(without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098A-1_COPY_255_717
Perfect score: 463
Sequence: 1 accgtgattccagctactgt.....attctccctgttgacag 463

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463	100.0	3505	3	AAA62932
2	152	32.8	135005	12	AD019501
3	150.4	32.5	23579	10	AD687112
4	149.4	32.3	186510	10	AD624797
5	148.8	32.1	151909	14	ABE96535
6	147.4	31.8	81099	11	ACN45018
7	147.2	31.8	110000	14	AEA61124_0
8	147	31.7	110000	10	ADG70447_0
9	147	31.7	110000	10	ABZ79565_0
10	146.8	31.7	7739	4	AA136824
11	146.8	31.7	7739	8	ABX59812
12	146.8	31.7	7739	12	ADJ30562
13	146.8	31.7	226475	9	AAD58279
14	146.4	31.6	41150	10	AD113819
15	146.4	31.6	41150	14	AD181843
16	146.4	31.6	44348	12	ADN48556
17	145.4	31.4	31749	4	AAK72959
18	145.4	31.4	78925	3	AAAC8988

19	145.4	31.4	143947	15	AEF38790	AEF38790 Human fib
20	145.4	31.4	143947	15	AEF38751	AEF38751 Human fib
21	145.4	31.4	143947	15	AEF35247	AEF35247 Human fib
22	145.4	31.4	143947	15	AEF64068	AEF64068 Human fib
23	145.4	31.4	143947	15	AEF63985	AEF63985 Human fib
24	144.8	31.3	53122	11	ACN43998_6	Continuation (7 of
25	144.8	31.3	110000	11	ACN43998_5	Continuation (6 of
26	144.6	31.2	2096	8	ACC72436	Acc72436 Human sec
27	144.6	31.2	93500	13	ADT77142	Adt77142 Type II d
28	144.4	31.2	32169	5	ABAI4358	Abai4358 Human ner
29	144	31.1	109906	6	ABK94411	ABK94411 DNA encod
30	144	31.1	109906	12	ADL08112	Adl08112 Human gen
31	144	31.1	158417	13	ADS36461	Ads36461 Human aut
32	143.8	31.1	11006	14	AEA61101	AEA61101 Human GUC
33	143.6	31.0	58822	9	ADA02540	Ada02540 Human TCO
34	143.6	31.0	58822	10	AD872278	Ad872278 Human TCO
35	143.6	31.0	58822	10	AD855788	Ad855788 Human TCO
36	143.6	31.0	110000	12	ADN06353_0	Adn06353 Human FLA
37	143.6	31.0	110000	13	ADS94372_0	Ads94372 Human 5-1
38	143.6	31.0	145616	14	AED17971	Aed17971 Fibrotic
39	143.6	31.0	174472	14	ADZ13139	Adz13139 Human can
40	143.6	31.0	174703	11	ACN44738	Acn44738 Human gen
41	143.6	31.0	276276	11	ACN44350	Acn44350 Human gen
42	143.4	31.0	2005	5	AAE93841	AAE93841 Human CDN
43	143.4	31.0	2005	14	ADY63190	Ady63190 Human c10
44	143.4	31.0	22428	4	AA541759	AA541759 Genomic s
45	143.4	31.0	22428	8	ABZ74201	Abz74201 Secreted

ALIGNMENTS

RESULT 1	AAA62932 standard; DNA; 3505 BP.
ID	AAA62932
AC	AAA62932;
XX	
DT	02-NOV-2000 (first entry)
XX	
DE	DNA containing human uncoupling protein-2 (UCP-2) promoter region.
XX	
KW	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;
KW	hypotension; hyperlipidaemia; anti-pyretic; ds.
XX	
OS	Homo sapiens.
XX	
PN	W0200039315-A1.
XX	
PD	06-JUL-2000.
XX	
PF	22-DEC-1999; 99NO-JP007198.
XX	
PR	24-DEC-1998; 98JP-00366719.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
PI	Toyoda Y, Kobayashi M, Igaki S;
DR	WPI; 2000-452407/39.
XX	
PT	DNA with promoter region containing regulator sequence of uncoupling
PT	protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,
PT	hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in
PT	therapy.
XX	
XX	Claim 4; Fig 1-6; 43p; Japanese.
XX	
PS	This invention relates to DNA comprising a promoter region containing the
CC	regulatory sequences of human uncoupling protein-2 (UCP-2). Included in
CC	the invention are a recombinant vector containing the DNA sequence, cells
CC	transformed by the vector, and a method for screening for compounds or
CC	salts that can promote or inhibit the UCP-2 promoter activity using the


```
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
PI WPI; 2003-335783/31.
DR P-PSDB; ADC87113.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 1; SEQ ID NO 1565; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85948-ADC87616 encode GPCR's of the
CC invention.
XX
SQ Sequence 23579 BP; 6524 A; 5062 C; 5419 G; 6574 T; 0 U; 0 Other;
Query Match 32.5%; Score 150.4; DB 10; Length 23579;
Best Local Similarity 72.4%; Pred. No. 6.6e-29;
Matches 223; Conservative 0; Mismatches 81; Indels 4; Gaps 2;
QY 2 CCTGTAAATTCGACGACTGTGAGAGCTCCGAGGTGAGAGAGCTTTGAGGCCAGAGATTCA 61
DB 14855 CCTATTAAGCCGAGCACTTTGGGAAGCTGAGGTGGTGCATCATCTTGAGGCCAGAGATTG 14914
QY 62 AGAGCAGCCTGGAACAACAAGGAGACCTGTCACTAACAAGATTAATTAATGACGAG 121
DB 14915 AGACGACGATGAGCCAACTGTGTAACCGTCTCTACTAAATAACAAATTAAGCCAGG 14974
QY 122 CTTAGTGGCTCATCCCTGTGGTCCACGACTACTAGAGAGGC--AGAAATGAGACTGCTTG 178
DB 14975 CTTGTGTGTGATGCTCTATATATCCAGCTACTTGGAGGCTGGAAGCAAGAAATCGGCTTG 15034
QY 179 TCCAGAGAGGTCAAGACTGCACTGAGAGTGAAGCCAGCCAGCTGCATTCAGCTGGGCA 238
DB 15035 AACCGGAGGCGGAGGTGCGAGTGAAGTGTGCCA--TTCACCTCCGGCTGGGCA 15093
QY 239 ACAAAGAAGAGACCTGTCTCAAAAATAAGTTAATAATAATAATAATAATAGTTTAA 298
DB 15094 ACGAGGCAAGACTGTCTCTAAAAATAATAATAATAATAATAATAATAAT 15153
QY 299 ACCCTAAA 306
DB 15154 AAAATAAA 15161
RESULT 4
ADE24797/c
ID ADE24797 standard; DNA; 186510 BP.
XX
AC ADE24797;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human endothelin-1, EDN1, gene.
XX
XX de; gene; human; vascular disease; endothelin-1; EDN1;
XX coronary artery disease; myocardial infarction.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(159908,T)
XX FT /*tag= b
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FT /standard_name= "Single nucleotide polymorphism"
XX US2003143544-A1.
XX
XX 31-JUL-2003.
XX
XX 09-JAN-2002; 2002US-00043715.
XX
XX 09-JAN-2002; 2002US-00043715.
XX
XX 09-JAN-2002; 2002US-00043715.
XX
XX (VIT1-) VITVITY INC.
XX
XX McCarthy J;
XX
XX WPI; 2003-874790/81.
XX
XX P-PSDB; ADE24798, ADE24801.
XX
XX Identifying a subject as a candidate for a particular therapy to treat a
XX vascular disease or disorder, particularly coronary artery disease or
XX myocardial infarction, comprises detecting polymorphisms of the
XX endothelin-1 gene.
XX
XX Claim 58; SEQ ID NO 1; 177bp; English.
XX
XX The invention relates to a method of identifying a subject as a candidate
XX for a particular therapy to treat a vascular disease or disorder
XX comprising determining the presence of nucleotides at polymorphic regions
XX of an endothelin-1 (EDN1) gene. The invention is used to determine risk
XX of developing a vascular disease or disorder, particularly coronary
XX artery disease or myocardial infarction. The present sequence represents
XX the human endothelin-1 gene.
XX
SQ Sequence 186510 BP; 56192 A; 36427 C; 37117 G; 56774 T; 0 U; 0 Other;
Query Match 32.3%; Score 149.4; DB 10; Length 186510;
Best Local Similarity 74.1%; Pred. No. 2.5e-28;
Matches 217; Conservative 0; Mismatches 71; Indels 5; Gaps 2;
QY 1 ACCGTAAATTCGAGTGTGAGAGTCCGAGGTGAGAGGACTGCTTGAGGCCAGAGATTC 60
DB 175801 ACCGTAAATTCGAGCTTTGGAGATGAGGCAAGAAATTAATTGAGGCGAGAGTTT 175742
QY 61 AAGAGCAGCCTGGAACAACAAGGAGAGCTGTCACTACAAAGAATAATAATTAATGACGAG 120
DB 175741 GAGACGAGCTGGTAAACAAGTGAAGCGCATCTCTACAAAAATAATAATAATTAATGCTGG 175682
QY 121 GCTTAATGCTCATCCCTGTGTGCTCCAGCTACTAAGGAGGCAAGATGAGA---CTGCT 176
DB 175681 GCATGTGTGTGTGCACTGTATGCTCCAGCTACTCAGAGGCTGAGGTGGAGATCGCTT 175622
QY 177 TGTCCGAGAGGTCAAGACTGCACTGAGCTGAGACCCAGCCAGCTGCATTCCAGCTGGG 236
DB 175621 GAGCCAAAGAGGTGAGACCTGTGTGAGCTGTGTTCATGCA--CTGCACTCAGCTGGG 175563
QY 237 CAACAAAAAAGAGACCTGTCTCAAAAATAAGTTAATAATAATAATAATAATAATA 289
DB 175562 CAACAGAGAGAGACCTGTCTCAACAAACAAACAAACAAACAAACAAACAA 175510
RESULT 5
AEB96535/c
ID AEB96535 standard; DNA; 151909 BP.
XX
XX AEB96535;
XX
XX 06-OCT-2005 (first entry)
XX
XX Human CABIN1 gene, SEQ ID 19.
XX
XX
XX hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;
XX liver cirrhosis; fibrosis; hepatoma; SNP detection; CABIN1; ds.
XX
XX Homo sapiens.
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FT	variation	10001
FT		/tag= b
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	10054
FT		/tag= c
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	15316
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FT	variation	21408
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FT	variation	21444
FT		/tag= g
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	28376
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FT		/tag= i
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FT	variation	33211
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FT	variation	54446
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ID	ACN45018/C
ID	ACN45018 standard; DNA; 81099 BP.
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XX	ACN45018;
DT	18-NOV--2004 (first entry)
XX	
DE	Human genomic sequence hCGI7395.
KW	Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
OS	Homo sapiens.
XX	
PX	WO2003073826-A2.
PN	
XX	12-SEP--2003.
PD	
PF	28-FEB--2003; 2003WO-US006235.
PR	
XX	01-MAR-2002; 2002US-00087192.
PA	(SAGR-) SAGRES DISCOVERY.
XX	
PI	Morris DW;
DR	
XX	WFI; 2003-328604/31.
PT	
PT	Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
PS	
PS	Claim 1; SEQ ID NO 1756; Opp; English.
CC	The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for:
CC	(i) screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
CC	
CC	US2002182586A1, for which no sequence data was published
CC	
XX	
SQ	Sequence 81099 BP; 20015 A; 18716 C; 19786 G; 22439 T; 0 U; 143 Other;
Query Match	31.8%; Score 147.4; DB 11; Length 81099;
Best Local Similarity	72.9%; Pred. No. 6,2e-28;
Matches 218; Conservative	0; Mismatches 76; Indels 5; Gaps 2;
Dy	2 CCTGTAATTCAGTACTGTGGAGCTCCAGGTCAGAGACTGTTGAGGCCAGAGTTCA 61
Db	18811 COTGAATCCAGACATTCTTGAGAGCCAGCAGAAGACTGCTTGAGCCCAGAGTTCC 1875
Dy	62 AGAGCAGCTTGAACAACACAGGAGAACCTGTCACTACATAAAAGATTAATTAATGCTAG 121
Db	18751 AGACCAGGCTGGGCAACATGAAAAGACCTCATCTCAAATAAAAAATTAATGACGAG 1869
Dy	122 CTTAGTGGCTCATCCCTGTGGTCCAGCTACTGAGGAGGAGAGTAGAGACTGTTG-- 179
Db	18651 CGTGTGTCTTAAGCCTGTGTACTCCAGCTACTACAGAGGCTGANAAGTGGAGAGACTCTTG 1863
Dy	180 --CCAGAGAGTCAAGACTGCAGTGAAGTGAAGCCAGCCAGCTGTCACTTCCAGCTGGAG 237
Db	18631 AGCTGGAGAGTTCAAGGCTACAGTAGACCCCTGATCGAGCCA-CGTGACCTCAGCTGGGT 1857
Dy	238 AACCAAAAGAGACCTGTCTCAAAAATTAAGTTAAATTAATTAATTAATTAATTAATTAAT 296
Db	18572 GACGAGGAGGAGCACCTGTCTCAAAAAACAAACAAAAAATCAATTAAGAGTGTTTT 18514

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RESULT 7
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WP Sequence split into 4 fragments LOCUS A661124 Accession A661124
WP Fragment Name Begin End
WP A661124_0 110000
WP A661124_1 210000
WP A661124_2 200001 310000
WP A661124_3 300001 383432
ID A661124 standard; DNA; 383432 BP.
XX
XX A661124;
AC
AC 25-AUG-2005 (first entry)
XX
XX Human SLC4A4 gene genomic sequence SEQ ID NO:34.
XX
XX DNA methylation; biomarker; cancer; gene; ds; SLC4A4.
XX
XX Homo sapiens.
XX
XX US2005130172-A1.
XX
XX 16-JUN-2005.
XX
XX 27-JAN-2004; 2004US-00765790.
XX
XX 16-DEC-2003; 2003US-00737082.
XX
XX (PARB ) BAYER CORP.
XX
XX Beard C, Burgess C, Gannon A, Harvey J, Lechner JF, Li Z;
XX
XX MPI; 2005-456991/46.
XX
XX GENBANK; AF011390, NM_003759.
XX
XX Identifying nucleic acid sequences as biomarker for disease, by
XX identifying nucleic acid sequences comprising methylated CpG site and
XX down-regulated in diseased cells and comparing its expression level with
XX demethylated nucleic acid.
XX
XX Claim 11; SEQ ID NO 34; 27pp; English.
XX
XX The invention relates to a method (M1) for identifying one or more
XX nucleic acid sequences useful as a biomarker for a disease to be
XX detected. (M1) involves identifying nucleic acid sequences comprising
XX methylated CpG site in promoter-first exon region and that are down-
XX regulated in diseased cells, comparing expression level of nucleic acid
XX sequences with that of demethylated nucleic acid sequences and
XX identifying nucleic acid sequences exhibiting increase in expression
XX after demethylation. Also described: (1) detecting (M2) the presence or
XX stage of a disease in a subject, which involves determining the degree of
XX methylation of one or more CpG sites on nucleic acid sequences in a
XX biological sample obtained from the subject, and determining the presence
XX of, predisposition to, or stage of the disease in the subject based on
XX the degree of methylation; (2) monitoring the onset, progression, or
XX regression of a disease in a subject; (3) determining the efficacy of a
XX test compound for inhibiting a disease in a subject; and (4) a kit (1)
XX useful for diagnosis, prognosis, staging, monitoring, and therapeutic
XX treatment of a disease. (M1) is useful for identifying one or more
XX nucleic acid sequences useful as a biomarker for a disease to be
XX detected, where the nucleic acid sequences are useful for detecting, the
XX presence or stage of a disease such as cancer e.g. colorectal cancer in a
XX subject. The present sequence represents a specifically claimed human
XX genomic sequence for use in the method of the invention. Note - The
XX sequence data for this patent is not represented in the printed
XX specification but was obtained in electronic format from the USPTO web
XX site.
XX
XX Sequence 383432 BP; 113010 A; 69169 C; 74959 G; 126294 T; 0 U; 0 Other;
XX
XX Query Match 31.8%; Score 147.2; DB 14; Length 110000;
XX Best Local Similarity 74.0%; Pred. No. 7.8e-28;
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Matches 213; Conservative 0; Mismatches 73; Indels 2; Gaps 2;
QY 2 CCTGTATTCCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAAGCCAGAGTTCA 61
Db 90502 CTTGTAGTCCAGACCTTTGAGAGGTGAGTGTGATCCCTTGAGCCCAAGATTGC 90561
QY 62 AGAGCAGCTTGACAAACACAGGAGACC-TGTCACTTCAAAAGATTAATTAATTAAGCCAG 120
Db 90562 AGACGAGCTGGGCAATATGACAAACCTTGTCTTCAAAAAAGACAAAGATTAAGCCAG 90621
QY 121 GCTTAGTGCTCATCCCTGTTGTCCTCAGCTACTAGGAGGAGCAGAGTAGGACTGCTTGTGC 180
Db 90622 GTGTGTGTGTGACACCTGTGTGTGCTCCAGCTACTTGGAGGCTGAGTGGACACTTGTGAC 90681
QY 181 CCAGAGGTCAGACAGTCAAGTCAAGTCAAGCCAGCCACTGCTTCAAGCTTGAGCCAC 240
Db 90682 CCAGAGGTCAGATCTGTAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 90740
QY 241 AAAAAGAGACCTGCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 288
Db 90741 AGAATGAGACCTGCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 90788

RESULT 8
ADG70447_0/c
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WP ADG70447_0 1 110000
WP ADG70447_1 100001 210000
WP ADG70447_2 200001 310000
WP ADG70447_3 300001 410000
WP ADG70447_4 400001 410846
ID ADG70447 standard; DNA; 410846 BP.
XX
XX ADG70447;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human ANGE-CLND8-CLND7 hybrid gene.
XX
XX ANGE; CLND8; CLND7; ANGE-CLND8; ANGE-CLND7; CLND7-CLND8;
XX ANGE-CLND8-CLND7; anti-allergic; antiasthmatic; dermatological;
XX antipyretic; anti-inflammatory; gene therapy; IgE-mediated disease;
XX ANGE 1; single nucleotide polymorphism; ds.
XX
XX Chimeric.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX variation replace(138770..G)
XX variation /*tag= b
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XX variation /*tag= c
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XX MO2003000727-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002MO-GB002859.
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XX 21-JUN-2001; 2001GB-00015211.
XX 21-JUN-2001; 2001GB-00015212.
XX 21-JUN-2001; 2001GB-00015213.
XX
XX (ISIS-) ISIS INNOVATIONS LTD.
XX
XX Zhang Y, Moffatt M, Cookson W, Tinsley J;
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Q1	AB279565_0/c	31.7%	Score 147, DB 10;	Length 110000;	Fragment 1
Q2	AB279565_1	68.8%	Pred. No. 8.8e-28;		Fragment 2
Q3	AB279565_2	0;	Mismatches 100;	Indels 5; Gaps 2;	Fragment 3
Q4	AB279565_3				Fragment 4
Q5	AB279565_4				Fragment 5
Q6	AB279565 standard; DNA; 410846 BP.				Fragment 6
Q7	AB279565;				Fragment 7
Q8	AB279565;				Fragment 8
Q9	AB279565;				Fragment 9
Q10	AB279565;				Fragment 10
Q11	AB279565;				Fragment 11
Q12	AB279565;				Fragment 12
Q13	AB279565;				Fragment 13
Q14	AB279565;				Fragment 14
Q15	AB279565;				Fragment 15
Q16	AB279565;				Fragment 16
Q17	AB279565;				Fragment 17
Q18	AB279565;				Fragment 18
Q19	AB279565;				Fragment 19
Q20	AB279565;				Fragment 20
Q21	AB279565;				Fragment 21
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Q84	AB279565;				Fragment 84
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OS	Unidentified.
XX	
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PN	WO2003000296-A2.
PD	
XX	03-JAN-2003.
XX	
PF	21-JUN-2002; 2002W0-GB002857.
PR	
XX	21-JUN-2001; 2001GB-00015211.
PA	(ISIS-) ISIS INNOVATIONS LTD.
PI	Zhang Y, Mofiat M, Cookson W;
DR	WPI; 2003-221370/21.
PT	Treating B-cell chronic lymphocytic leukemia in an individual by
PS	modulating the expression of the CLD8 and/or the NY-REN-34 gene.
XX	Disclosure; Fig 1; 154bp; English.
CC	The invention relates to a method for treating B-cell chronic lymphocytic
CC	leukemia (BCLL), comprising modulating the expression of the CLD8
CC	and/or the NY-REN-34 gene. The polynucleotide sequence or gene product of
CC	the CLD8 and/or NY-REN-34 gene or agent is useful for the manufacture of
CC	a diagnosis and treatment of BCLL. The current sequence represents CLD8
CC	and NY-REN-34 encoding DNA
SQ	Sequence 410846 BP; 125177 A; 83172 C; 81704 G; 120793 T; 0 U; 0 Other;
	Query Match 31.7%; Score 147; DB 10; Length 110000;
	Best Local Similarity 68.8%; Pred. No. 8.8e-28;
	Matches 232; Conservative 0; Mismatches 100; Indels 5; Gaps 2;
OY	2 CCTGTAAATTCAGTACTGTGAGAAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGACTTCA 61
DB	98790 CCTGTAAATTCAGACACTTTTGGAGAGCGAGGCGGGCGGATCAGCTGAGCTCAGAAATTGG 98731
OY	62 AGAGCAGCCTTGACAACACAGGAGN-CCTGTCACTAACAAATAAATAATTAATACCAG 120
DB	98730 AGACACACCCGAGCAACATGGCGAAAACCCGCTCTTAATAAATAAATAATTAAGCCAG 98677
OY	121 GCTTAGGAGCTCATCCCTGTGTCTCCAGACTACTAGGAGGAGCAAAATAGGA---CTGCT 176
DB	98670 GCGGTGGTGGCCGCCTGTAAATCCAGCTACTCCGGGGGGCTGAGACAGAAATACATT 98611
OY	177 TGTCACGAGAGGTCAAGACTGCAGTAGACTGAGACCCAGCCACTTGCAATTCAGCCTGG 236
DB	98610 GAACCCGAGAGCGGAGTGTGACAGTAGCCGAGATCGAGCCACTCGCACCTCAGCCTAG 98551
OY	237 CAACAAAAAAGACCCCTGTCTCAAAAAATAAGTTAATAATAATAATAATAATAGTTT 296
DB	98550 CAACAGAGAGACTGTCTCAAAATAATAATAATAATAATAATAATAATAATAATAATA 98491
OY	297 AAACCCTAACACATCTTTTTTTCAAAGAGACTTC 333
DB	98490 TAATAATTTGTTGAACCTTTTAAAAAGGTGGGAATC 98454

RESULT 10
AAL36824/c
ID AAL36824 standard; DNA; 7739 BP.
XX
XX AAL36824;
AC
XX 08-JAN-2002 (first entry)
DT
XX
XX Human musculoskeletal system related polynucleotide SEQ ID NO 3189.
DE
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antinflammatory; anticancer;
KW vulnery; anticonvulsant; antibacterial;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ds.
XX musculoskeletal system; ds.
OS Homo sapiens.
XX
XX WO200155367-A1.
XX
XX 02-AUG-2001.
PD
XX
XX 17-JUN-2001; 2001WO-US001338.
PF
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
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PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235634P.
PR 27-SEP-2000; 2000US-0235636P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
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PR 08-NOV-2000; 2000US-0244647P.
PR 08-NOV-2000; 2000US-02446475P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.

02-0CT-2000; 2000US-0237037P.
PR 02-0CT-2000; 2000US-0237038P.
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PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;
WPI; 2003-128199/12.

Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.

Disclouseure; SEQ ID NO 3189; 321pp; English.

The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animal or humans. The nucleic acid stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since RGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; increases tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells; besides, haematopoietic lineage, modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammalian state or physical state by influencing biorhythms, cardiac rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This sequence encodes a novel human musculoskeletal system antigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at ftp://seqlata.uspto.gov/sequence.html?DocID=20020147140

Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;

Query Match 31.7%; Score 146.8; DB 8; Length 7739;
Best Local Similarity 77.5%; Pred. No. 46-26; Indels 6; Gaps 3;
Matches 217; Conservative 0; Mismatches 57;

2 CCTGTAATCCAGTACTGTGAGAGTCGCCAGGTCCAGACGCTTGAGCGCAGAGATTCA 61
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Db 5631 CCTATTAATCCAACTTTGGAGGCCAGAGTGGGAGAGATGCTTGATCCAGTAGTCCA 557Z
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62 AGAGGAGCCTTGAGCAACACAGGAGA-CCTGTCACTTACAAGAAATAATTAATTAGCCAG 120

Db	5511	AGACGACGCTGGGCAACATATAGGGAGACCTTGACTCTCAATAATATTTAAAAATTCGCTGG	5512
Oy	121	GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTTAGGAGGCAGAAATGAGA----	CTGCT 176
Db	5511	GTGTAGTGGCAACATACCTGTGTCTCCAGCTAGTTGGAGGCCGAGGAGGATCGCTT	5452
Oy	177	TGTCCCGAGGAGGTCAACACTGCACTGAGCTGAGACCAGGCACCTGCATTCAGCTGGG	236
Db	5451	GAGCCCGAGAGGTAAAGAGCTGCATATGAGCTGCATCTTGGCA-CTGCATCTCAGCTGGG	5393
Oy	237	CAACAAAAAGAGACCTGTCTCAAAAAATGATTAAATAA	276
Db	5392	CAACGACTGAGACCTGTCTCAAAAAACAAAAA	5353
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ID	ADJ30562/c		
XX	ADJ30562 standard; DNA; 7739 BP.		
AC	ADJ30562;		
DT	20-MAY-2004 (first entry)		
XX	Human musculoskeletal system-associated genomic DNA - SEQ ID 3189.		
DE	musculoskeletal system; cytoskeletal; osteopathic; cancer; osteoporosis;		
XX	gene therapy; vaccine; human; ds.		
KM	Homo sapiens.		
XX	US2004009488-A1.		
PN	15-JAN-2004.		
XX	13-SEP-2002; 2002US-00242515.		
XX	31-JAN-2000; 2000US-0179066P.		
PR	04-FEB-2000; 2000US-0180628P.		
PR	24-FEB-2000; 2000US-0184664P.		
PR	02-MAR-2000; 2000US-0186350P.		
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Ruben SM, Barash SC;
XX WPI, 2004-090458/09.
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX
XX Disclosure; SEQ ID NO 3189; 289pp; English.
PS
XX
XX The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytoskeletal and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated genomic DNA of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC http://seqdata.uspto.gov/sequence.html?docID=20040009488.
XX
XX Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
SQ
Query Match 31.7%; Score 146.8; DB 12; Length 7739;
Best Local Similarity 77.5%; Pred. No. 4e-28;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;
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QY 121 GCTTAGTGCTATCCCTGTGTGTCAGCTACTAGGAGGAGAGAGTGA---CTGCT 176
Db 5511 GTGTAGTGCACTACTGTGTGTCAGCTAGTTGGAGGAGCCAGGAGGAGATCGCTT 5452
QY 177 TGTCCAGAGGTCAGAGCTGAGTGAAGTGAACCCAGGACCTGATTCAGCCCTGG 236
Db 5451 GAGCCAGAGGTCAGAGGCTGCAATGATGCAATCTTGCCA-CTGCACTCAGCCTGG 5393

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 ; Search time 3206.07 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_717

Perfect score: 463

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150.8	32.6	836	13	CZ458737 MCF746k19
2	146.8	31.7	1033	3	BM556801 AGNCOURT
3	146.4	31.6	315	1	AI961957 w40904.x
4	146.4	31.6	592	4	EX486310 DKFZP868B
5	145.2	31.4	554	11	AQ784105 HS_350_A
6	143.8	31.1	675	11	AQ313572 RPI11-10
7	143.6	31.0	444	11	AQ088791 HS_3002_A
8	143.6	31.0	721	8	CR773238 DKFZP470D
9	143.4	31.0	417	11	AQ215619 HS_3217_B
10	143.4	31.0	454	9	DB322788 DB322788
11	143.4	31.0	551	4	EX487140 DKFZP866G
12	142.8	30.8	2821	6	BC029972 Homo sapi
13	142.6	30.7	916	14	AG014790 Homo sapi
14	142.6	30.6	444	8	CR980253 CR980253
15	141.8	30.6	641	3	BE349022 ht48a11.x
16	141.8	30.6	641	3	BM555373 AGNCOURT
17	141.8	30.6	809	12	BZ603262 BZ603262
18	141.8	30.6	1792	6	CR602256 CR602256
19	141.8	30.6	1941	6	CR616604 CR616604

C 20	141.4	30.5	751	12	BZ606730	BZ606730 WHAAT71TR
C 21	141.2	30.5	483	10	W45205	W45205 zc24f10..x1
C 22	141.2	30.5	558	11	AQ480483	AQ480483 RPI1-11-2
C 23	141	30.5	408	7	BE138484	BE138484 x775h02.x
C 24	141	30.5	749	14	AG014791	AG014791 Homo sapi
C 25	141	30.5	1295	2	BG432839	BG432839 602496047
C 26	140.8	30.4	374	4	BX954311	BX954311 DKFZP781A
C 27	140.8	30.4	561	9	DB358919	DB358919 DB358919
C 28	140.8	30.4	4833	6	CR936701	CR936701 Homo sapi
C 29	140.6	30.4	400	11	AQ007744	AQ007744 CIT-HSP-2
C 30	140.2	30.3	589	9	DB382632	DB382632 DB382632
C 31	140.2	30.3	647	7	BB883545	BB883545 BB883545
C 32	140.2	30.3	750	14	AG015272	AG015272 Homo sapi
C 33	140.2	30.3	2149	6	CR936757	CR936757 Homo sapi
C 34	139.8	30.2	470	4	CD102612	CD102612 AGNCOURT
C 35	139.8	30.2	606	13	CZ465897	CZ465897 MCF75111
C 36	139.8	30.2	705	14	AG013775	AG013775 Homo sapi
C 37	139.8	30.2	723	14	DX360777	DX360777 MGOQ_CH25
C 38	139.6	30.2	547	9	DA315473	DA315473 DA315473
C 39	139.6	30.2	821	13	CZ449889	CZ449889 MCF730G23
C 40	139.4	30.1	721	9	DA571947	DA571947 DA571947
C 41	139.2	30.1	500	1	AL712995	AL712995 DKFZP686K
C 42	139.2	30.1	510	7	AW949355	AW949355 EST361425
C 43	139.2	30.1	556	3	BG64577	BG64577 C118n11.
C 44	139.2	30.1	564	7	BE300855	BE300855 ba77h08.x
C 45	139.2	30.1	624	7	AW945152	AW945152 EST361345

ALIGNMENTS

RESULT 1	CZ458737	836 bp	DNA	linear	GSS 20-OCT-2005
LOCUS	MCF746k19TF Human MCF7 breast cancer cell line library (MCF7_1)				
DEFINITION	Homo sapiens genomic clone MCF7_46k19, genomic survey sequence.				
ACCESSION	CZ458737				
VERSION	CZ458737.1	GI:77931089			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 836)				
AUTHORS	Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brehner,J.H., Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L., Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de Jong,P., Pezner,P., and Collins,C.				
TITLE	Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project				
JOURNAL	Unpublished (2005)				
COMMENT	Contact: Volik SV Colin Collins' lab UCSF Comprehensive Cancer Center UCSF Box 0808, San Francisco, CA 94143-0808, USA Tel: 415 502 7066 Fax: 415 502 5665 Email: svolik@cc.ucsf.edu This clone is available from Amplicon Express http://www.genomex.com Class: BAC ends.				
FEATURES	Location/Qualifiers				
SOURCE	1. 836 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="MCF7_46k19" /sex="female" /clone_id="Human MCF7 breast cancer cell line library (MCF7_1)" /note="Vector: pECBAC1, site_1: HindIII, This library was				

ORIGIN

constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

Query Match 32.6%; Score 150.8; DB 13; Length 836;
Best Local Similarity 73.7%; Pred. No. 1.7e-18;
Matches 233; Conservative 0; Mismatches 77; Indels 6; Gaps 3;

QY 1 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCAAGAGCACTGTGAGGCCAGGAGTTC 60
DB 158 ACCGTATATCCAGACATTTTGAGGCTGAGGAGAGGATCCCTTGAGTCCAGAGATT 217
QY 61 AAGAGAGCCTTGACACACAGAGGAGA-CCTGTCACTACAAAGATTAATTAATTAGCCA 119
DB 218 GAGACGAGCCTGTGACATAGGAGAGACCTGTCTCAGAGATTAATTAATTTAGCTG 277
QY 120 GAGTTAGTGGCTATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAGTAGA---CTGC 175
DB 278 GGCCTGTGTGACACCTGTGTGCCAGCTACTTGGAGAGCTGAAGCAGAGATCACT 337
QY 176 TTGTCCAGAGAGTCAAGTCACTGAGTGAAGCCAGCCAGCTGCATTCAGAGCTGG 235
DB 338 TGAACCGAGAGGTGAGGCTGACAGTGAAGCCGAGATTGCCCA-CTACACTCCAGCTGG 396
QY 236 GCAACAAAAGAGACCTGTCTCAAAAATTAATTAAATTAATTAATTAATTAATAGTT 295
DB 397 GTGACGAGAGTGAACCTGTCTCAAAAAGAGAGAGAGATTAATTAATTAATTAATTAAGT 456
QY 296 TAAACCTTAACACAT 311
DB 457 CAACCTTAATTCAT 472

RESULT 2
BM556801/c 1033 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6540722 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737964
DEFINITION 5', mRNA sequence.

ACCESSION BM556801.1 GI:18798321
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1033)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: L1AM12748 row: 0 column: 21
High quality sequence stop: 606.

FEATURES

Source

1. 1033
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737964"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT5;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;

ORIGIN

oligo-dt primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

Query Match 31.7%; Score 146.8; DB 3; Length 1033;
Best Local Similarity 77.5%; Pred. No. 9.1e-18;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;

QY 2 CCTGTAAATCCAGTACTGTGAGAGTCCGAGTCAAGAGCACTGTGAGGCCAGGAGTTCA 61
DB 316 CCTATTAATCCCAACTTTTGGAGGCCGAGGTGGAGATGCTTAAGTCCAGTATTCA 257
QY 62 AGAGCAGCCTTGACACACAGGAGA-CCTGTCACTACAAAGATTAATTAATTAGCCAG 120
DB 256 AGACGAGCCTGGGCAATAGGAGAGACCTGACTTACAAATTAATTAATTTCCCTGG 197
QY 121 GCTTAATGCTATCCCTGTGTGCTCCAGCTACTAGGAGGAGAGAGTAGA---CTGCT 176
DB 196 GTGTAGTGGACATACCTGTGTGCCAGCTAGTTGGAGAGCCGAGGAGAGAGTGCCTT 137
QY 177 TTGTCCAGAGAGTCAAGTCACTGAGTGAAGCCAGCCAGCTGCATTCAGAGCTGG 236
DB 136 GAGCCAGAGAGTCAAGCTGCATAGCTGCATTTGCCA-CTGCATCCAGCTGG 78
QY 237 CAACAAAAGAGACCTGTCTCAAAAATTAATTAAATTA 276
DB 77 CAACAGCCGAGACCTGTCTCAAAAACAAAACAAA 38

RESULT 3
A1961957/c 315 bp mRNA linear EST 09-MAR-2000
LOCUS w40g04.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2509974 3'
DEFINITION similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION A1961957.1 GI:5754659
VERSION A1961957.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 315)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bdrp/image/image.html
Insert length: 1397 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 314.

FEATURES

Source

1. 315
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2509974"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_id="NCI-CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT5; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN

Query Match 31.6%; Score 146.4; DB 1; Length 315;
Best Local Similarity 74.6%; Pred. No. 1.4e-17;
Matches 212; Conservative 0; Mismatches 66; Indels 6; Gaps 2;

Qy	2	CCTGTAATTCAGTACTGTGAGAGTCCAGGTCAGAGACTGCTTGAGGCCAGAGATTCA	61
Db	284	CCTGTAATCCCATCCTTTGGGAGGCCAGGCGAAGAAGATTGCTTGAATCCAGAGATTG	225
Qy	62	AGAGCAGCCTGCGACAACACAGGAGACC--TGTCATTACAAAGAATTAATTAATGACC	118
Db	224	AGACTAGCCTGGGCAACATAGTAGAGCACTCTCTACAAAATAATGAACAAATTTAGCC	165
Qy	119	AGGCTTAATGTCATTCCTGTGTGTCCAGACTACTAGGAGGACAGAAAT---AGACTGC	175
Db	164	GGGCTCTGTGTGTGCATGTGCTTAGTCCAGACTACTGGGGAAGCTGAGGTGGAGGATTC	105
Qy	176	TTGTGCCAGGAGGTCGAAGCTGAGTGAAGCTGAGGCCAGGCACCTGATTCAGGCTGG	235
Db	104	TGACCTCGGAGGTCTAAGAGCTGCAATGAGCTGAGATCATGCGCAATGTGACTTCGACCTAA	45
Qy	236	GCAACAAATAAGACCCGTCTCAAAAATAATGAATTAATAATA	279
Db	44	GCGACAGGCAAGACCCGTCTCAAAAAAAAAAAAAAAAAAAAAA	1

RESULT 4	LOCUS	DEFINITION
BX486310/c	BX486310	592 bp mRNA linear EST 04-SEP-2003
	DKFZp668B08251_r1 686 (synonym: h1cc3)	Homo sapiens CDNA clone
	DKFZp668B08251_5', mRNA sequence.	

ACCESSION	BX486310
VERSION	BX486310.1
KEYWORDS	GI:31949871
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
Ansoerje, W., Krieger, S., Regiert, T., Rittmeller, C., Schwager, B.,
Hominidae, Homo
1 (bases 1 to 592)
Mammalia: Eutheria; Euarchontoglires; Primates; Catarrhini;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amniota; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE	JOURNAL	COMMENT
Meeus, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.	EST (Ansooge, W., Krieger, S., Regiert, T., Rittmeller, C., et al.)	Unpublished (2003)
Contact: MIPS		

Ingolstaedter Landstr.1, D-85764 Neuburg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysts, German Cancer
Research Center (DKFZ): Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.

This clone (DKFZp686B08251) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.

FEATURES	Location/Qualifiers
source	1. .592

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686B08251"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="686 (synonym: hlec3)"
/note="Vector: pTritipleX2; Site_1: SfiIA, Site_2: SfiIB
cDNA-collection"

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ORIGIN			
Query Match	31.6%	Score 146.4;	DB 4; Length 592;
Best Local Similarity	74.3%;	Pred. No. 1.2e-17;	
Matches 211; Conservative	0;	Mismatches 71;	Indels 2; Gaps 2;

QY	1	ACCTGAATATCCAGTACTGTGAGAGTCCAGAGTCAAGAGCTCTTGAGGCTCAGAGATTCC	60
Db	287	ACCTGAATATCCAGCACTTTGGGAGGCTAAGCAGAGTGAATCACTTGAATCCAGAGATTCC	22
QY	61	AAGACGAGCTTGGACAAACAAGGGAGACCT-GTCACTACAAAGATTAATTAATTAGCCA	113
Db	227	GAGACGAGCTTGGGACAACATAGTGAACCTCATCTCTTACAAAAAATAACAAAAATTAGCCA	168
QY	120	GACCTAGTGGCTCATCCCTGTGTGCTCCACACTACTAGGAGGACGAAGTAGAGACTGTGT	178
Db	167	GCTGTGTGTGGCAGTATGCTGTAGTTTACTACTACCTGGAGACTCAGTGGATCACTTGAG	108
QY	180	CCGACGAGGTCAAGACTGAGCTGAGACCCACCACTTGCATTTCCAGCTTGGCCAA	233
Db	107	CCCGGAGAGGAGAGGTTCAGTGAAGCTGGAATGTACCA-CTGCACCTCCACGCTGGCCAA	49
QY	240	CAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATA	283
Db	48	CAGAGTGAGACCTCTTCTCAAAAGAAAAAATTAATTAATTAATA	5

LOCUS	DEFINITION	554 bp	DNA	linear	GSS 03-AUG-1999
AQ784105	HS 3250 A2 H10 T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3250 Col=20 Row=0, genomic survey sequence.				

ACCESSION	AQ784105
VERSION	AQ784105.1
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
Mahaffay, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
1 (bases 1 to 554)
Hominidae: Homo.
Mammalia: Eutheria: Euarchontoglires; Primates, Catarrhini;
Eucaryota: Metazoa: Chordata: Vertebrata: Euteleostomi;
Hominidae: Homo.

TITLE
JOURNAL
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.

PUBLISHED 10/4/93/64
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com)
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 3250 row: O column: 20
Seq primer: T7
Class: BAC ends
High quality sequence: 554.

FEATURES	Location/Qualifiers
source	1. .554

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate:3250 Col:20 Row:0"
/sex="male"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
B-Coli DH10B"

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ORIGIN			
Query Match	31.4%	Score 145.2; DB 11;	Length 554;
Best Local Similarity	74.3%	Pred. No. 2.1e-17;	
Matches 211; Conservative	0;	Mismatches 68;	Indels 5; Gaps 2;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCAGAGTCAGAGAGCTGCTTGAGGCCAGAGTTCA 61
| | | | |
DB 140 CCTATATATCTAGACATTGGAGAGCCAGAGTGGGCGATTACTTGAAGTCAGAGATTCA 199
| | | | |
QY 62 AAGAGCAGCTTGACACACAGGAGACCTGTCTACAAAGAAATTAATTAATTAAGCCAG 121
| | | | |
DB 200 AAGACGAGCTGGGCAATATGTTAAACCTGTCTCTCTAAATAATACAAAATTCAGACAG 259
| | | | |
QY 122 CTATAGTGGCTCATCCCTGTGTGTCCAGACTACTAGAGGAGGAGAGTGTCTGT-- 179
| | | | |
DB 260 TGTGTGTGGCAGATGCTGTATCTCCAGCTACTCAGAGAGGCTGAGCAGAGAAATTTGTTG 319
| | | | |
QY 180 --CCAGAGAGTCAAGACTGCACTGAGCTGAGACCCAGCCACTTCAGCTTGAGG 237
| | | | |
DB 320 AACCCAGAGAGTTGAGAGGCTGCAATGAGCTGAGATTGTGCGCA-CTGACATCCAGCTGGGT 378
| | | | |
QY 238 AACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATAA 281
| | | | |
DB 379 GATTAAGCGAGACCTGTCTCAAAAAATTAATTAATTAATAA 422
| | | | |

RESULT 6
AQ313572/c 675 bp DNA linear GSS 04-MAY-1999
LOCUS RPCI11-101F17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-101F17,
DEFINITION genomic survey sequence.
ACCESSION AQ313572
VERSION AQ313572.1 GI:4045035
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 675)
Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
COMMENT Other GSSs: RPCI11-101F17.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@delong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..675
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7538536"
/db_xref="taxon:9606"
/clone="RPCI-11-101F17"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN

Query Match 31.1%; Score 143.8; DB 11; Length 675;
Best Local Similarity 69.8%; Pred. No. 3.7e-17;
Matches 238; Conservative 0; Mismatches 97; Indels 6; Gaps 3;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCAGAGTCAGAGAGCTGCTTGAGGCCAGAGTTTC 60
| | | | |
DB 444 ACCTGTAATTCAGTACTGTGAGAGTCCAGAGTGGGCGATTACTTGAAGTCAGAGATTCA 385
| | | | |
QY 61 AAGAGCAGCTTGACACACAGGAGACCTGTCTACAAAGAAATTAATTAATTAAGCCAG 119
| | | | |
DB 384 AAGATAGAGCTGGGCAACATGTTAAACCTGTCTCTCTAAATAATACAAAATTAAGCCA 325
| | | | |
QY 120 GCTTATAGTGGCTCATCCCTGTGTGTCCAGACTACTAGAGGAGGAGAGTGTCTGT--CTGC 175
| | | | |
DB 324 GCGATGTGTGGCAGATGCTGTATCTCCAGCTACTTGGAGGTGAGAGCAGAGAAATTCACC 265
| | | | |
QY 176 TGTCCAGAGAGTCAAGACTGCACTGAGCTGAGACCCAGCCACTTCAGCTTGAGG 235
| | | | |
DB 264 TGAATTCAGAGAGCGAGGCTGCACTGAGACCAAGATCGTGCA-CTGCACTCCAGCTGG 206
| | | | |
QY 236 GCAACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATGTT 295
| | | | |
DB 205 GTGACAAAGTGAAGATTCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 146
| | | | |
QY 296 TAAACCTTAAGACATCTTCTTTTCAAGAGAGACTTCTTA 336
| | | | |
DB 145 CTATACCTTTCTTCACTTACTTGGAGATGATCCATATTA 105
| | | | |

RESULT 7
AQ088791/c 444 bp DNA linear GSS 26-AUG-1998
LOCUS HS_3002.AI.P05.MP.CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone plate=3002 Col=9 Row=K, genomic survey
sequence.
ACCESSION AQ088791
VERSION AQ088791.1 GI:3457702
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 444)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,T., Young,T., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence tagged Connector
Plate: 3002 row: K column: 9
Class: BAC ends
High quality sequence stop: 444.

FEATURES
source

Location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3002 Col=9 Row=K"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: Sperm; Vector: pBeloBAC11; BAC clones in
E-Coli DH10B"

ORIGIN

Query Match 31.0%; Score 143.6; DB 11; Length 444;
Best Local Similarity 70.3%; Pred. No. 4.3e-17;
Matches 222; Conservative 0; Mismatches 89; Indels 5; Gaps 2;

[illegible]

	Best Local Similarity	71.9%; Matches 230;	Pred. No.	3.9e-17; Conservative 0;	Mismatches 84;	Indels 6;	Gaps 3;
OY	2	CCTGTAAATTCAGTACTGTTAGAGACGCCAGACTCAGAGAGACTGGTTAGAGCCAGAGATTCA	61				
Dd	95	CCGTACTCCAGACAATTGGGAGGCCAAGAAGTAATCACCTTGAGGTGAGAGATTCA	154				
OY	62	AGAGCACCCTTGAGCAACACAGAGGAGA-CCTGTCACTCAAAAGATAATTAATTAGGCAG	120				
Dd	155	AGAGTAGCCTTGCGCCAATGGTGAAGACCTGCTCTTAATAAATAAAAATTAGGCAG	214				
OY	121	GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGCAAGTAGA----CTGCT	176				
Dd	215	GCATGTGTGGGTGACACTGTGTAGTCCCAGCTAATTGGGAGGCTGAGGCAAGGAATCACTT	274				
OY	177	TGTCCAGAGAGGTCAACAGCTGCAGTGAAGTGAGACCCAGCACCTGCATTCCAGCCTGAG	236				
Dd	275	AATCCCGGGGGCCGABGTGCBAATGACTGAGACTCCGCA-CTGCATCTGCAGCTCGAG	333				
OY	237	CAACAAAAAGAGACCCTGTCTCAAAAAAAAAATTAATTAAATATATAAAAAATAGTTT	296				
Dd	334	CAACAGAGTGAAGACTCAGTCTCAAAAAAAAAAAAAAAAAAAGATTAACAGAAAAATATATA	393				
OY	297	AAACCCCTAACACATCTTCT	316				
Dd	394	AAAGATATTAATAATTTTTTT	413				

RESULT 9	417 bp	DNA	linear	GSS 19-1998
LOCUS	AO215619/c			
DEFINITION	AO215619			
	HS_3217_B2_A01_MR_CIT	Approved Human Genomic Sperm Library D Homo sapiens genomic clone	Plate=3217 Col=2 Row=B,	genomic survey
ACCESSION	AO215619			
VERSION	AO215619.1			
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae; Homo.			
REFERENCE	1 (bases 1 to 417)			
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shakeri,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.			
	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	96 (17),	9739-9744	(1999)
PUBMED	10449764			
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L			
	High Throughput Sequencing Center			
	University of Washington			
	401 Queen Anne Avenue North, Seattle, WA 98109, USA			
	Tel: (206) 616-3618			
	Fax: (206) 616-3887			
	Email: jwallace@u.washington.edu			
	Sequence Tagged Connector			
	Plate: 3217 row: B column: 2			
	Class: BAC ends			
	High quality sequence stop: 417.			
FEATURES	Location/Qualifiers			
source	1..417			
	/organism="Homo sapiens"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:9606"			
	/clone="Plate=3217 Col=2 Row=B"			
	/sex="male"			
	/clone_1lb="CIT Approved Human Genomic Sperm Library D"			
	/note="Organ: sperm; Vector: pBeloBAC11, BAC clones in E-Coli DH10B"			
ORIGIN				

Query Match 31.0%; Score 143.4; DB 11; Length 417;
Best Local Similarity 74.0%; Pred. No. 4,8e-17;
Matches 208; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

QY 2 CCTGTAATTCACACTGAGAGTCCAGAGTCAGAGAGCTGCTAGAGCCAGAGTTCA 61
DB 413 CCTATATCCCACTACTCTTATATAGTGAAGCCGAGTGCACCTTGAAGTCAGAGTTG 354
QY 62 AGAGCAGCCTGAGCAACACAGAGAGACT-GTCACTACAAAGATTAATTAATTAAGCCAG 120
DB 353 AGACCAAGCTAGCTAATCATGTGTAAACCTCATCTCTACTAATAAATTCAAATTAACAG 294
QY 121 GCTTAAGTGTCTATCCCTGTGTCCAGCTACTAGGAGGCAAGATAGAGCTGCTTGT 180
DB 293 GTGTGTGTGGACATGTCTGTAGTCCAGCTGTGTGGAGAGCTGAGGCAAGATAGCTTGA 234
QY 181 CCGAGAGGTCAACACTGAGAGTGAAGCCAGCAGCTGATTCAGCTGGGAGAC 240
DB 233 CCGGGGGGCAAAAGGCTGAGAGTGAAGTGTGCCA-CTGCACTCCAAAGCTGGGGGAC 175
QY 241 AAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATAA 281
DB 174 AGAAAGAGACTGTCTCAAAAAATTAATTAATTAATAA 134

RESULT 10
DB322788/c 454 bp mRNA linear EST 04-DEC-2005
LOCUS DB322788 NT2NE2 Homo sapiens cDNA clone NT2NE2000864 3', mRNA
DEFINITION DB322788 NT2NE2 Homo sapiens cDNA clone NT2NE2000864 3', mRNA
sequence.
VERSION DB322788
KEYWORDS DB322788.1 GI:83261293
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 454)
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsutitani, K., Makaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
Toneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
Miyakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isega, T., and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
JOURNAL PUBMED
COMMENT Contact: Takao Isegai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
1..454
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2NE2000864"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_id="NT2NE2"
/note="Vector: pME18SFLJ3; mRNA from NT2 neuron after the

ORIGIN differentiation of NT2 neuronal precursor cells"

Query Match 31.0%; Score 143.4; DB 9; Length 454;
Best Local Similarity 73.4%; Pred. No. 4,7e-17;
Matches 212; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 CCTGTAATTCACACTGAGAGTCCAGAGTCAGAGAGCTGCTAGAGCCAGAGTTCA 61
DB 293 CCTGTAGTCCAGACACTTTTGGAGGCGAGGTGGGAGTGTGCTTGAAGTCAGAGTTTC 234
QY 62 AGAGCAGCCTGAGCAACACAGAGAGGAG-CCGTGACTACAAAGATTAATTAATTAAGCCAG 120
DB 233 AGAGCAGCCTGAGCAACAGTGAACCCGTGTCTACTAATAAATTCAAATTAAGCCAG 174
QY 121 GCTTAAGTGTCTATCCCTGTGTCCAGCTACTAGGAGGAGAGATAGGA-----CTGC 175
DB 173 GCATGTGTGGCGACAGCGCTGTGTGTTACGTAACCTGAGAGCTGAGCAAGAAATTCCT 114
QY 176 TTGTCCAGAGAGGTCAAGACTGAGTGAAGCCAGCCAGCTGCACTTCAGCCTGG 235
DB 113 TGAGCCTGGAGGTGAGAGGCTGAGTGGGCAAGATGTATCCCACTGCACTTCAGCCTGG 54
QY 236 GCAACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATAA 284
DB 53 GCAACAGAGCAAGACTGTCTCAAAAAATTAATTAATTAATAA 5

RESULT 11
BX487140/c 551 bp mRNA linear EST 04-SEP-2003
LOCUS BX487140
DEFINITION BX487140 DKFZp686G22255 r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
DKFZp686G22255 5', mRNA sequence.
VERSION BX487140
KEYWORDS BX487140.1 GI:31951470
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 551)
Behr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Oesinger, A.,
Fodor, G., Han, M., and Wiemann, S.
EST (Behr, A., Lauber, J., Mewes, H.W., Weill, B., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Olagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686G22255) is available at the RZPD in Berlin.
Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..551
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686G22255"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="686 (synonym: h1cc3)"
/note="Vector: pT7p18x2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 31.0%; Score 143.4; DB 4; Length 551;
Best Local Similarity 72.4%; Pred. No. 4,5e-17;

Matches 228; Conservative 0; Mismatches 81; Indels 6; Gaps 3;

QY 1 ACCGTAAATCCAGTACTGTGAGAGTCCGAGAGCTGCTTGAAGCCAGAGCTTC 60
|||||
Db 325 ACCGTAAATCCAGTACTGTGAGAGTCCGAGAGCTGCTTGAAGCCAGAGCTTC 266

QY 61 AAGAGCAGCTTGAACACACAGGAGAGCT-GTCACTACAAAGATAATTAATTAACCA 119
|||||
Db 265 AAGAGCAGCTTGAACACACAGGAGAGCTGCTTGAAGCCAGAGCTTC 206

QY 120 GCGTAAATGCTCACTCCCTGTGTCCCAAGCTTACAGGAGGAGAGTGAAGTGA 175
|||||
Db 205 GGCACAGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 146

QY 176 TTGTCCAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 235
|||||
Db 145 TGAACCCAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 87

QY 236 GCAACAAAGAGAGAGCTGCTCAAAAAATTAATTAATTAATTAATTAATTAAT 295
|||||
Db 86 GTAAACAGAGTGAAGCTGTGTGCAAAAAATTAATTAATTAATTAATTAATTA 27

QY 296 TAAACCTTAACACA 310
|||||
Db 26 GAAAAATTAATAATA 12

RESULT 12
BC029972 2821 bp mRNA linear HTC 28-JUN-2005
LOCUS
DEFINITION
Homo sapiens clusterin (complement lysin inhibitor, SP-40/40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J), mRNA (cdna clone IMAGE:4939961).
BC029972
2821 bp mRNA linear HTC 28-JUN-2005
LOCUS
DEFINITION
Homo sapiens (human)
HTC
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homidae; Homo.
1 (bases 1 to 2821)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Tishiyuki, S., Abramson, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulhany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.D., Malek, U.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Viallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, U., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 2821)

CONSTRM
TITLE
JOURNAL
AUTHORS
PUBMED
REFERENCE
REMARK
COMMENT

NIH MGC Project
Direct Submission
Submitted (06-May-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk

Email: cgabs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louis, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nannavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Series: IRAC Plate: 42 Row: h Column: 7
This clone has the following problem: no 5' EST match.

FEATURES
Location/Qualifiers
1. 2821
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4939961"
/tissue_type="Brain, anaplastic oligodendroglioma with 1p/19q loss"
/clone_id="NCI CGAP_Brn67"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6"

ORIGIN
Query Match 30.8%; Score 142.8; DB 6; Length 2821;
Best Local Similarity 71.4%; Pred. No. 4.3e-17;
Matches 230; Conservative 0; Mismatches 87; Indels 5; Gaps 3;

QY 2 CTTGTAATCCAGTACTGTGAGAGTCCGAGAGCTGCTTGAAGCCAGAGCTTC 61
|||||
Db 1686 CTTGTAATCCAGTACTGTGAGAGTCCGAGAGCTGCTTGAAGCCAGAGCTTC 1745

QY 62 AGAGCAGCTTGAACACACAGGAGAGCTGCTCAAAAGATAATTAATTAATTAAT 120
|||||
Db 1746 AGAGCAGCTTGAACACACAGGAGAGCTGCTCAAAAGATAATTAATTAATTA 1805

QY 121 GCTTAATGCTCACTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 177
|||||
Db 1806 GCTTAATGCTCACTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1865

QY 178 GTCCAGAGAGTCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 237
|||||
Db 1866 GTCCAGAGAGTCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1924

QY 238 AACCAAAAGAGCTGCTCAAAAAATTAATTAATTAATTAATTAATTAATTAAT 297
|||||
Db 1925 AACCAAAAGAGCTGCTCAAAAAATTAATTAATTAATTAATTAATTAATTAAT 1984

QY 298 AACCTTAACACATCTCTTTT 319
|||||
Db 1985 AACCTTAACACATCTCTTTT 2006

RESULT 13
AG014790 746 bp DNA linear GSS 16-FEB-2005
LOCUS
DEFINITION
Homo sapiens genomic DNA, 21q region, clone: 762015N19, genomic survey sequence.
AG014790 AG006505
VERSION
AG014790.1 GI:3650008
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homidae; Homo.
1

REFERENCE
1

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE 2 (bases 1 to 746)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (23-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences Center, RIKEN Yokohama Institute, Yokohama Research Promotion Division, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@sc.riken.jp, Tel:81-45-503-9111, Fax:81-45-503-9113)
COMMENT On Feb 6, 1999, this sequence version replaced gi:2992383.
FEATURES
source Ag006505; Submitted (27-Mar-1998).
Location/Qualifiers
1..746
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="762015N19"
ORIGIN
Query Match 30.8%; Score 142.6; DB 14; Length 746;
Best Local Similarity 73.8%; Pred. No. 6.1e-17;
Matches 220; Conservative 0; Mismatches 72; Indels 6; Gaps 3;
QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGAGTCAAGAGTCTGAGCCAGAGTTCA 61
DB 44 CCGTAATTCAGTACTGTGAGAGTCCGAGAGTCAAGAGTCTGAGCCAGAGTTCC 103
QY 62 AGAGCAGCTTGAGCAACACAGGAGA-CCTGTCACTACAAAGATTAATTAATTAAGCCAG 120
DB 104 AGACAGCCTTGAGCAACACAGGAGA-CCTGTCACTACAAAGATTAATTAATTAAGCCAG 163
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGAGGACAGAGTACAGTCTGT- 179
DB 164 GCATTAATGACATGCTGTGATCTCAGCTACTGAGGAGAGCTGAGGTGAGAGGCTTCTT 223
QY 180 ---CCGAGAGGTCAAGACTGAGTGAAGACCCAGCCACTGATTCAGAGCTGG 236
DB 224 GAGCCAGAGGAGGAGGAGGAGTGCAGTGAAGTCAAGCCCA-CTGATCTCAGAGCTGG 282
QY 237 CAACAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAAGT 294
DB 283 TGACAGAGCCAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAAGTACAGT 340
RESULT 14
CR980253 916 bp mRNA linear EST 24-JUN-2005
LOCUS CR980253 RZPD no.9017 Homo sapiens cDNA clone RZPDp9017H083 5',
DEFINITION mRNA sequence.
ACCESSION CR980253
VERSION CR980253.1 GI:68218587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Hell,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
and Korn,B.
TITLE Human T-lymphocytes library
JOURNAL Unpublished (2005)
COMMENT Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: RZPDp9017H083.
RZPDLIB: (Human T-lymphocytes) RZPD LIB No. 9017
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:

Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPDp9017H083
contact RZPD (product-support@rzpd.de) for further information.
Primer name: q93.4, Primer sequence: CGGATACCAATTCACACAG.
FEATURES
source 1..916
Location/Qualifiers
1..916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPDp9017H083"
/issue_type="T-lymphocytes"
/dev_stage="adult"
/lab_host="DH10B"
/lab_lib="RZPD no. 9017"
/note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
NotI; Vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned.pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-lymphocytes with a NotI-oligo(dT) primer [5'
GACTAGTTCAGATCGGAGCGGCCCTTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to SalI adaptor,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN_cloned vector"
ORIGIN
Query Match 30.7%; Score 142; DB 8; Length 916;
Best Local Similarity 70.7%; Pred. No. 7.6e-17;
Matches 232; Conservative 0; Mismatches 90; Indels 6; Gaps 3;
QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGAGTCAAGAGTCTGAGCCAGAGTTCA 61
DB 671 CCGTAATTCAGTACTGTGAGAGTCCGAGAGTCAAGAGTCTGAGCCAGAGTTCA 612
QY 62 AGAGCAGCTTGAGCAACACAGGAGACCT-GTCACTACAAAGATTAATTAATTAAGCCAG 120
DB 611 AGACAGCCTTGAGCAACACAGGAGACCT-GTCACTACAAAGATTAATTAATTAAGCCAG 552
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGAGGACAGAGTACAGTCTGT- 176
DB 551 GCATGAGGACATGCTGTGATCCAGCTGCTCGGAGAGCTGAAGTAAAGATCACTT 492
QY 177 TGTCACAGAGTCAAGACTGAGTGAAGACCCAGCCACTGATTCAGAGCTGG 236
DB 491 GAAACCCAGAGGAGGAGGAGTGCAGTGAAGTCAAGGCCA-CTGCACTCCAGAGCTGG 433
QY 237 CAACAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAAGTT 296
DB 432 CGACAGAGTGAAGCCCATCTCAAAACAAATTAATTAATTAATTAATTAATTAAGTT 373
QY 297 AAACCTTAACACATCTCTTTTCAAA 324
DB 372 ATACAAACAGAGTCTTCTGCTTAA 345
RESULT 15
BE349022 444 bp mRNA linear EST 18-JUN-2000
LOCUS BE349022
DEFINITION ht48a11.x1 NCI CGAP Mel15 Homo sapiens cDNA clone IMAGE:314948 3',
similar to contains Alu repetitive element; contains element MER35
repetitive element ;, mRNA sequence.
ACCESSION BE349022
VERSION BE349022.1 GI:9260875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
1 (bases 1 to 444)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 414.
Location/Qualifiers

FEATURES

source
1..444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3149948"
/tissue_type="malignant melanoma, metastatic to lymph
node"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mel15"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
library constructed by Life Technologies."

ORIGIN

Query Match 30.6%; Score 141.8; DB 7; Length 444;
Best Local Similarity 74.6%; Pred. No. 9.5e-17;
Matches 220; Conservative 0; Mismatches 67; Indels 8; Gaps 3;
QY 1 ACCTGTAATTCAGTACCTGAGAGTCGAGAGTCAAGAGACTGCTTGAGGCCAGAGATTTC 60
DB 129 ACCTGTAATTCAGTACCTGAGAGTCGAGAGTCAAGAGACTGCTTGAGGCCAGAGATTTC 188
QY 61 AAGAGCAGCCTGAGCAACACAGAGAGA-CCTGTCACTACAAAGAATAATAATTAGCCA 119
DB 189 GAGACCAACCTGGGCAACAGAGCGAGATCCATCACTACAAATAATTCAAAAAATTAGCCA 248
QY 120 GGCTTAGTGGCTCATTCCTGTGTGCCAGCTACTAGGGAGGCAGAGTAGGA---CTGC 175
DB 249 GGCATGTGTGGTGCACACTTGTAGTCCAGCTACTCAGGAGGCTGAGGTGGAGAAATTGCT 308
QY 176 TTGTCCAGAGAGTCAAGAGCTGAGAGTGAAGCCAGCCACTGCATTCCAGCCTGG 235
DB 309 TGGGCCCAAGAAATCAAGGCTAGAGTAGAGCCGTATC--ACCAAGTCACTTAGCCTGG 365
QY 236 GCAACAAAAAGAGACCTGTCTCAAAAAAATAAGTTAAATAATAATAATAAAAA 290
DB 366 GCAACAGAGAAAGACCTGTCTCAAAAAAATAAGTTAAATAATAATAATAAAAA 420

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Job time : 3207.07 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:58:22 ; Search time 118.608 Seconds
(without alignments)
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Title: US-09-869-098A-1_COPY_255_717

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	461.4	99.7	11808	US-09-949-016-15281	Sequence 15281, A
2	461.4	99.7	39754	US-09-949-016-14689	Sequence 14689, A
3	153.4	33.1	601	US-09-949-016-165996	Sequence 165996, A
4	152.2	32.9	61461	US-09-949-016-16419	Sequence 16419, A
5	149.6	32.3	126237	US-09-949-016-16674	Sequence 16674, A
6	149.6	32.3	126237	US-09-949-016-16675	Sequence 16675, A
7	149.4	32.3	13023	US-09-949-016-16292	Sequence 16292, A
8	149.4	32.3	63783	US-09-949-016-13576	Sequence 13576, A
9	149	32.2	601	US-09-949-016-6338	Sequence 6338, A
10	148.4	32.1	29171	US-09-949-016-12283	Sequence 12283, A
11	148.4	32.1	29171	US-09-949-016-13509	Sequence 13509, A
12	147.2	31.8	601	US-09-949-016-28523	Sequence 28523, A
13	147.2	31.8	601	US-09-949-016-60956	Sequence 60956, A
14	147.2	31.8	99370	US-09-949-016-12816	Sequence 12816, A
15	146.8	31.7	601	US-09-949-016-17540	Sequence 17540, A
16	146.8	31.7	601	US-09-949-016-17561	Sequence 17561, A
17	146.8	31.7	35493	US-09-949-016-16780	Sequence 16780, A
18	146.6	31.7	24221	US-09-949-016-14964	Sequence 14964, A
19	146	31.5	119981	US-09-949-016-11884	Sequence 11884, A
20	146	31.5	119982	US-09-949-016-13606	Sequence 13606, A
21	144.6	31.2	93778	US-09-949-016-15096	Sequence 15096, A
22	144.6	31.2	131254	US-09-949-016-13734	Sequence 13734, A
23	144.4	31.2	601	US-09-949-016-56159	Sequence 56159, A

ALIGNMENTS

24	144.2	31.1	16230	US-09-949-016-14788	Sequence 14788, A
25	144.2	31.1	17607	US-09-949-016-15968	Sequence 15968, A
26	143.8	31.1	601	US-09-949-016-150302	Sequence 150302, A
27	143.8	31.1	39601	US-09-949-016-16045	Sequence 16045, A
28	143.6	31.0	18508	US-09-949-016-13883	Sequence 13883, A
29	143.6	31.0	157032	US-09-949-016-16502	Sequence 16502, A
30	143.2	30.9	601	US-09-949-016-71235	Sequence 71235, A
31	143.2	30.9	601	US-09-949-016-71236	Sequence 71236, A
32	143.2	30.9	40641	US-09-949-016-13376	Sequence 13376, A
33	143.2	30.9	55130	US-09-949-016-11890	Sequence 11890, A
34	143	30.9	30820	US-09-949-016-17145	Sequence 17145, A
35	143	30.9	58821	US-09-949-016-15897	Sequence 15897, A
36	143	30.9	58824	US-09-949-016-12615	Sequence 12615, A
37	142.8	30.8	8133	US-09-659-791A-10	Sequence 10, Appl
38	142.8	30.8	17348	US-09-949-016-17403	Sequence 17403, A
39	142.4	30.8	601	US-09-949-016-162454	Sequence 162454, A
40	142.4	30.8	57605	US-09-949-016-13259	Sequence 13259, A
41	142.4	30.8	68702	US-09-949-016-13638	Sequence 13638, A
42	142.2	30.7	93894	US-09-949-016-13629	Sequence 13629, A
43	141.8	30.6	15222	US-09-949-016-11916	Sequence 11916, A
44	141.8	30.6	15223	US-09-949-016-16912	Sequence 16912, A
45	141.8	30.6	44971	US-09-949-016-17049	Sequence 17049, A

RESULT 1	US-09-949-016-15281	Sequence 15281, Application US/09949016
1	Patent No. 6812339	GENERAL INFORMATION:
2	APPLICANT: VENTUR, J. Craig et al.	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
3	FILE REFERENCE: CL001307	CURRENT APPLICATION NUMBER: US/09/949,016
4	CURRENT FILING DATE: 2000-04-14	PRIOR APPLICATION NUMBER: 60/241,755
5	PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/237,768
6	PRIOR FILING DATE: 2000-10-03	PRIOR APPLICATION NUMBER: 60/231,498
7	PRIOR FILING DATE: 2000-09-08	NUMBER OF SEQ ID NOS: 207012
8	SOFTWARE: FASTSEQ for Windows Version 4.0	SEQ ID NO 15281
9	LENGTH: 11808	TYPE: DNA
10	ORGANISM: Human	US-09-949-016-15281
Query Match	99.7%; Score 461.4; DB 3; Length 11808;	
Best Local Similarity	99.8%; Pred. No. 1.9e-117;	
Matches 462; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	ACCTGTAATTCAGTACTGTGAGAGTCCGAGGCTGAGGAGCTGTTAGGCCGAGATTC 60
DB	23	ACCTGTAATTCAGTACTGTGAGAGTCCGAGGCTGAGGAGCTGTTAGGCCGAGATTC 82
QY	61	AAGAGCAGCTGAGCAACAGAGGAGCTGCTCACTCAAGATTAATTAATTAAGCAG 120
DB	83	AAGAGCAGCTGAGCAACAGAGGAGCTGCTCACTCAAGATTAATTAATTAAGCAG 142
QY	121	GCTTATGCTCATCCCTGTGTCCTCAGCTACTAGGAGGAGGAGGAGGAGGAGGAGG 180
DB	143	GCTTATGCTCATCCCTGTGTCCTCAGCTACTAGGAGGAGGAGGAGGAGGAGGAGG 202
QY	181	CCAGAGGCTGAGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB	203	CCAGAGGCTGAGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 262
QY	241	AAAAAGAGCCCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 300

;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16419
;; LENGTH: 61461
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-16419

Query Match 32.9%; Score 152.2; DB 3; Length 61461;

Best Local Similarity 70.6%; Pred. No. 9.4e-32; Mismatches 92; Indels 4; Gaps 2;

Matches 231; Conservative 0; Mismatches 92; Indels 4; Gaps 2;

QY 2 CCTGTATTCAGTACTGTGAGAGTCCAGGTCAGAGCTGTTGAGGCCAGAGTTCA 61
DB 50081 CTTGTATCCAGACTTTGAGAGCCAGGCAAGTGTGAGTCCAGGATTTG 50140
QY 62 AGAGCAGCTTGACACACAGGAGACCTGTCTACTACAAAGATTAATTAATGACAG 121
DB 50141 AGAGCAGCTTGACACACAGGAGACCTGTCTACTACAAAGATTAATGAGTGG 50200
QY 122 CTGATGGCTCATCCCTGTGTCCAGTACTAGGAGGAGCA--AGTAGACTGTG 178
DB 50201 CATGTGTGCTACTCTCTGTATCCAGCTTCTGTGGAGCTGAGGAGGAGAAATTTG 50260
QY 179 TCCAGAGAG-TCAGAGCTCAGTGTGAGAGCCAGCCAGCTGATTCAGCTGGC 237
DB 50261 AACGAGGGGTGTGAGGTTGAGAGCCAGATCCATGCCCTGCACTCAAGTCTGGC 50320
QY 238 AACAAAAAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTA 297
DB 50321 AACGAGTGTGAGTCTGTCTCAAAAAACAAACAAACAAAGTAATGA 50380
QY 298 AACCTTAACACATCTTCTTTTCAA 324
DB 50381 AAACGTGAGTGTGAGCTCTTTGCAA 50407

RESULT 5

US-09-949-016-16674/c
;; Sequence 16674, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: C1001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16674
;; LENGTH: 126237
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-16674

Query Match 32.3%; Score 149.6; DB 3; Length 126237;
Best Local Similarity 75.0%; Pred. No. 6.4e-31;
Matches 213; Conservative 0; Mismatches 69; Indels 2; Gaps 2;

QY 1 ACTGTATTCAGTACTGTGAGAGTCCAGGTCAGAGCTGTTGAGGCCAGAGTTTC 60
DB 21590 ACTGTATTCAGTACTGTGAGAGTCCAGGTCAGAGCTGTTGAGGCCAGAGTTTC 21531
QY 61 AAGAGCAGCTTGACACACAGGAGAG-CCTGTCTACTACAAAGATTAATTAATTAAGCA 119
DB 21530 GAGACGAGTCTGGCAACACAGGAGAGCCCATCTCTACAAACAAACAAATTAAGTGTG 21471
QY 120 GGCTTAGTGTCTACCTGTGTGTCCTGAGTCTGAGGAGGAGGAGGAGGAGTGTGT 179
DB 21470 GGCTTAGTGTCTACCTGTGTGTCCTGAGTCTGAGGAGGAGGAGGAGGAGTGTGT 21411
QY 180 CCAGAGGTCAGAGTGTGAGTGTGAGAGCCAGCCAGCTGATTCAGCTGGCA 239
DB 21410 GCCCGAGGTCAGAGTGTGAGTGTGAGAGCTGAGTGTGCA-CTGCACTACAGCTGGGTGA 21352
QY 240 CAAAAAGAGCCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTA 283
DB 21351 CAGAGTGTGAGCCTGTCTGTGAAAAACAAACAAACCAAGCA 21308

RESULT 6

US-09-949-016-16675/c
;; Sequence 16675, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: C1001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16675
;; LENGTH: 126237
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-16675

Query Match 32.3%; Score 149.6; DB 3; Length 126237;
Best Local Similarity 75.0%; Pred. No. 6.4e-31;
Matches 213; Conservative 0; Mismatches 69; Indels 2; Gaps 2;

QY 1 ACCTGTATTCAGTACTGTGAGAGTCCAGGTCAGAGCTGTTGAGGCCAGAGTTTC 60
DB 21590 ACCTGTATTCAGTACTGTGAGAGTCCAGGTCAGAGCTGTTGAGGCCAGAGTTTC 21531
QY 61 AAGAGCAGCTTGACACACAGGAGAG-CCTGTCTACTACAAAGATTAATTAATTAAGCA 119
DB 21530 GAGACGAGTCTGGCAACACAGGAGAGCCCATCTCTACAAACAAACAAATTAAGTGTG 21471
QY 120 GGCTTAGTGTCTACCTGTGTGTCCTGAGTCTGAGGAGGAGGAGGAGTGTGT 179
DB 21470 GGCTTAGTGTCTACCTGTGTGTCCTGAGTCTGAGGAGGAGGAGGAGTGTGT 21411
QY 180 CCAGAGGTCAGAGTGTGAGTGTGAGAGCCAGCCAGCTGATTCAGCTGGCA 239
DB 21410 GCCCGAGGTCAGAGTGTGAGTGTGAGAGCTGAGTGTGCA-CTGCACTACAGCTGGGTGA 21352
QY 240 CAAAAAGAGCCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTA 283
DB 21351 CAGAGTGTGAGCCTGTCTGTGAAAAACAAACAAACCAAGCA 21308

RESULT 7
US-09-949-016-16292


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QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 60
DB 290 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 231
QY 61 AAGAGCAGCTGAGCAACACAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCCA 119
DB 230 AAGAGCAGCTGAGCAACACAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCCA 171
QY 120 GGGTGTAGTGCATCCCTGTGTGCTCCAGCTACTAGGAGAGCAGA---AGTAGAGCTGCT 176
DB 170 GGGTGTAGTGCATCCCTGTGTGCTCCAGCTACTAGGAGAGCAGA---AGTAGAGCTGCT 111
QY 177 TGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGCATTCAGACCTGGG 236
DB 110 TGAACCGGAGAGTGAAGAGTGTGAGTGAAGATTTGTGCCA-CGGCACTCTAGCCTGGG 52
QY 237 CAACAAAAGAGACCTGTCTCAAAAATAATTAATTAATTAATTA 284
DB 51 CAATAGAGTGAAGACCTGTCTCAAAAATAATTAATTAATTAATTA 4
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RESULT 13

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US-09-949-016-60956/c
; Sequence 60956; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60956
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60956
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Query Match 31.8%; Score 147.2; DB 3; Length 601;
Best Local Similarity 76.4%; Pred. No. 4.2e-31;
Matches 220; Conservative 0; Mismatches 63; Indels 5; Gaps 3;
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QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 60
DB 290 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 231
QY 61 AAGAGCAGCTGAGCAACACAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCCA 119
DB 230 AAGAGCAGCTGAGCAACACAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCCA 171
QY 120 GGGTGTAGTGCATCCCTGTGTGCTCCAGCTACTAGGAGAGCAGA---AGTAGAGCTGCT 176
DB 170 GGGTGTAGTGCATCCCTGTGTGCTCCAGCTACTAGGAGAGCAGA---AGTAGAGCTGCT 111
QY 177 TGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGCATTCAGACCTGGG 236
DB 110 TGAACCGGAGAGTGAAGAGTGTGAGTGAAGATTTGTGCCA-CGGCACTCTAGCCTGGG 52
QY 237 CAACAAAAGAGACCTGTCTCAAAAATAATTAATTAATTAATTA 284
DB 51 CAATAGAGTGAAGACCTGTCTCAAAAATAATTAATTAATTAATTA 4
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RESULT 14

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US-09-949-016-12816
; Sequence 12816; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12816
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12816
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Query Match 31.8%; Score 147.2; DB 3; Length 99370;
Best Local Similarity 73.5%; Pred. No. 2.7e-30;
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QY 3 CTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 62
DB 66673 CTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 66732
QY 63 GAGCAGCTGAGCAACACAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCAG 121
DB 66733 GAGCAGCTGAGCAACACAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCAG 66792
QY 122 CTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 177
DB 66793 CTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTG 66852
QY 178 GTCCAGAGAGTCAAGACTGAGTGAAGCCAGCCACTGCATTCAGACCTGGG 237
DB 66853 GTCCAGAGAGTCAAGACTGAGTGAAGCCAGCCACTGCATTCAGACCTGGG 66912
QY 238 AACAAAAGAGACCTGTCTCAAAAATAATTAATTAATTAATTAAT 291
DB 66913 AACAAAAGAGACCTGTCTCAAAAATAATTAATTAATTAATTAAT 66966
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RESULT 15

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; Sequence 17540; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540
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GenCore version 5.1.9
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	152	32.8	135005	9 US-10-723-860-2320	Sequence 2320, Ap
C 3	152	32.8	135005	10 US-10-756-149-1719	Sequence 1719, Ap
C 4	150.6	32.5	558	4 US-09-925-065A-822292	Sequence 822292,
C 5	150.6	32.5	558	4 US-09-925-065A-839930	Sequence 839930,
C 6	150.6	32.5	558	5 US-09-925-065A-822292	Sequence 822292,
C 7	150.6	32.5	558	5 US-09-925-065A-839930	Sequence 839930,
C 8	150.4	32.5	23579	7 US-10-017-161-1909	Sequence 1909, Ap
C 9	150.4	32.5	23579	7 US-10-292-798-1565	Sequence 1565, Ap
C 10	149.4	32.3	186510	7 US-10-043-715-1	Sequence 1, Appl1
C 11	148.2	32.0	561515	8 US-10-741-601-5682	Sequence 5682, Ap
C 12	148.2	32.0	561515	9 US-10-741-601-17730	Sequence 17730, A
C 13	147.4	31.8	636	4 US-09-925-065A-696683	Sequence 696683,
C 14	147.4	31.8	636	4 US-09-925-065A-696684	Sequence 696684,
C 15	147.4	31.8	636	5 US-09-925-065A-696683	Sequence 696683,
C 16	147.4	31.8	636	5 US-09-925-065A-696684	Sequence 696684,
C 17	147.4	31.8	81099	6 US-10-087-192-1756	Sequence 1756, Ap

C 18	147.2	31.8	814	4 US-09-925-065A-930127	Sequence 930127,
C 19	147.2	31.8	814	5 US-09-925-065A-930127	Sequence 930127,
C 20	147.2	31.8	383432	10 US-10-737-082-34	Sequence 34, Appl
C 21	147.2	31.8	383432	10 US-10-765-790-34	Sequence 34, Appl
C 22	147	31.7	636	4 US-09-925-065A-696682	Sequence 696682,
C 23	147	31.7	636	5 US-09-925-065A-696682	Sequence 696682,
C 24	147	31.7	410846	10 US-10-481-613-1	Sequence 1, Appl1
C 25	146.8	31.7	7739	3 US-09-764-877-3189	Sequence 3189, Ap
C 26	146.8	31.7	7739	7 US-10-242-515-3189	Sequence 3189, Ap
C 27	146.6	31.7	1369	6 US-10-027-632-86881	Sequence 86881, A
C 28	146.6	31.7	1369	6 US-10-027-632-86881	Sequence 178961,
C 29	146.6	31.7	1369	7 US-10-027-632-86881	Sequence 86881, A
C 30	146.6	31.7	1369	7 US-10-027-632-86881	Sequence 178961,
C 31	146.4	31.6	853	12 US-10-301-480-591007	Sequence 591007,
C 32	146.4	31.6	853	12 US-10-301-480-591007	Sequence 1204416,
C 33	146.4	31.6	44348	8 US-10-301-832-11	Sequence 11, Appl
C 34	145.4	31.4	611	4 US-09-925-065A-500442	Sequence 500442,
C 35	145.4	31.4	611	5 US-09-925-065A-500442	Sequence 500442,
C 36	145.4	31.4	894	12 US-10-301-480-553001	Sequence 553001,
C 37	145.4	31.4	894	12 US-10-301-480-553001	Sequence 553001,
C 38	145.4	31.4	87467	8 US-10-741-601-5634	Sequence 5634, Ap
C 39	145.4	31.4	87467	9 US-10-741-601-17624	Sequence 17624, A
C 40	145.4	31.4	87672	10 US-10-995-561-13237	Sequence 13237, A
C 41	145.4	31.4	143947	16 US-11-193-771-37	Sequence 37, Appl
C 42	145.4	31.4	143947	16 US-11-193-789-37	Sequence 37, Appl
C 43	145.4	31.4	143947	16 US-11-193-806-37	Sequence 37, Appl
C 44	145.4	31.4	143947	16 US-11-193-857-37	Sequence 37, Appl
C 45	145.4	31.4	143947	16 US-11-193-561-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-10-719-993-6827/C
; Sequence 6827, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719, 993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6827
; LENGTH: 160556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(160556)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-719-993-6827

Query Match	34.1%	Score 157.8;	DB 9;	Length 160556;
Best Local Similarity	68.3%	Pred. No. 2e-30;		
Matches 233;	Conservative 1;	Mismatches 103;	Indels 4;	Gaps 1;
QY	2	CCTGTAATTCAGTACTGTGAGAGTCCAGAGTCAGAGCACTGTTAGGCCAGACTTCA	61	
DB	30072	CTGTATCTCTAGCACTTTGGAGGCGCAAGCGAGTGATTAAGTGAAGTCAGAGTTGC	30013	
QY	62	AGAGCAGCTTGACACACAGGAGACCTGTCTACTACAAAGATTAATTAATGACAGG	121	
DB	30012	AGAGCAGCTTGACACACAGGAGACCTGTCTACTACAAAGATTAATTAATGACAGG	29953	
QY	122	CTTAGTGTCTATCCCTGTGTGTCCAGCTACTAGGAGGAGCAAGTAGA-----CTGCTT	177	
DB	29952	YGTGTTGTGCGGCGCTGTAGTCCAGCTACTAGGAGGAGGAGCAAGTAGA-----CTGCTT	29893	
QY	178	GTCACGAGGAGTCAAGACTGACAGTGAAGCCAGGACCACTGCATTTCCAGCTGGGC	237	

Db 29892 AACCCAGAGGTGGAGGTACAGGACCTTGAGATTGACCACTGCACCTCGAGCT 298333

Qy 238 AACAAAAAGAGACCCCTGTCTCAAAAAATTAAGTTAAATTAATAATAATAATAGTTTA 297

Db 29832 GACGAGGTGAGACCTCTGTCTCAAAAAAATTAATAACAATGGAAAAAATTTAAATAAT 297733

Qy 298 AACCTAAACACATCTTCTTTTCAAGAGAGACTCTTAAG 338

Db 29772 ATAGCTAGAACAACTTGATGACAAAAATGTGTACTAAG 29772

```

RESULT 2
US-10-723-860-2320/c
; Sequence 2320. Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

```

Query Match	32.8%	Score 152	DB 9	Length 135005
Best Local Similarity	80.0%	Pred. No. 6.6e-29		
Matches 216	Conservative 0	Mismatches 50	Indels 4	Gaps 3
QY	1	ACCTGTAATTCCTCACTCTGTGAGAGTCCGAGAGTTCAGAGGACTGCTTGAGGCCAGAGATTCC	60	
Db	84820	ATCTGTAATTCACACACTTTTGAGGAGGAGAGAGTAGAGGATTCTTGAGGGCAGGAGTTCC	84761	
QY	61	AAGAGCAGCCTGACCAACACAGGAGA--CCTGTCACTACAAAGAAATTAATTAATTAGCC	118	
Db	84760	AAGACTATCTCGGGGAACATATGTAGAGACCCTGTCTTCAAAAAAATAGAAAAATTATAGTC	84701	
QY	119	AGGCTTATGTGGCTCATCCCTGTGTGCCAGCTACTTAGGAGGCGAAGTAGTGAAGCTCTTG	178	
Db	84700	GGATATGTGTGCACATGTCTTATGTCCAGCTACTTCAGAGGCTGAGAGTAGAGTTGGTG	84641	
QY	179	-TCCAGAGAGTCAAGACTGCAAGTAGCTGAGACCAGCAGCCTGTCAATTCAGCCTTGAGG	237	
Db	84640	AGCTCAGAGGATCGAGGCGGACAGTAGAGCTGAGACAGTGCA--CTGTACTCAACTTGAGG	84587	
QY	238	AAACAAAAGAGACCTGTCTCAAAAAATTA	267	
Db	84581	AAACAGAACAGACCTGTCTCAAAAAATTA	84552	

```

RESULT 3
US-10-756-149-1719/C
; Sequence 1719, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818

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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1719
;
; LENGTH: 135005
;
; TYPE: DNA
;
; ORGANISM: Homo Sapiens
US-10-756-149-1719

```

	Query Match	Best Local Similarity	32.84%;	Score 152;	DB 10;	Length 135005;
	Matches 216;	Conservative 0;	Mismatches 50;	Indels 4;	Gaps 3;	
Qy	1	ACCTGTAAATTCAGACTCTGTGAGAGTCCGAGGTCAAGAGGACTGTGTAAGGCCAGAGTTTC	60			
Db	84820	ATCTGTAAATTCAGACTCTTTGGGAGGACAGAGTGAAGAGATTGCTTGAAGGCCAGAGTTTC	84761			
Qy	61	AAGAGCAGCCTTGACAAACACAGGGAGA--CTGTCACTACAAAGATTAATTAATTAGCC	118			
Db	84760	AAGACTATCTCTGGGCAACATAGGAGACCCTGTCTCTCAAAAAATTAACAAAATTAATGTC	84701			
Qy	119	AGGCTTAGTGGCTCATCCCTGTGTGTCCTCCAGCTACTAGAGGACGAGAAGTAGAGACTGTCTTG	178			
Db	84700	GGGTATGTGTGGCACTATGCCCTGTATGTCCCAAGCTACTAGAGAGGTGAGTGAATTTGCTTG	84641			
Qy	179	-TCCAGAGAGTCAAGAATGTCAGATGAGTGAAGACCCAGCCACTGTCATTCAGACTGTGGCC	237			
Db	84640	AGCTCAGAGAGTGAAGGCGGCAAGTGAAGTGAAGCAAGTGCA-CTGTATCTCCAACTGTGGCC	84582			
Qy	238	AACAAAAAGAGACCTGTCTCAAAAAATTA 267				
Db	84581	AACGAAACAAAGACCTGTCTCAAAAAATTA 84552				

```

RESULT 4
US-09-925-065A-822292/c
; Sequence 822292, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 822292
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-822292

```

Query Match	32.5%	Score 150.6	DB 4	Length 558
Best Local Similarity	74.1%	Pred. No. 1.4e-29		
Matches 217	Conservative 1	Mismatches 70	Indels 5	Gaps 2
Q7	2	CCTGTAATTCAGACTGTGAGGTCCAGAGGTCAAGGACTGTTGAGGCCAGAGTTCA	61	
Db	345	CCTGTAATCCAGACCTTTGGAGAGCCAGGACAGGTGATTACTTGAAGTCAGAGTTCA	286	
Q7	62	AGAGAGGCTGACAAACACAGAGAGACCTGTCACTACAAAGAAATTAATTAATGACCAAG	121	
Db	285	AGACGAGCTTCCCAACACGGTGAACCCGCTCTTCACTAAATAATACAAAAATTGACCAAG	226	

```

Oy 122 CTTAGAGGCTCATCCCTGGGATGCCAGGTACTTGGGAGGAGGAAGTAGACTGTTG -- 179
Db 225 TGTGGTGGTCAGTCCCTGATGTCCTGAGCTTATGGGAGGCTGAGGAGGGGGGTTGCTTG 166
Oy 180 --CCGAGAGGTCGAAGTCACTGAGTGAAGTGAAGCCAGCCAGCTGCATTCAGAGCTGGGC 237
Db 165 AACCTGGGAGGATGGAGGTTGCACTGAGCCAGATCAAGTCA -CTGCCCTCAGAGCTGGGG 107
Oy 238 AACAAAAAGAGACCCTGTCTCAAAAATAAAGTAAATAAATAATAATAATAATAATA 290
Db 106 AACCTAGTAGACTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 54

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US-09-925-065A-839930
; RESULT 5
US-09-925-065A-839930
; Sequence 839930, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSeq For Windows Version 4.0
; SEQ ID NO 839930
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-839930
```

Query Match	32.5%	Score 150.6	DB 4	Length 558
Best Local Similarity	74.1%	Pred. No. 14e-29		
Matches 217	Conservative 1	Matches 70	Indels 5	Gaps 2
Qy	2	CCTGTAATTCAGTACTGTGAGATGTCACAGGTCAGAGACTGCTTGAGGCCAGAGTTC	61	
Db	215	CCTGTAATCCAGACACTTTGGAGGCCAAGGACAGGTGATTACTTGAGGTCAAGAGTTCA	274	
Qy	62	AGAGCAGCCTGGACAACA CAGGGAGACCTGTCACTTCAAAAGATTAATTAATTAGCCAGG	121	
Db	275	AGACCAGCTGGCAACACGGTGAACCCGCTTCTACTTAATAATCAAAAATTACCAAG	334	
Qy	122	CTTAGTGCTATCCCTGTGTGCCAGTACTAGGAGGACAGAAATGAGACTGCTTGT-	179	
Db	335	TGTGTGTGATGCTGCTAGTCCAGCTACTTGGAGGCTGAGGACAGGGGGTGTCTTG	394	
Qy	180	--CCCAGAGGTCAGAGCTGACGTGAGCTGAGACCCAGCCACTGCAATTCAGCCTGGGC	237	
Db	395	AACCTGGAGGTCAGGTTCAGTGAAGCCAAAGATACGTCACCTGCCAGCCTGGGG	453	
Qy	238	AAACAAAAGAGACCTGTCTCAAAAATAATGAATTAATTAATTAATTAATAA	290	
Db	454	AACTAAGTGAAGCTGTGTCTCAAAAATAATTAATTAATTAATTAATTAATAA	506	

RESULT 6
US-09-925-065A-822292/c
; Sequence 822292, Application US/0995065A;
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

```

; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 822292
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-822292

Query Match      32.5%   Score 150.6;   DB 5;   Length 558;
Beech Local Similarity 74.1%;   Pred. No. 1.4e-29;
Matches 217; Conservative 1; Mismatches 70; Indels 5; Gaps 2

```

Qy	2	CCTTAATATTCAGAGTACGTGAGAGTCCGAGGTCAAGAGATCTGTAGAGGCCAGAGATTCA	61
Db	345	CTGTAAATCCAGACCTTTGGAGGCCAAGCAGGTGATTAATTGTAGAGTCAAGAGTTCA	286
Qy	62	AGAGCAGCCTTGACAACAACAGGAGACCTGTCACTACAAAGATTAATTAATTAGCCAGG	121
Db	285	AGACCAACCTGGCCAAACAGGTGAAACCGCTCTACTATAAAAAATACAAAAATTAGCCAGG	226
Qy	122	CTTAGTGGTTCATCCCTGTGGTCCGACGTACTAGGAGGACGAAGTGGATGCTGTG--	179
Db	225	TGTGTGTGTGCATCCTCTGTAGTCCGAGTACTTGGAGGCTGGAGCAGGGGGGTTGCTTG	166
Qy	180	--CCAGAGGTCAAAGCTGCAGTGAAGCTGAGCCCAAGCCACTGCAATTCAGCCTGGGC	237
Db	165	AACTGGAGGATGAGGTTGTCAGAGACCAAGATCAGGYCA-CTGCCCTCAGCCTGGGG	107
Qy	238	AAACAAAAAGAGACCCCTGTCTCAAAAAATTAATTAAATTAATTAATTAATTAATAA	290
Db	106	AACTAAGTGAACCTCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATAA	54

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RESULT 7
US-09-925-065A-839930
, Sequence 839930, Application US/09925065A
, Publication No. US20050228172A9
, GENERAL INFORMATION:
, APPLICANT: Wang, David G.
, TITLE OF INVENTION: Identification and Mapping of Single
, TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
, FILE REFERENCE: 108827.135
, CURRENT APPLICATION NUMBER: US/09/925, 065A
, PRIOR FILING DATE: 2001-08-08
, PRIOR APPLICATION NUMBER: US 60/243, 096
, PRIOR FILING DATE: 2000-10-24
, PRIOR APPLICATION NUMBER: US 60/252, 147
, PRIOR FILING DATE: 2000-11-20
, PRIOR APPLICATION NUMBER: US 60/250, 092
, PRIOR FILING DATE: 2000-11-30
, PRIOR APPLICATION NUMBER: US 60/261, 766
, PRIOR FILING DATE: 2001-01-16
, PRIOR APPLICATION NUMBER: US 60/289, 846
, PRIOR FILING DATE: 2001-05-09
, NUMBER OF SEQ ID NOS: 957086
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 839930
, LENGTH: 558

```


[illegible]

```

RESULT 10
US-10-043-715-1/c
; Sequence 1, Application US/10043715
; Publication No. US20030143544A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: MMI-009
; CURRENT APPLICATION NUMBER: US/10/043,715
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 186510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-043-715-1

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Query Match	32.3%	Score	149.4	DB	7	Length	186510
Best Local Similarity	74.1%	Pred	No. 3.8e-28				
Matches	217	Conservative	0	Mismatches	71	Indels	5
						Gaps	2

OY	1	ACCTTAATTCAGTAAGTGTGAGAGTCCAGGTCAGAGACCTCTTGAGGCCAGAGATTC	60
Db	175801	ACCTTAATCCAGCAGCACTTTGGGAGATCGAGGCAAGAGATTATTGGGCCAGGAGTTT	175742
OY	61	AAGACGACCTTGGAACAACAAGGAGACCTGTCACTACAAAGATTAATTAATTCAG	120
Db	175741	GAGACACACCTTGGAACAAGATGAGACCCATCTTAACAAAAATTAATTAATTCAGTGG	175682
OY	121	GCTTAGTGGCTATCCCTGTGGTCCAGGTACTAGGAGAGGCAATTAAGA-----CTGGCT	176
Db	175661	GCATGTGTGTGTCACCTGTAGTCCAGCTACTCAGAGAGGCTGAGGTTGGAGGATGCTT	175622
OY	177	TGTCCAGAGAGGTCAAGACTGAGTGAAGTGAAGCCAGCCACTTGATTTCCAGCCTGG	236
Db	175621	GAGCCCAAGAGGTTCAGAGCTGTAGTGAAGCTGTATTCATGCCA-CTCAGTCCAGCCTGG	175633
OY	237	CAACAAAAGAGACCTGTCTCAAAAAATAAGTTAATTAATTAATTAATTAATTAATTAAT	289
Db	17562	CAACGAGAGAACCTGTCTCAAAACAAACAAACAAACAAACAAACAAACAAACAAACAA	175510

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RESULT 11
US-10-741-601-5682/c
; Sequence 5682, Application US/10741601
; Publication No. US2004016619A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C10001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5682
; LENGTH: 561515

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ..(561515)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
; IS-10-741-601-5682

```

Query Match	32.0%	Score 148.2;	DB 8;	Length 56151;
Best Local Similarity	70.0%	Pred. No. 1,3e-27;		
Matches 229;	Conservative 0;	Mismatches 93;	Indels 5;	Gaps 2;

```

RESULT 12
US-10-741-600-17730/C
Sequence 17730, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17730
LENGTH: 561515
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(561515)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-741-600-17730

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RESULT 13
US-09-925-065A-696683
; Sequence 696683, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 696683
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-696683

```

Query Match	Similarity	31.8%	Score 147.4	DB 4	Length 636	
Best Local	Similarity	73.7%	Pred. No. 16-28			
Matches	216	Conservative	0	Mismatches 71	Indels 6	Gaps 2
QY	2	CCTGTAATTCACGTA	CTGTGAGATGCCAGAGTCGAGAGAC	CTGCTTTGAGGCCAGAGTTCA	61	
Db	15	CCTGTAATTC	TAAACCTTTGGAGGCTGAGGGGAGAGATGCTTGACCT	TAGAGATTCA	74	
QY	62	AGAGCAGCCTGGA	CACAACAGGAGACCTGTCTACTACAAAGAATTAATTAATTAAGCAGG	121		
Db	75	AGACCAGCCTGGA	CAACAATGGCAACCCCTGCTTTACAAAAGATACAAAATTTAGCCAGA	134		
QY	122	CTTAATGCTCAT	CCCTGTGTGTTCCAGCTACTAGGAGGCAGAAATAGACTGCT	-----	176	
Db	135	TGTGTGTGCAT	TACGGCTGTGTGTTCCAGCTACTCAGAGAGCTGAGGCAGAGAGGTTGCTTG	194		
QY	177	TGTC	CCAGAGAGTCAAGACTGACAGTGAAGCCAGCCACTGCATTTCCAGCCTGGG	236		
Db	195	AGCC	CAGAGAGGTTCAGAGTTGCAGTGAAGTGAATTGGGCCA-CTGCACACCAAGCCTGGG	253		
QY	237	CACCAAAAAGAGA	CCCTGCTCTCAAAAAATTAAGTTAATTAATTAATTAATTAATAA	289		
Db	254	CACAGAGGCACA	CTTAATCTCAAAAAATTAATTAATTAATTAATTAATTAATAA	306		

RESULT 14
US-09-925-065A-696684
; Sequence 696684, Application US/09925065A

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; Publication No.: US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,036
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ. ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO: 696684
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-696684

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	Query Match	31.8%	Score 147.4	DB 4	Length 636	
	Best Local Similarity	73.7%	Pred. No. 1e-28			
	Matches	216	Conservative	0	Mismatches	71
					Indels	6
					Gaps	2
OY	2	CCTGTAAATCCAGTACTGTGTGAGAGTCCGAGAGTCAGAGGACCTGTCTTGTAGGCCACGAGACTTCA	61			
Db	15	CCTGTAAATCCTTAACACTTTGTGGAGAGCTGAGGTGTGAGAGATTGTCTGAGCCTTGAAGATTCA	74			
OY	62	AGACGAGCTGTGACAAACAAGAGAGACCTGTCTCACTACCAAGATTAATTAATTTAATAGCCAG	121			
Db	75	AGACGAGCTGTGACAAACATGTGCAAGCCCTGTCTTTACAAAAGATCAAAAAATTATAGCCAGA	134			
OY	122	CTTATGTGCTCATCCCTGTGTGTCTCCAGTACTTATAGGAGGCAAGATAGACTGTCT-----	176			
Db	135	TGTGTGTGCATACACCTGTGTGTCTTCAGCTACTCAGGAGAGCTGTGAGCAGAGAGGTGTCTTG	194			
OY	177	TGTCCCAAGAGAGTCAAGACTGACAGTGTGAGCTGAGACCCAGCCACTGTCACTTCAGCCTGGG	236			
Db	195	AGCCCAAGAGAGTGTGAGGTGTGCACTGTGAGCTGAATTTGGCCA-CTGCACACCAAGCCTGGG	253			
OY	237	CAACAAAAGAGACCTGTCTCAAAAAAATAAGTTAAATTAATTAATTAATTAATAA	289			
Db	254	CAACGAGCCCAAGCCTTAATCTCAAAAAAATAATTAATTAATTAATTAATAA	306			

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/ RESULT 15
/ US-09-925-065A-696683
/ Sequence 696683, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925.065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/

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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 696683
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-696683

Query Match 31.8%; Score 147.4; DB 5; Length 636;
Best Local Similarity 72.7%; Pred. No. 1e-28;
Matches 216; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY	2	CTGTAAATTCAGTACTGTGTGAGAGTCCGAGGTCAGAGACTGCTTGAGGCCAGAGTTCA	61
Db	15	CTGTAAATTCCTAACACTTTGGAGGCTGAGGTGGAGGATTGCTTGAGCCTAGAGATTCA	74
QY	62	AGAGCAGCCTGAGCAACACAGGGAGACTGTCACTACAAAGATTAATTAATTAGCCAGG	121
Db	75	AGACCAAGCCTGAGCAACATGGCAAGCCCTGTCTTTACAAAGATACAAATAATTAGCCAGA	134
QY	122	CTTAGTGGTCAATCCCTGTGGTCCAGCTACTAGGAGGACAGAGTGAAGTGAAGTGGCT----	176
Db	135	TGTGTGCCAATACGCCCTGTGTTCAGCTACTCAGAGGCTGAGGACAGAGGTTGCTTG	194
QY	177	TGTCCAGAGAGTCAAGACTGCACTGAGAGACCCAGCCACTGCATTCCAGCTTGGG	236
Db	195	AGCCAGAGAGGTGAGGTTGCACTGAGCTGAGATTGGCCA-CTGCACACACAGCTTGGG	253
QY	237	CAACAAAAGAGACCCCTGTCTCAAAAAATAAGTTAATAATAATAATAATAA	289
Db	254	CAACAGAGCCAGACTTATCTCAAAAAATAATAATAATAATAATAATAA	306

Search completed: June 6, 2006, 00:21:07
Job time : 924.76 secs

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/ Publication No. US20060105381A1
/ GENERAL INFORMATION:
/ APPLICANT: Ellipsis Biotherapeutics Corporation
/ APPLICANT: Peltekova, Vanya D
/ APPLICANT: Siminovitsh, Katherine A
/ APPLICANT: St George-Hyslop, Peter H
/ APPLICANT: Rubin, Laurence A
/ APPLICANT: Peltekova, Vanya D
/ APPLICANT: Muntle, Richard F
/ TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIATED WITH INFLAMMATORY BOWEL DISORDERS
/ FILE REFERENCE: ELP-020
/ CURRENT APPLICATION NUMBER: US/11/318,813
/ CURRENT FILING DATE: 2005-12-27
/ PRIOR APPLICATION NUMBER: US/10/327,188
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/362,700
/ PRIOR FILING DATE: 2002-03-08
/ PRIOR APPLICATION NUMBER: 60/343,338
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/427,529
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: 60/362,717
/ PRIOR FILING DATE: 2002-03-08
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 42
/ LENGTH: 54550
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
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Query Match 29.5%; Score 136.8; DB 7; Length 54550;

Best Local Similarity 69.5%; Pred. No. 3.1e-20;

Matches 228; Conservative 0; Mismatches 94; Indels 6; Gaps 3;

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QY 2 CCTGTATTCAGTACTGTGAGAGTCCGAGGTGAGAGGACTGCTTGAGGCCAGAGTTCA 61
DB 46202 CATGTATCCACACACTTTGGNAGGCCAAGGTAGTGAATCAGCTGAGGCCAGAGTTCA 46261
QY 62 AGAGGAGCCTGGACAACACAGGAGA-CCTGTACTCAAGAAATTAATTAATTAAGCAG 120
DB 46262 AGACGAGCCTGGACAAGTGTGAACCTGTCTCTAATAAATAAATAAATAAATTAAGCAG 46321
QY 121 GCTTAGTGTCTCATCCCTGTGTGCTCCAGCTACTAGGAGGACAGAAAGTAGAGCTGTGT- 179
DB 46322 GTGTGTGTGGAGGAGTGTGAATCCGGCTACTCTGAGGCTGAGGTAGAGAAATGCTT 46381
QY 180 ---CCACGAGGCTCAGACTGCACTGAGTGAAGCCAGCCACTGATTCAGGCTGG 236
DB 46382 GAACCCAGGAGGAGGCTGCAGTGAGTGAAGTTGACCA-CTGCACTCCAACTGGG 46440
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QY 237 CAACAAAAGAGACCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAAGTTT 296
DB 46441 CAACAAAGCAAACTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAAGTTAA 46500
QY 297 AAACCTTAACACATCTCTTTTTCAAA 324
DB 46501 ACACACAAATTAACATTAATATATGTAA 46528
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RESULT 3

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US-11-293-697-1292
Sequence 1292, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIORITY FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1292
LENGTH: 2252
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-1292
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Query Match 29.1%; Score 134.6; DB 7; Length 2252;

Best Local Similarity 72.1%; Pred. No. 5.9e-20;

Matches 204; Conservative 0; Mismatches 74; Indels 5; Gaps 2;

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QY 2 CCTGTATTCAGTACTGTGAGAGTCCGAGGTGAGAGGACTGCTTGAGGCCAGAGTTCA 61
DB 1891 CTTGTATCCACACACTTTGGATGTGAGGTGGCGGATCACTTGAGGTGAGAGTTCA 1950
QY 62 AGAGGAGCCTGGACAACACAGGAGGAGCTGTCTACTCAAAAGAAATTAATTAATTAAGCAG 121
DB 1951 AGACGAGCCTGGACAAGTGTGAACCTGTCTCTAATAAATAAATAAATAAATTAAGCAG 2010
QY 122 CTTAGTGTCTATCCCTGTGTGCTCCAGCTTACTAGGAGGAGGAGAAATAGGA----CTGCTT 177
DB 2011 TGTGTGTGGACGGGCGCTGTGAATCGACGCCCTTGAAAGGCCAGGAGGAATGCGCTC 2070
QY 178 GTCCAGAGAGTCAAGACTGAGTGAAGCCAGCACTGCAATTCAGGCTGGGC 237
DB 2071 AACACTGAGAGTGAAGTTCAGTGAAGTGAATGAGCA-CTGCACTCCAGGCTGGGC 2129
QY 238 AACAAAAGAGACCTGTCTCAAAAAATAGTTAAATTAATTA 280
DB 2130 AATGAGGCAAGACCTGTCTCAAAAAATTAATTAATTA 2172
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RESULT 4

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US-11-293-697-441/c
Sequence 441, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIORITY FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 441
LENGTH: 2374
TYPE: DNA
ORGANISM: Homo sapiens
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SOFTWARE: PatentIn 3.2
SEQ ID NO 433
LENGTH: 4987
TYPE: DNA
ORGANISM: Homo sapiens
US-10-505-928-433

Query Match 28.0%; Score 129.6; DB 6; Length 4987;
Best Local Similarity 71.5%; Pred. No. 6.9e-19;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 3805 CCTGTAATTCAGAGCTTTGGAGGCTGAGGTGGGAGATCACTTGAGGTGAGAGTTT 3746
QY 62 AGAGCAGCTTGACAACACAGGAGAGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3745 AGACCAAGCTGGCCACATGAGTGAACCTGTCTCTAATAAATAATTAGCCAG 3686
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGGAGAGAGTGAAGA---CTGCT 176
DB 3685 GTGTGGTGGACACACCTGTAATCCAGCTACTTGGAGGCCAAGGAGAGAAATCACTT 3626
QY 177 TGTCCAGAGGTCAAGACTGCACTGAGTGAAGACCAAGCCACTGCTTCCAGCTGG 236
DB 3625 GAACCTGGTGGTGAAGGTTGCAGTGAGGCGAGATTGCAACA-CTGCATCTCAGCCTGG 3567
QY 237 CAACAAAAGAGACCCCTGTCTCAAAAATAAGTAATAATAATAATAATACT 294
DB 3566 TGACACAGTGAAGACTATCGCAAAAATAATAATAATAATAATAATAAGT 3509

RESULT 8

US-11-251-465-4/C
Sequence 4, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tonne, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30.172-A USA
CURRENT APPLICATION NUMBER: US/11/251.465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 4987
TYPE: DNA
ORGANISM: Homo sapiens
US-11-251-465-4

Query Match 28.0%; Score 129.6; DB 7; Length 4987;
Best Local Similarity 71.5%; Pred. No. 6.9e-19;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 3805 CCTGTAATTCAGAGCTTTGGAGGCTGAGGTGGGAGATCACTTGAGGTGAGAGTTT 3746
QY 62 AGAGCAGCTTGACAACACAGGAGAGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3745 AGACCAAGCTGGCCACATGAGTGAACCTGTCTCTAATAAATAATTAGCCAG 3686
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGGAGAGAGTGAAGA---CTGCT 176
DB 3685 GTGTGGTGGACACACCTGTAATCCAGCTACTTGGAGGCCAAGGAGAGAAATCACTT 3626

QY 177 TGTCCAGAGGTCAAGACTGCACTGAGTGAAGACCAAGCCACTGCAATTCAGCCTGG 236
DB 3625 GAACCTGGTGGTGAAGGTTGCAGTGAGGCGAGATTGCAACA-CTGCATCTCAGCCTGG 3567
QY 237 CAACAAAAGAGACCCCTGTCTCAAAAATAAGTAATAATAATAATAATAATACT 294
DB 3566 TGACACAGTGAAGACTATCGCAAAAATAATAATAATAATAATAATAAGT 3509

RESULT 9

US-11-251-465-5/C
Sequence 5, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tonne, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30.172-A USA
CURRENT APPLICATION NUMBER: US/11/251.465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 5014
TYPE: DNA
ORGANISM: Homo sapiens
US-11-251-465-5

Query Match 28.0%; Score 129.6; DB 7; Length 5014;
Best Local Similarity 71.5%; Pred. No. 6.9e-19;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 3832 CCTGTAATTCAGAGCTTTGGAGGCTGAGGTGGGAGATCACTTGAGGTGAGAGTTT 3773
QY 62 AGAGCAGCTTGACAACACAGGAGAGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3772 AGACCAAGCTGGCCACATGAGTGAACCTGTCTCTAATAAATAATTAGCCAG 3713
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGGAGAGAGTGAAGA---CTGCT 176
DB 3712 GTGTGGTGGACACACCTGTAATCCAGCTACTTGGAGGCCAAGGAGAGAAATCACTT 3653
QY 177 TGTCCAGAGGTCAAGACTGCACTGAGTGAAGACCAAGCCACTGCAATTCAGCCTGG 236
DB 3652 GAACCTGGTGGTGAAGGTTGCAGTGAGGCGAGATTGCAACA-CTGCATCTCAGCCTGG 3594
QY 237 CAACAAAAGAGACCCCTGTCTCAAAAATAAGTAATAATAATAATAATAATACT 294
DB 3593 TGACACAGTGAAGACTATCGCAAAAATAATAATAATAATAATAATAAGT 3536

RESULT 10

US-11-293-697-1324
Sequence 1324, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: Helix Research Institute
TITLE OF INVENTION: Novel Full Length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1

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/ SEQ ID NO 1324
/ LENGTH: 2682
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-293-697-1324

Query Match      27.9%; Score 129.4; DB 7; Length 2682;
Best Local Similarity 71.1%; Pred. No. 7.1e-19;
Matches 214; Conservative 0; Mismatches 81; Indels 6; Gaps 3;

QY      2 CCTGTATTCCTAGTCTGAGAGTCCGAGTCAGAGGAGCTGTTAGGCGCAGAGTTCA 61
DB      2090 CCTGTATTCCTAGTCTGAGAGTCCGAGTCAGAGGAGCTGTTAGGCGCAGAGTTG 2149
QY      62 AGAGCAGCTGAGCAACACAGGAGA-CCTGTACTACAAAGATTAATTAATTAAGCCAG 120
DB      2150 AGAGCAGCTGAGCAACAGTGTAAACCCGTCTCTAATAAATTAATAATTAAGCCAG 2209
QY      121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGGAGGAGAGAGTAGGACTGCTGT- 179
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DB      2270 GAACTGGAGAGGCGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2328
QY      237 CAACAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 296
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QY      297 A 297
DB      2389 A 2389

RESULT 11
US-11-318-813-42/c
/ Sequence 42, Application US/11318813
/ Publication No. US20060105381A1
/ GENERAL INFORMATION:
/ APPLICANT: Ellipse Biopharmaceuticals Corporation
/ APPLICANT: Peltekova, Yanya D
/ APPLICANT: Siminovitsh, Katherine A
/ APPLICANT: St George-Hyslop, Peter H
/ APPLICANT: Rubin, Laurence A
/ APPLICANT: Peltekova, Yanya D
/ APPLICANT: Wintle, Richard F
/ TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIAT
/ FILE REFERENCE: ELLP-020
/ CURRENT APPLICATION NUMBER: US/11/318,813
/ CURRENT FILING DATE: 2005-12-27
/ PRIOR APPLICATION NUMBER: US/10/327,188
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/362,700
/ PRIOR FILING DATE: 2002-03-08
/ PRIOR APPLICATION NUMBER: 60/343,338
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/427,529
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: 60/362,717
/ PRIOR FILING DATE: 2002-03-08
/ NUMBER OF SEQ ID NOS: 42
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/ SEQ ID NO 42
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DB 16640 AAGACAGCCTGGGTAACTAGTGAACCCGTCTCTACTAATAATTAATTAGCTG 16581
QY 120 GGCTTAGTGCTCATCCCTGTGCTCCAGCTACTAGGAGGACAGAGTAGGA--CTGCT 176
DB 16580 GGCACGCTGGCAGTGCTGTATCCAGCTACTTGGAGACTGAGCAGAGAGTTCT 16521
QY 177 TGTCCAGAGGTCAAGACTGCACTGAGCTGAGACCCAGCCACTGCACTTCCAGCTGGG 236
DB 16520 TGAGCCTGAGGTGAGGTTGCACTGAGTCAACACCA-CTGCACCTCCAGCTGGG 16462
QY 237 CAACAAAAGAGACCCTGTCTCAAAAATAAGTAATAATAATAATA 283
DB 16461 CAACAAAGTAGACTCTCATCTCAACAAACACACAAACAACTATA 16415
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RESULT 12
US-11-293-697-1206/c
; Sequence 1206, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentln Ver. 2.1
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; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1206
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Matches 208; Conservative 0; Mismatches 73; Indels 6; Gaps 3;
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DB 2323 CCTGTATTCAGACTTTGGAGGCCAAGGTGGGACGATCACTTGGAGCCAGAGTTCA 2264
QY 62 AGAGCAGCTTGAACAACAGGAGGA-CCTGTCACTACAAGATAATAATTAGCCAG 120
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:46 ; Search time 2823.19 Seconds
(without alignments)
9445.379 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133

Perfect score: 417
Sequence: 1 gccacgggggacattcttgcg.....gctctggtccctcagctgt 417

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_env: *
2: gb_pat: *
3: gb_ph: *
4: gb_pl: *
5: gb_pr: *
6: gb_ro: *
7: gb_rts: *
8: gb_ay: *
9: gb_un: *
10: gb_vi: *
11: gb_ov: *
12: gb_hcg: *
13: gb_in: *
14: gb_om: *
15: gb_ba: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	100.0	3270	5 AF306570	AF306570 Homo sapi
2	417	100.0	3505	2 ES4511	ES4511 UCP-2 promo
3	417	100.0	12177	5 DQ087219	DQ087219 Homo sapi
4	417	100.0	155668	12 AC024029	AC024029 Homo sapi
5	417	100.0	156370	5 AP003717	AP003717 Homo sapi
6	417	100.0	199384	5 AP003531	AP003531 Homo sapi
7	405	97.1	3301	5 AF208500	AF208500 Homo sapi
8	400.2	96.0	197031	12 AC019121	AC019121 Homo sapi
9	87	20.9	7218	2 I66494	I66494 Sequence 14
10	76.4	18.3	170579	12 AC020985	AC020985 Homo sapi
11	76.4	18.3	179380	5 AL355501	AL355501 Human DNA
12	75.8	18.2	110000	4 AP008217_231	Continuation (232
13	75.8	18.2	128848	4 AC104844	AC104844 Oryza sat
14	74.4	17.8	154957	5 AC019270	AC019270 Homo sapi
15	74.4	17.8	160556	12 AC013645	AC013645 Homo sapi
16	74.4	17.8	170414	12 AC026019	AC026019 Homo sapi
17	74.4	17.8	197198	12 AC148630	AC148630 Callithrix
18	74.4	17.8	317499	12 AC117407	AC117407 Homo sapi

19	73.8	17.7	184251	12 AC173434	AC173434 Gorilla g
20	73.2	17.6	44515	5 AC114914	AC114914 Homo sapi
21	73.2	17.6	97129	5 HS292H14	AL008710 Human DNA
22	73.2	17.6	114279	12 AC083907	AC083907 Homo sapi
23	73.2	17.6	171941	12 AC026531	AC026531 Homo sapi
24	73.2	17.5	187927	5 AC046142	AC046142 Homo sapi
25	72.6	17.4	858	11 AY522982	AY522982 Colinus v
26	72.6	17.4	130119	12 AC117906	AC117906 Rattus no
27	72.6	17.4	161690	6 AC115697	AC115697 Mus muscu
28	72.6	17.4	211149	6 AC148019	AC148019 Mus muscu
29	72.6	17.4	236159	12 AC130109	AC130109 Rattus no
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35	71.8	17.2	148950	5 CT027658	CT027658 Macaca mu
36	71.8	17.2	153726	5 AC120194	AC120194 Homo sapi
37	71.8	17.2	155468	5 AC022730	AC022730 Homo sapi
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42	71.6	17.2	193953	12 AC149623	AC149623 Papio anu
43	71.4	17.1	186038	6 AC117612	AC117612 Mus muscu
44	71.4	17.1	211604	6 AC113491	AC113491 Mus muscu
45	71	17.0	185608	12 AC149179	AC149179 Papio anu

ALIGNMENTS

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AF306570 3270 bp DNA linear PRI 30-OCT-2000
LOCUS AF306570
DEFINITION Homo sapiens uncoupling protein 2 gene, promoter region and exon 1;
nuclear gene for mitochondrial product.
ACCESSION AF306570
VERSION AF306570.1 GI:11037742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 3270)
Schneitler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.
UCP2 promoter region and exon 1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3270)
Schneitler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.
Direct Submission
TITLE Submitted (18-SEP-2000) Laboratory Medicine, Landeskranken
JOURNAL Salzburger, Melchner Hauptstr. 48, Salzburg A-5020, Austria
location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-103;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	GCACGGGGGACAATTTTGGTCTGGAGGCGCTTGGATCTGTTCTGCTGGTCTAGCAAT	60
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OY	61	CTCACAGCAAAATTGGCCGAGCCTCTCCGGAAATGCACAGCCAGACAGGCTCAGCGCAAA	120
Db	1692	CTCACAGCAAAATTGGCCGAGCCTCTCCGGAAATGCACAGCCAGACAGGCTCAGCGCAAA	1751
OY	121	GCTAGAGAACTGGCGGAGGGAGACTCAAGTGCCACAAAATACTTATCTTTTCTTTT	180
Db	1752	GCTAGAGAACTGGCGGAGGGAGACTCAAGTGCCACAAAATACTTATCTTTTCTTTT	1811
OY	181	TTTTTTTCTTTTCTTTCTCTCTCTTTCTTCTGCTCTTCTGCTCTTCTCTCTCTCT	240
Db	1812	TTTTTTTCTTTTCTTTCTCTCTCTTTCTTCTGCTCTTCTGCTCTTCTCTCTCTCT	1871
OY	241	CTGTCTTCTTCTCTCTCTCTTTCTTTTCTTATTCACATATGCAGAAATCTCCTCATGCGAG	300
Db	1872	CTGTCTTCTTCTCTCTCTCTTTCTTTTCTTATTCACATATGCAGAAATCTCCTCATGCGAG	1931
OY	301	AAATATCTGCTTGACTTCTGTTTCCAAGCTGCTTCTGCCAGAGCAATGCGCTTCGCGCT	360
Db	1992	AAATATCTGCTTGACTTCTGTTTCCAAGCTGCTTCTGCCAGAGCAATGCGCTTCGCGCT	1991
OY	361	GTTTTTCTTTCGGCATATAATATCCAGGCGCATCCCAAGCTCTGGGCGCCCTCAGCGCT	417
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RESULT 2			
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LOCUS	E54511	3505 bp	DNA
DEFINITION	UCP-2 promoter and use thereof.		linear
			PAT 31-JAN-2002

VERSION	534311.1	GI:188238
KEYWORDS	JP 2000236886-A/1.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE	1 (bases 1 to 3505)
AUTHORS	Toyota, Y., Kobayashi, M. and Igaki, S.
TITLE	UCP-2 promoter and use thereof
JOURNAL	Patent: JP 2000236886-A 1 05-SEP-2000;

COMMENT	OS	Homo sapiens (human)

PN	JP 2000236886-A/1
PD	05-SEP-2000
PF	22-DEC-1999 JP 1999364724

PI YUKIO, TOKYOTA, MAKOTO KOBAAYASHI, SHIGERU IGAKI
PC C12N15/00, A61K45/00, A61P3/04, A61P3/06, A61P3/10, A61P9/12, PC
A61K29/00, C12N1/21
PC C12N5/10, C12D1/02, G01N33/15, G01N33/50//A61K31/711, A61K38/00,
PC A61K9/00,
PC (C12N15/09, C12R1:19), (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
PC C12R1:19),
PC (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)

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ORIGIN

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RESULT 3	LOCUS	DEFINITION
DO087219	DQ087219	12177 bp DNA linear PRI 18-JUN-2005
		Hom sapiens uncoupling protein 2 (mitochondrial, proton carrier) (UCP2) gene, complete cds; nuclear gene for mitochondrial product.

VERSION DQ087219.1 GI:67515418

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Mammalia; Eutheria; Euarchontoglires; Primates; Cetartiodactyla; Homi-
 nidae; Homo.
 1 (bases 1 to 12177)
 Livingston, R.J., Rieder, M.J., Shaffer, T., Bertucci, C., Baler, C.N.,
 AUTHORS

TITLE Nguyen, C.P., Gilderleeve, H., Cassidy, C.M., Johnson, E.J., Swanson, J.E., McFarland, I., Yool, B., Park, C. and Nickerson, D.A. Direct Substitution
JOURNAL Submitted (07-JUN-2005) Genome Sciences, University of Washington.

COMMENT To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS E815478, Department of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).

FEATURES	Location/Qualifiers
source	1. .12177

repeat_region

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repeat_region

12177 bp DNA linear PRI 18-JUN-2005
mammals uncoupling protein 2 (mitochondrial, proton carrier)
gene, complete cds; nuclear gene for mitochondrial product.
. .1 GI:67515418

mammals (human)

Homo sapiens
Homo sapiens
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homos.

Accession: U01191 (1 to 12177)
Author: Olson,R.V., Rieder,M.J., Shaffer,T., Bertucci,C., Baler,C.N.,
Barnes,N., Wills,H.T., Daniels,M., Downing,T.K., Stanaway,I.B.,
Simpson,P., Gilderaleevs,H., Cassidy,C.M., Johnson,E.J.,
J.E., McFarland,I., Yoo!,B., Park,C. and Nickerson,D.A.
Submission
and (07-JUN-2005) Genome Sciences, University of Washington,
Pacific, Seattle, WA 98195, USA
This work please use: NIEHS-SNPs, Environmental Genome
NIHES ES15478, Department of Genome Sciences, Seattle, WA
<http://sepp.gs.washington.edu>.

Location/Qualifiers

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/rpt_type=dispersed
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/frequency="0.02"
/replace="t"
2900 /gene="UCP2"
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/replace="t"
3310 /gene="UCP2"
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/translation="MVGFKATDVPTATVFKLAGTAACTADLTTPPLDPAKVLQIQ
GESQGPVRAASAQVGRVGMGTILTMVTEGPRSLYNGLVAGLQROMSFASRLGLYS
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NAYKTARBERGFRGKMGKTSPTNARNAIVNCAELVYTDILKDALIKANLTDDPCHF
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6779 /gene="UCP2"
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6787 /gene="UCP2"
/frequency="0.46"
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6850 /gene="UCP2"
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/replace="a"
7113.7334
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/replace="t"
7361.7480
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/rpt_type=dispersed
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7486.7570
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7723 /gene="UCP2"
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               /frequency="0.02"
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Query Match      100.0%; Score 417; DB 5; Length 12177;
Best Local Similarity 100.0%; Pred. No.5.4e-103;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGGGACAAATTTTGTCTGACAGCCCTTTCATCTGTCTGTCTGCTCAGCAAT 60
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DB 515 GCCAGGGGACAAATTTTGTCTGACAGCCCTTTCATCTGTCTGTCTGCTCAGCAAT 574
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QY 61 CTCACAGCAAAATTTGCCAGCCTCTCCGAAATGACAGCCAGACAGCTCAGCGCAAA 120
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DB 575 CTCACAGCAAAATTTGCCAGCCTCTCCGAAATGACAGCCAGACAGCTCAGCGCAAA 634
   |||||

QY 121 GCTAGAGAACTCGCGGAGGAGAGCTCAGAGTGCACAAAAAATTATCTTTCTTT 180
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DB 635 GCTAGAGAACTCGCGGAGGAGAGCTCAGAGTGCACAAAAAATTATCTTTCTTT 694
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QY 181 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 240
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QY 241 CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 300
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DB 755 CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 814
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QY 301 AAATTAATCTGAGCTTGAATCTGCTTTCAGCGCTGCTGCGAGAGACAGCGCTCGAGCT 360
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DB 815 AAATTAATCTGAGCTTGAATCTGCTTTCAGCGCTGCTGCGAGAGACAGCGCTCGAGCT 874
   |||||

QY 361 GTTTTCTTTCCGTATATATATATATATATATATATATATATATATATATATATAT 417
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RESULT 4
AC024029/c 155668 bp DNA linear HTG 07-JUL-2000
LOCUS      Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
DEFINITION
SEQUENCE 15 unordered pieces.
AC024029
AC024029.3 GI:7230916
VERSION    HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
            Bkayayote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 155668)
            Waterston,R.H.
REFERENCE 1
AUTHORS    The sequence of Homo sapiens clone
TITLE      Unpublished
JOURNAL    2 (bases 1 to 155668)
REFERENCE 2
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (20-FEB-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            On Mar 13, 2000 this sequence version replaced gi:7109555.
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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NH0167N04
Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q40
Consensus quality: 151087 bases at least Q20
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.38 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
* 11378 14368: contig of 2991 bp in length
* 14369 14468: gap of unknown length
* 14469 20130: contig of 5662 bp in length
* 20131 20230: gap of unknown length
* 20231 25513: contig of 5283 bp in length
* 25514 25613: gap of unknown length
* 25614 30765: contig of 5152 bp in length
* 30766 30865: gap of unknown length
* 30866 37337: contig of 6472 bp in length
* 37338 37437: gap of unknown length
* 37438 45571: contig of 8134 bp in length
* 45572 45671: gap of unknown length
* 45672 60199: contig of 14528 bp in length
* 60200 60299: gap of unknown length
* 60300 71424: contig of 11125 bp in length
* 71425 71524: gap of unknown length
* 71525 86218: contig of 14694 bp in length
* 86219 86318: gap of unknown length
* 86319 104104: contig of 17786 bp in length
* 104105 104205: gap of unknown length
* 104206 155668: contig of 51464 bp in length.
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1807..1906
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1907..4798
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4799..4898
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misc_feature
misc_feature
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20131..20230
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25514..25613
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Best Local Similarity 100.0%; Pred. No.6.2e-103;
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Db 69697 GCCAGGGGGAATTTTGGTCTGCAAGCCTTTGCATCTGTTGCTGCTCAGCAAT 69638
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Db 69637 CTCACAGCAAAATTTGCCGAGCCTCTCTCGGAATGACAGCAGACAGACTCAGCGCAAA 69578
QY 121 GCTAGAGAACTGGCGGAGGAGACTCAGTGCACAAAAAACTTATCTTTCTTT 180
Db 69577 GCTAGAGAACTGGCGGAGGAGACTCAGTGCACAAAAAACTTATCTTTCTTT 69518
QY 181 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 240
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QY 241 CTGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 300
Db 69457 CTGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 69398
QY 301 AAATTAATCTGCTTGAATTTATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 417
Db 69397 AAATTAATCTGCTTGAATTTATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 69281
QY 361 GTTTTCTTTCCGCTAATTAATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 417
Db 69337 GTTTTCTTTCCGCTAATTAATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 69281

RESULT 5
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LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-167N4, complete
DEFINITION
ACCESSION AP003717
VERSION AP003717.3 GI:20334343
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submision
JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
COMMENT (E-mail:hattori@gsc.riken.go.jp; URL:http://hnp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Apr 26, 2002 this sequence version replaced gi:16904692.
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ORIGIN
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Best Local Similarity 100.0%; Pred. No.6.2e-103;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGGGGGAATTTTGGTCTGCAAGCCTTTGCATCTGTTGCTGCTCAGCAAT 60
Db 44411 GCCAGGGGGAATTTTGGTCTGCAAGCCTTTGCATCTGTTGCTGCTCAGCAAT 44352
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Db 44351 CTCACAGCAAAATTTGCCGAGCCTCTCTCGGAATGACAGCAGACAGACTCAGCGCAAA 44292
QY 121 GCTAGAGAACTGGCGGAGGAGACTCAGTGCACAAAAAACTTATCTTTCTTT 180
Db 44291 GCTAGAGAACTGGCGGAGGAGACTCAGTGCACAAAAAACTTATCTTTCTTT 44232
QY 181 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 240
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[illegible]

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Db	181653	AAATAATTCGCTTGAATCTCTTTTCACAGCTGCTTTCGACAGACATGGCGTGGCGGT	181594
Qy	361	GTTTTCTTTCGCTTGAATTCACAGGCGCATCCAGACTCTGGTCCCTCAGCTGT	417
Db	181593	GTTTTCTTTCGCTTGAATTCACAGGCGCATCCAGACTCTGGTCCCTCAGCTGT	181537
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LOCUS	AF208500	3301 bp	DNA linear PRI 09-JAN-2000
DEFINITION	Homo sapiens uncoupling protein 2 (UCP2) gene, promoter and exon 1.		
ACCESSION	AF208500		
VERSION	AF208500.1	GI:6684000	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1. (bases 1 to 3301)		
AUTHORS	Tu, N., Chen, H., Wilmkes, U., Reinert, I., Marmann, G., Pirke, K.M. and Lenters, K.U.		
TITLE	Molecular cloning and functional characterization of the promoter region of the human uncoupling protein-2 gene		
JOURNAL	Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)		
PUBMED	10558866		
REFERENCE	2. (bases 1 to 3301)		
AUTHORS	Tu, N., Chen, H., Wilmkes, U., Reinert, I., Pirke, K.M. and Lenters, K.-U.		
TITLE	Functional characterization of the 5'-flanking and promoter regions of the human UCP3 gene		
JOURNAL	Biochem. Biophys. Res. Commun. (2000) In press		
AUTHORS	3. (bases 1 to 3301)		
	Lenters, K.-U., Tu, N. and Chen, H.		
JOURNAL	Direct Submission		
AUTHORS	Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics, Center for Psychobiological and Psychosomatic Research, University of Trier, Friedrich-Wilhelm-Strasse 23, Trier D-54290, Germany		
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Qy	61	CTCAGACAAATTTGCGAGAGCTCTCCGGAATGACAGGACAGACAGAGCTCAGCGCAAAA	120
Db	1844	CTCAGACAAATTTGCGAGAGCTCTCCGGAATGACAGGACAGACAGAGCTCAGCGCAAAA	1902

Oy	121	GTGAGAGAACTGGGGGAGGAGATCAAGTGCACAAAAAAATTATCTTTTCTTT	180
Db	1903	CGTAGAGAACTGGGGGAGGAGATCAAGTGCACAAAAAAATTATCTTTTCTTT	19632
Oy	181	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	240
Db	1963	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	20222
Oy	241	CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT	300
Db	2023	CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT	20822
Oy	301	AAATATATCGCTTACTCTCTTTTCCACAGCGCTTTCGACAGACATGCGCTG	360
Db	2083	AAATATATCGCTTACTCTCTTTTCCACAGCGCTTTCGACAGACATGCGCTG	21422
Oy	361	GTTTTCTTTCCGCTAATATATTCACAGGCCATCCACGCTGTGCTCCCTCAGCT	417
Db	2143	GTTTTCTTTCCGCTAATATATTCACAGGCCATCCACGCTGTGCTCCCTCAGCT	2199
RESULT 8			
LOCUS	AC019121	197031 bp	DNA linear HTG 07-JUL-2000
DEFINITION		Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT	
ACCESSION	AC019121		
VERSION	AC019121.3	GI:8440022	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
TITLE	Hominidae; Homo.		
JOURNAL	1 (bases 1 to 197031)		
AUTHORS	Waterston,R.H.		
REFERENCE	Unpublished		
TITLE	2 (bases 1 to 197031)		
JOURNAL	Waterston,R.H.		
AUTHORS	Direct Submission		
REFERENCE	University (30-DEC-1999) Genome Sequencing Center, Washington		
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,		
JOURNAL	MO 63108 USA		
COMMENT	On Jun 10, 2000 this sequence version replaced gi:7105573.		
	----- Genome Center -----		
	Center: Washington University Genome Sequencing Center		
	Center code: WUGSC		
	Web site:http://genome.wustl.edu/gsc/index.shm1		
	----- Project Information -----		
	Center project name: H_NH0535C12		
	----- Summary Statistics -----		
	Sequencing vector: M13; 55%		
	Sequencing vector: plasmid; 45%		
	Chemistry: Dye-primer ET; 55% of reads		
	Chemistry: Dye-terminator Big Dye; 45% of reads		
	Assembly program: Phrap; version 0.990319		
	Consensus quality: 182418 bases at least Q40		
	Consensus quality: 187565 bases at least Q30		
	Consensus quality: 190012 bases at least Q20		
	Insert size: 190000; agarose-fp		
	Insert size: 194831; sum-of-contigs		
	Quality coverage: 4.10 in Q20 bases; agarose-fp		
	Quality coverage: 4.05 in Q20 bases; sum-of-contigs		
	----- NOTE: -----		
	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 23 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		

	* as soon as it is available and the accession number will be preserved.
	* 1
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	2972
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	3072
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	5765
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	8568: contig of 2704 bp in length
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	8669
	12865: contig of 4197 bp in length
	12866
	12965: gap of unknown length
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	18581: contig of 5616 bp in length
	18582
	18681: gap of unknown length
	18682
	23851: contig of 5170 bp in length
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	23951: gap of unknown length
	23952
	28414: contig of 4463 bp in length
	28415
	38514: gap of unknown length
	33195: contig of 4681 bp in length
	33196
	33295: gap of unknown length
	33296
	38648: contig of 5353 bp in length
	38649
	38748: gap of unknown length
	38749
	44525: contig of 6177 bp in length
	44926
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	45026
	51784: contig of 6759 bp in length
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	58855: contig of 6971 bp in length
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	68290
	68389: gap of unknown length
	68390
	77123: contig of 8734 bp in length
	77124
	77223: gap of unknown length
	77224
	87292: contig of 10069 bp in length
	87293
	87392: gap of unknown length
	87393
	96029: contig of 8637 bp in length
	96030
	96129: gap of unknown length
	96130
	104791: contig of 8662 bp in length
	104792
	104891: gap of unknown length
	104892
	116512: contig of 12021 bp in length
	116513
	117012: gap of unknown length
	117013
	131368: contig of 14356 bp in length
	131369
	131468: gap of unknown length
	131469
	142993: contig of 11525 bp in length
	142994
	143093: gap of unknown length
	143094
	154361: contig of 11268 bp in length
	154362
	154461: gap of unknown length
	154462
	173802: contig of 19341 bp in length
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	173902: gap of unknown length
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gap	2972..3071
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Matches 413; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GCCAGGGGAGACATTTTGGTCGACAGCCCTTGACATCTGTCGTGCTGACCAAT 60
DB 163820 GCCAGGGGAGACATTTTGGTCGACAGCCCTTGACATCTGTCGTGCTGACCAAT 163879

QY 61 CTCACGCAAAATTTGCCGAGCCTCTCCGAAATGCAACGCAACAGCTCAGCGCAAA 120
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QY 121 GCTAGGAACCTGGGAGGAGAGACTCACAGTGCACAAAACCTTAATCTTTCTTT 180
DB 163940 TCTAGGAACCTGGGAGGAGAGACTCACAGTGCACAAAACCTTAATCTTTCTTT 163999

QY 181 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 240
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DB 164060 CTGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 164119

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DB 164120 AATAATCGCCCTTGACTCTGTTTCCAGCGCTCTGCGACGACATGCGCGCTG 164178

QY 361 GTTTTCTTTCCGCTAATTAATTAATCAAGCCCATCCAGCTCTGCTCCCTCACTG 417
DB 164179 GTTTTCTTTCCGCTAATTAATTAATCAAGCCCATCCAGCTCTGCTCCCTCACTG 164235

RESULT 9
166494 7218 bp DNA linear PAT 28-DEC-1997
LOCUS Sequence 14 from patent US 5670367.
DEFINITION 166494
ACCESSION 166494.1 GI:2724471
VERSION 166494.1
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 7218)
AUTHORS Dörner, F., Scheiflinger, F. and Falkner, F. Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SBP-1997;
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ORIGIN

Query Match 20.9%; Score 87; DB 2; Length 7218;
Best Local Similarity 4.3%; Pred. No. 5e-13;
Matches 12; Conservative 197; Mismatches 72; Indels 0; Gaps 0;

QY 131 CTGGCGGAGGAGACTCACAGTGCACAAAACCTTAATCTTTCTTTTCTTTCTT 190
DB 1046 CAGGTGAGGAGACTTGCATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1105

QY 191 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 250
DB 1106 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1165

QY 251 TTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 310
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ORIGIN

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Matches 140; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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DB      111144 GAACCTGCGGAGGAGAGACTGAGCTAATAAATACCTTTCTCTCTCTCTTC 111203

QY      187 TCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246
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DB      111204 TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 111263

QY      247 TCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 306
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DB      111264 TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 111323

QY      307 TCTGACCTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 366
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DB      111324 TCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 111383

QY      367 CTTTCC 372
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DB      111384 CTTTCC 111389

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RESULT 11
AL355501/c 179380 bp DNA 1linear PRI 18-MAY-2005
LOCUS Human DNA sequence from clone RP11-360P7 on chromosome 10 Contains
DEFINITION the 5' end of the gene for a novel protein (FLJ37798), a zinc
finger protein pseudogene and a CpG island, complete sequence.

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ACCESSION        AL355501
VERSION          AL355501.26 GI:15384628
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SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE        1 (bases 1 to 179380)
AUTHORS          Kay, M.
TITLES           Direct Substitution
JOURNAL          Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
COMMENT          On June 31, 2001 this sequence version replaced gi:14329345.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL, Sw: SWISSPROT, Tr: TrEMBL, Wp: WORMPEP, Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-360P7 is from the library RPCT-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk
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FEATURES

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mRNA

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Db 154732 CTTTCC 154727

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WPCOMMENT

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AP008217_142	14200001	14310000
AP008217_143	14300001	14410000
AP008217_144	14400001	14510000
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AP008217_146	14600001	14710000
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AP008217_150	15000001	15110000
AP008217_151	15100001	15210000
AP008217_152	15200001	15310000
AP008217_153	15300001	15410000
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AP008217_156	15600001	15710000
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AP008217_158	15800001	15910000
AP008217_159	15900001	16010000
AP008217_160	16000001	16110000
AP008217_161	16100001	16210000
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AP008217_169	16900001	17010000
AP008217_170	17000001	17110000
AP008217_171	17100001	17210000
AP008217_172	17200001	17310000
AP008217_173	17300001	17410000
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AP008217_176	17600001	17710000
AP008217_177	17700001	17810000
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AP008217_180	18000001	18110000
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AP008217_183	18300001	18410000
AP008217_184	18400001	18510000
AP008217_185	18500001	18610000
AP008217_186	18600001	18710000
AP008217_187	18700001	18810000
AP008217_188	18800001	18910000
AP008217_189	18900001	19010000
AP008217_190	19000001	19110000
AP008217_191	19100001	19210000
AP008217_192	19200001	19310000
AP008217_193	19300001	19410000
AP008217_194	19400001	19510000
AP008217_195	19500001	19610000
AP008217_196	19600001	19710000

[illegible]

LOCUS	AC104844/C	128848 bp	DNA	linear	PLN 22-JAN-2004
DEFINITION	Oryza sativa (japonica cultivar-group)	chromosome 11	BAC clone		
ACCESSION	AC104844				
VERSION	AC104844.2	GI:11058064			
KEYWORDS	HTG.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
REFERENCE	Oryza sativa (japonica cultivar-group)				
AUTHORS	*Currie,J., *Collura,K., *Soderlund,C., *Wing,R., Gaur,A., Raghuvanshi,S., Khurana,P. and Tyagi,A.K.				
JOURNAL	Submitted (21-DEC-2001) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India				
REMARK	# The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873, USA				
REFERENCE	2 (bases 1 to 128848)				
AUTHORS	Khurana,J.P., #Linton,E.W., #Messing,J., *Yu,Y., *Rambo,T., Raghuvanshi,S., Khurana,P. and Tyagi,A.K.				
JOURNAL	Submitted (22-JAN-2004) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India				
REMARK	On Jan 22, 2004 this sequence version replaced gi:11976554. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. There are Bacterial Transposons at base 4874-8468 and 101808-105050 and from base 104112-104122 there are only transposon reads. The assembly overlaps from base 11302-128848 with OSJNBa0034K24 (accession #AF161269). The overlap is from bases 127311-124852 on OSJNBa0034K24. The nucleotide sequence of this BAC clone was completed to Phase 2 jointly by the Indian Initiative for Rice Genome Sequencing Project and The Plant Genome Initiative at Rutgers, and Finished/Annotated (Phase 3) at the Arizona Genomics Institute under the Indo-USA collaboration.				
FEATURES	Location/Qualifiers				
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	/clone="OSJNB00301L19"				
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ORIGIN					
Query Match	18.2%;	Score 75.8;	DB 4;	Length 128848;	
Best Local Similarity	80.2%;	Pred. No. 6.7e-10;			

[illegible]

REFERENCE
AUTHORS

Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 154957)

Birren, B., Linton, L., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glnde, S., Gord, S., Goylette, M., Graham, L., Grand-pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Lahocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M., Mcwan, P., McKernan, K., Meldrum, J., Menes, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Punthang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnuppach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stefanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vasaliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, J., Zemek, L., Zimmer, A. and Zody, M.

TITLE
 Direct Submission

JOURNAL
 Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 20, 2002 this sequence version replaced gi:18252020.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RW/RepeatMasker.html>

COMMENT

----- Genome Center -----
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: MIR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information -----
 Center project name: L3046
 Center clone name: 10_C_8

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 /db_xref="taxon:9606"
 /chromosome="8"
 /map="g"
 /clone="RP11-10C8"
 /clone_lib="RPC1-11 Human Male BAC"
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 /rpt_family="MIR3"
 3423..3731
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 4785..4905
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 5524..5693
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/rpt_family="MST7A"
repeat_region complement(11165. .11453)
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repeat_region 11881. .12074
/rpt_family="MSTB1"
repeat_region 12076. .12202
/rpt_family="FLAM_C"
repeat_region 12216. .12456
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repeat_region 12601. .12909
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repeat_region 13972. .13992
/rpt_family="AT_rich"
repeat_region 14119. .14422
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repeat_region 15630. .15932
/rpt_family="AluY"
repeat_region 16793. .16823
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repeat_region 17216. .17279
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/rpt_family="L2"
repeat_region complement(21297. .21594)
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repeat_region complement(23766. .24061)
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repeat_region 24391. .24412
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repeat_region complement(24565. .24737)
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repeat_region 24738. .24767
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QY 167 TTATCTTTTCTTTTTCYTTCTTTCTTTCTTTCTTTCTTTGTCTTTCTGCTT 226

[illegible]

RESULT 15	
AC013645	
LOCUS	AC013645
DEFINITION	Homo sapiens clone RP11-17H6, WORKING DRAFT SEQUENCE, 11 unordered pieces.
ACCESSION	AC013645
VERSION	AC013645.3
KEYWORDS	GI:7381812
SOURCE	HTG: HTGS PHASE1; HTGS_DRAFT.
ORGANISM	Homo sapiens (human)
	Homo sap lens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 160556)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RPL-17H6
Unpublished
2 (bases 1 to 160556)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

TITLE	Direct Submission
JOURNAL	Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Apr 1, 2000 this sequence version replaced gi:64789998.

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

```
----- Project Information
Center project name: L3643
```

Center clone name: 17_H_6
----- Summary Statistics -----

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731
Consensus quality: 156212 bases at least Q40

Consensus quality: 157480 bases at least Q30
Consensus quality: 158348 bases at least Q20

Insert size: 157000; agarose-1p
Insert size: 159556; sum-of-contigs

Quality coverage: 7.7 in Q20 bases; agarose-tp
Quality coverage: 7.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

*	1	1050: contig of 1050 bp in length
*	1051	1150: gap of 100 bp
*	1151	4281: contig of 3131 bp in length
*	4282	4381: gap of 100 bp
*	4382	12996: contig of 8615 bp in length
*	12997	13096: gap of 100 bp
*	13097	23348: contig of 10452 bp in length
*	23549	23648: gap of 100 bp
*	23649	36288: contig of 12640 bp in length
*	36289	36288: gap of 100 bp
*	36289	50226: contig of 13838 bp in length
*	50227	50326: gap of 100 bp
*	50327	63487: contig of 13161 bp in length
*	63488	63587: gap of 100 bp
*	63588	82132: contig of 18545 bp in length
*	82133	82232: gap of 100 bp
*	82233	101188: contig of 18956 bp in length
*	101189	101288: gap of 100 bp
*	101289	128638: contig of 27250 bp in length
*	128639	128638: gap of 100 bp
*	128639	160556: contig of 31918 bp in length.

FEATURES
Source

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misc_feature      |1..1050  
gap               |note="assembly_fragment"  
                  |1051..1150  
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gap              |4282..4381  
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                  |4382..12966  
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                  |36289..36388  
misc_feature     |estimated_length=100  
                  |36389..50236  
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gap              |50227..50326  
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                  |50327..63487  
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gap              |63488..63587  
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gap              |101189..101288  
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ORIGIN
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128639..160556
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[illegible]

Search completed: June 5, 2006, 22:27:11
Job time : 2830.19 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 362.801 Seconds
(without alignments)
803.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133
Perfect score: 417
Sequence: 1 gccagcgggacacattcttg.....gtctgtgcccctcagctgt 417

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq.8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	417	100.0	3505	AAA62932 DNA conca
2	71.6	17.2	188888	ABQ75562 Human rel
3	70.4	16.9	1548	ABZ43078 Human GPC
4	70	16.8	472	ACH29376 Human adu
5	69.2	16.6	231222	ADL13693 Osteoarth
6	67.4	16.2	288563	AEE05135 Cancer-as
7	67.2	16.1	3326	ADP28980 Homo prot
8	67	16.1	1755	ADP28980 Human sec
9	67	16.1	277616	ABD32602 Human can
10	66.8	16.0	170834	AAD62833 Human BAC
11	66	15.8	180821	ADL13761 Osteoarth
12	65.6	15.7	3583	ADQ23651 Human sof
13	65.4	15.7	849	AA89073 DNA encof
14	65.4	15.7	1073	AD148332 Maize oil
15	65.4	15.7	11456	AAK59400 Human imm
16	65.4	15.7	37590	AA512439 DNA encof
17	65.4	15.7	99544	AD213273 Human can
18	65.4	15.7	99588	ACN45034 Human gen

C	19	65.4	15.7	144392	15	AEE75162 Human pol
	20	65.4	15.7	272022	12	ADQ97126 Human can
	21	65.2	15.6	563	5	ABV50724 Human pro
	22	65.2	15.6	42998	8	ADA14747 Human rib
	23	65.2	15.6	42999	6	AB855032 Invertebr
	24	65.2	15.6	42999	10	AA61411 Human rib
	25	65.2	15.6	42999	13	ADR43949 Human rib
	26	65.2	15.6	42999	14	ABE25475 Human rib
	27	65	15.6	432	5	ABV58626 Human pro
	28	64.6	15.5	504	5	ABV58626 Human pro
	29	64.6	15.5	42999	8	ABX11086 Human rib
	30	64.6	15.5	89625	11	ACN45194 Human gen
	31	64.4	15.4	1096	10	AD14268 Human enz
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	33	64	15.3	73465	6	ABO88161 Human ost
	34	63.8	15.3	248	13	ACN55172 Cotton an
	35	63.8	15.3	392	5	ABV48356 Human pro
	36	63.6	15.3	712	4	AAE81806 Human pro
	37	63.6	15.3	1121	15	AEE30075 Lead Cere
	38	63.6	15.3	3578	13	ADR07968 Full leng
	39	63.6	15.3	8317	4	AA835779 Human car
	40	63.6	15.3	8317	10	ADE6473 Human car
	41	63.6	15.3	8317	13	AD07891 Human car
	42	63.6	15.3	330973	11	ACN44846 Human gen
	43	63.4	15.2	540	5	ABV58372 Human pro
	44	63.4	15.2	770	4	AA195041 Human neu
	45	63.4	15.2	1840	10	ADC87550 Human GPC

ALIGNMENTS

RESULT 1	AAA62932	standard; DNA; 3505 BP.
ID	AAA62932	
XX	AAA62932;	
AC	XX	
DT	02-NOV-2000	(first entry)
XX	XX	
DE	DNA containing human uncoupling protein-2 (UCP-2) promoter region.	
XX	XX	
KM	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;	
KW	hypotension; hyperlipidaemia; anti-pyretic; ds.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	WO200039315-A1.	
XX	XX	
PD	06-JUL-2000.	
XX	XX	
PF	22-DEC-1999;	99WO-JP007198.
XX	XX	
PR	24-DEC-1998;	98JP-00366719.
XX	XX	
PA	(TAKE) TAKEDA CHEM IND LTD.	
XX	XX	
PI	Toyoda Y, Kobayashi M, Igaki S;	
XX	XX	
DR	WPI; 2000-452407/39.	
XX	XX	
PT	DNA with promoter region containing regulator sequence of uncoupling	
XX	XX	
PT	protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,	
XX	XX	
PT	hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in	
XX	XX	
PS	Claim 4; Fig 1-6; 43pp; Japanese.	
XX	XX	
CC	This invention relates to DNA comprising a promoter region containing the	
XX	XX	
CC	regulatory sequences of human uncoupling protein-2 (UCP-2). Included in	
XX	XX	
CC	the invention are a recombinant vector containing the DNA sequence, cells	
XX	XX	
CC	transformed by the vector, and a method for screening for compounds or	
XX	XX	
CC	salts that can promote or inhibit the UCP-2 promoter activity using the	

CC transformants. The DNA and cells transformed using it can be used to
 CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidaemic
 CC and anti-pyretic drugs. The present sequence represents DNA containing
 CC the UCP-2 promoter sequences

XX SQ Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 417; DB 3; Length 3505;
 Best Local Similarity 100.0%; Pred. No. 2.5e-79;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGGGACAAATTTGGTCTGACAGGCTTGTGCACTGTTGCTGTCAGCAAT 60

DB 717 GCCAGGGGACAAATTTGGTCTGACAGGCTTGTGCACTGTTGCTGTCAGCAAT 776

QY 61 CTCACGCAAAATTTGGCGAGCCCTCCGAAATGCAAGCCAGACAGGCTCAGCGGAAA 120

DB 777 CTCACGCAAAATTTGGCGAGCCCTCCGAAATGCAAGCCAGACAGGCTCAGCGGAAA 836

QY 121 GCTAGAGAACTGGCGAGGAGACTCACAGTCCCAAAAAAATTATCTTTCTTT 180

DB 837 GCTAGAGAACTGGCGAGGAGACTCACAGTCCCAAAAAAATTATCTTTCTTT 896

QY 181 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 240

DB 897 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 956

QY 241 CCGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 300

DB 957 CCGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 1016

QY 301 AATAATTCGCTTGAATCTTCTGTTTCCACGCTGCTTCCGACAGACATGCGTGGCGT 360

DB 1017 AATAATTCGCTTGAATCTTCTGTTTCCACGCTGCTTCCGACAGACATGCGTGGCGT 1076

QY 361 GTTTTCTTTCCGCTATATATATCCAGGCCATCCAGCTCTGTCCCTCACTGT 417

DB 1077 GTTTTCTTTCCGCTATATATATCCAGGCCATCCAGCTCTGTCCCTCACTGT 1133

RESULT 2

ABQ75562/c

ID ABQ75562 standard; DNA; 18888 BP.

AC ABQ75562;

DT 11-NOV-2002 (first entry)

DE Human related CYP 27C1 clone RP11-30F3 SEQ ID NO:21.

XX Cloning; characterisation; human; cytochrome P450; CYP 27C1; cytostatic;

KM chryomimetic; antidiabetic; antipsoriatic; tuberculostatic; osteoparitic;

KM vitamin D metabolite deficiency; hyperparathyroidism; hypoparathyroidism;

KM medullary carcinoma; psoriasis; sarcoidosis; tuberculosis; osteomalacia;

KM chronic renal disease; vitamin D dependent rickets; anticonvulsant;

KM fibrogenesis imperfecta ossium; osteitis fibrosa cystica; osteoporosis;

KM osteoparitis; osteosclerosis; renal osteodystrophy; rickets; steatorrhea;

KM glucocorticoid antagonism; idiopathic hypercalcaemia; tropical sprue;

KM malabsorption syndrome; cholesterol steroid; lipid metabolic disorder;

XX gene; de.

XX Homo sapiens.

XX MO200264765-A2.

XX 22-AUG-2002.

XX 11-FEB-2002; 2002MO-CA000163.

XX 09-FEB-2001; 2001US-0267410P.

XX (CYTO-) CYTOCHROME INC.

XX WIPI; 2002-657595/70.

XX New nucleic acid molecules encoding cytochrome P450 proteins, human CYP

PT 27C1 and a hybrid homologs from Xenopus laevis, useful for treating

PT diseases related to vitamin D or vitamin D metabolite deficiency, e.g.

PT parathyroidism and diabetes.

XX Example 1; Fig 1A; 209pp; English.

XX The present invention describes an isolated nucleic acid molecule (1)

CC encoding human cytochrome P450, CYP 27C1, and a hybrid homologe from

CC xenopus laevis. (1) has chryomimetic, antidiabetic, cyostatic,

CC antipsoriatic, tuberculostatic, osteoparitic, dermatological and

CC antihyperemic activities, and can be used in gene therapy and in vaccines.

CC The nucleic acid molecules, proteins and methods from the present

CC invention are useful for treating diseases related to vitamin D or

CC vitamin D metabolite deficiency, e.g. hyper- and hypo-parathyroidism,

CC pseudohypo-parathyroidism, Secondary hyperparathyroidism, diabetes,

CC medullary carcinoma, psoriasis, sarcoidosis, tuberculosis, chronic renal

CC disease, hypophosphatemic VDR, vitamin D dependent rickets,

CC anticonvulsant treatment, fibrogenesis imperfecta ossium, osteitis

CC fibrosa cystica, osteomalacia, osteoporosis, osteoparitis, osteosclerosis,

CC renal osteodystrophy, rickets, glucocorticoid antagonism, idiopathic

CC hypercalcaemia, malabsorption syndrome, steatorrhea, and tropical sprue,

CC or cholesterol, steroid and other lipid metabolic disorders. The present

CC sequence represents a human related CYP 27C1 clone designated RP11-30F3,

CC which is given in an example from the present invention

XX Sequence 18888 BP; 51055 A; 42661 C; 43560 G; 47708 T; 0 U; 3904 Other;

SQ

Query Match 17.2%; Score 71.6; DB 6; Length 18888;

Best Local Similarity 78.2%; Pred. No. 2e-05;

Matches 86; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 165 CTTATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCC 224

DB 44890 CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCC 44831

QY 225 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCC 274

DB 44830 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCC 44781

RESULT 3

ABZ43078/c

ID ABZ43078 standard; DNA; 1548 BP.

AC ABZ43078;

DT 06-MAR-2003 (first entry)

XX Human GPCR polynucleotide SEQ ID NO 417.

XX Human GPCR; G protein coupled receptor; signal transduction; olfactory;

XX drug development; gustatory; taste; fragrance; gene; de.

XX Homo sapiens.

XX MO200216548-A2.

XX 28-FEB-2002.

XX 30-JUL-2001; 2001MO-IB001446.

XX 04-AUG-2000; 2000JP-00237818.

XX 13-FEB-2001; 2001JP-00034434.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Haga T, Takeda S, Mitaku S,

PI

XX	WPI. 2002-304118/34.
DR	P-P8DB; ABP955804.
PR	Database global search for G protein-coupled receptors, proteins and
PT	p encoded genes for studying in vivo signal transduction mechanism and
xx	identifying targets for drug development.
xx	
PS	Claim 9; SEQ ID NO 417; 97pp + Sequence Listing; Japanese.
CC	The invention relates to a method for screening G protein-coupled
CC	receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC	ABP95992) by extracting open-reading frames containing 6-8 transmembrane
CC	domains with 250-1000 amino acid residues to give a gene homologous with
CC	a known GPCR gene. The receptor proteins and encoded genes are useful for
CC	studying in vivo signal transduction mechanism and identifying targets
CC	for drug development e.g. based on olfactory and gustatory receptors in
CC	form of agonists and antagonists by screening intrinsic and extrinsic
CC	ligands as bitter taste inhibitors, taste enhancers and fragrance
CC	improvers. Note: The sequence data for this patent did not form part of
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ	Sequence 1548 BP; 577 A; 219 C; 320 G; 332 T; 0 U; 100 Other;
OY	Query Match 16.9%; Score 70.4; DB 6; Length 1548;
	Best Local Similarity 78.2%; Pred. No. 1.6e-05;
	Matches 97; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
Dd	168 TATCTTTCTTTTTTTCCTTTCTTTCTTTCTTTCTTTCTTTGCTTGTCTT 227
	1148 TCTCTTTCTTTTAATTATTTCTTTCTTTCTTTCTTTCTTTCTTC-TCTTTCTTTC 10950
Oy	228 CCTCTCTCTCTCGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTTCCACAGCAAGAT 287
Dd	1089 TTCTTTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCCCTCC 10300
Oy	288 CTCC 291
Dd	1029 CTCCTC 1026
RESULT 4	
ACH29376/C	
ID	ACH29376 standard; cDNA; 472 BP.
XX	ACH29376;
XX	
DT	13-OCT-2003 (first entry)
XX	
DE	Human adult spleen cDNA #395.
XX	
KM	Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX	genome mapping; biodiversity; genetic disorder.
OS	Homo sapiens.
PN	US2003073623-A1.
PD	17-APR-2003.
PF	30-JUL-2001; 2001US-00918995.
PR	30-JUL-2001; 2001US-00918995.
PA	(DRAVA/) DRMANAC R T.
PA	(LABA/) LABAT I.
PA	(STAC/) STACHE-CRAIN B.
PA	(DICK/) DICKSON M C.
PI	(JONE/) JONES L W.
XX	
PI	Drmanac RT, labat I, Stache-Crain B, Dickson MC, Jones LW;
XX	

XX	DR	WPI; 2003-615964/58.
PT	FT	New polynucleotide sequences obtained from various cDNA libraries, useful
PT	as hybridization probes, as oligomers for PCR, for chromosome and gene	
PT	mapping, in the recombinant production of protein, or in generating	
PT	antisense DNA or RNA.	
PS	Claim 1; SEQ ID NO 16588; 44pp; English.	
XX	CC	The invention relates to an isolated polynucleotide comprising any one of
CC	CC	38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC	CC	determined by the technique of SSH (sequencing by hybridisation). Also
CC	CC	included is a purified polypeptide comprising a sequence corresponding to
CC	CC	a reading frame of the novel polynucleotide. The nucleic acid sequences
CC	CC	are useful in diagnostics as expressed sequence tags (EST) for
CC	CC	identifying expressed genes or for physical mapping of the human genome,
CC	CC	in forensics, in assessing biodiversity, or in identifying mutations
CC	CC	responsible for genetic disorders and other traits. The nucleotide
CC	CC	sequences are also useful as hybridisation probes, as oligomers for PCR,
CC	CC	for chromosome and gene mapping, in the recombinant production of
CC	CC	protein, or in generating antisense DNA or RNA. The purified polypeptide
CC	CC	is useful for generating antibodies specific for it. The present sequence
CC	CC	is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC	CC	for this patent did not form part of the printed specification, but was
CC	CC	obtained in electronic format directly from USPTO at
CC	CC	seqdata.uspto.gov/sequence.html?docID=20030073623
SQ	XX	Sequence 472 BP; 194 A; 52 C; 92 G; 115 T; 0 U; 19 Other;
		Query Match 16.8%; Score 70; Denom 472;
		Best Local Similarity 65.8%; Pred. No. 1.6e-05;
		Matches 100; Conservative 0; Mismatches 52; Indels 0; Gaps 0
Qy	Db	154 CCACAAAAAACTTATCTTTCTTTTTTTTTCTTTCTTTCTTTCTTTCTT 213
		325 CCCCAANNAATTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 266
Qy	Db	214 GTCTTTCTGTTCCTCCTCTCTCTCTGCTTTCTTCCCTCTTCTTTCTTTC 273
		265 GTTTC 206
Qy	Db	274 CTACATGGCAAGATCTCCTCATGGCAGAATA 305
		205 CACAAAAACAAGCGCCTTATTCAGTATTA 174
RESULT 5		
ADL13693/C		
ID	ADL13693	standard; DNA; 231222 BP.
XX	AC	
XX	ADL13693;	
XX	DT	06-MAY-2004 (first entry)
DE	XX	Osteoarthritis-associated polymorphic nucleotide #225.
XX	KW	ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW	KW	joint space narrowing; osteophyte development; joint pain;
KW	KW	osteoarthritis; SNP; single nucleotide polymorphism.
OS	XX	Homo sapiens.
XX	MO	WO2003054166-A2.
PD	XX	03-JUL-2003.
PF	XX	19-DEC-2002; 2002WO-US041225.
PR	XX	20-DEC-2001; 2001US-0342603P.
PA	(INCY-) INCYTE GENOMICS INC.
Jones KA, Schafer A;		

[illegible]

XX		Disclousure; SEQ ID NO 453; 148bp; English.
PS		The invention relates to new isolated cancer-associated nucleic acid and
CC		polypeptide sequences. Also included are the following: a host cell
CC		comprising the recombinant nucleic acid or expression vector; an
CC		expressing vector comprising the isolated nucleic acid; a microarray for
CC		detecting a cancer associated (CA) nucleic acid comprising at least one
CC		probe comprising at least 10 contiguous nucleotides of the sequence given
CC		in the specification; an isolated polypeptide encoded within an open
CC		reading frame of a CA sequence; an isolated antibody or its antigen
CC		binding fragment that binds to the polypeptide; a hybridoma that produces
CC		the monoclonal antibody; a kit for detecting cancer cells comprising the
CC		antibody; a kit for diagnosing the presence of cancer in a test sample;
CC		comprising at least one polynucleotide that selectively hybridizes to a
CC		CA polynucleotide sequence; a method for detecting a presence or an
CC		absence of cancer cells in an individual; an electronic library
CC		comprising the polynucleotide or polypeptide or its fragment comprising
CC		the CA polynucleotide or polypeptide sequence, or its complement; a
CC		method of screening for anticancer activity; a method for detecting
CC		cancer associated with expression of a polypeptide in a test cell sample;
CC		a method for screening for a bioactive agent capable of modulating the
CC		activity of a CA protein (CAP), where the CAP is encoded by the nucleic
CC		acid sequence given in the specification; a method for diagnosing cancer;
CC		a method for treating cancer; and a method for inhibiting expression of a
CC		cancer associated (CA) gene in a cell. Inhibiting expression of a cancer
CC		associated (CA) gene in a cell comprises contacting a cell expressing a
CC		CA gene with a double stranded RNA comprising a sequence capable of
CC		hybridizing to a cancer associated (CA) mRNA corresponding to the
CC		polynucleotide sequences given in the specification, in an amount
CC		sufficient to elicit RNA interference and inhibiting expression of the CA
CC		gene in the cell. The double stranded RNA is provided by introducing a
CC		short interfering RNA (siRNA) into the cell by transfection,
CC		electroporation or microinjection. The double stranded RNA is provided by
CC		introducing a short interfering RNA (siRNA) into the cell by an
CC		expression vector. The polynucleotides are useful in preparing a
CC		composition for diagnosing or treating cancer. The present sequence
CC		represents a cancer-associated DNA of the invention. Note: This sequence
CC		is not shown in the specification but was obtained in electronic format
CC		directly from WIPO at
CC		ftp.wipo.int/pub/published_pct_sequences/17.11.2005/.
XX		
SO		Sequence 288563 BP; 79385 A; 61331 C; 62963 G; 83030 T; 0 U; 2854 Other;
Query Match	16.2%;	Score 67.4; DB 14; Length 288563;
Best Local Similarity	71.2%;	Pred. NO. 0.00017;
Matches	89; Conservative	0; Mismatches 36; Indels 0; Gaps 0;
OY	166	TTTATCTTTCTTTTTTTTTTTTCCTTCTTCTGCTCCTTGTGCTTGCTCT 225
DB	17138	TCTCTCTCTCTTTTCTTTTCTCTTTCATCTCTCTCTCTCTCTCTCTTTCT 17139
OY	226	TTCTCTCTCTCTCTGCTGCTTCTTCCCTCTCTCTCTTCTTCCACATGGCAAG 285
DB	17198	TTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTGAAGAAG 1725
OY	286	ATCTC 290
DB	17258	TTTTC 17262
RESULT 7		
ADK00688/c		
ID	ADK00688	standard; DNA; 3226 BP.
XX		
AC	ADK00688;	
XX		
DT	06-MAY-2004	(first entry)
XX		
DE	HOMO protein encoding sequence #33.	
XX		
KW	cancer; Cytostatic; cancer; ds; HOMO; ds.	
XX		


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XX DR WPI; 2004-348438/32.
XX XX New nucleic acid molecule for diagnosing, preventing or treating diseases
XX PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
XX PT genetic, bacterial and viral diseases.
XX PS Claim 1; SEQ ID NO 978; 428bp; English.
CC CC The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein encoding sequence. The
CC present sequence is available on MIPOMEB and is not in the specification.
SQ SQ Sequence 1755 BP; 715 A; 325 C; 396 G; 319 T; 0 U; 0 Other;
Query Match 16.1%; Score 67; DB 12; Length 1755;
Best Local Similarity 76.6%; Pred. No. 8.9e-05;
Matches 82; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 165 CTCTAATCTTTCTTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTGTCCTTCCTTC 224
Db 1450 CTTTCCTTTTCTTTCTTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTC 1391
QY 225 TTTCCTCTCTCCTCCTCCTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTT 271
Db 1390 CTCCTCTTCCTTTCTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 1344
RESULT 9
ABD32602
ID ABD32602 standard; DNA; 277616 BP.
AC ABD32602;
XX 18-NOV-2004 (first entry)
XX DS Human cancer-associated genomic DNA HD7-221.
XX KM Human; ds; cancer-associated protein; gene; cytosolic; cancer;
XX KM leukaemia; lymphoma; CAP.
OS Homo sapiens.
PN WO2004074320-A2.
PD 02-SEP-2004.
PF 17-FEB-2004; 2004WO-US004730.
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
PA (SAGR-) SAGRES DISCOVERY INC.
XX PI Morris DW, Morris DW, Malandro MS;
DR WPI; 2004-652914/63.
XX PT New isolated cancer-associated polynucleotides and polypeptides useful
XX PT for diagnosing, preventing or treating cancers, especially lymphoma and
XX PT leukemia, or in screening for agents that modulate cancer.
PS claim 16; seqid 109; 310pp; English.
XX

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CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells/comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcc_sequences
XX
XX Sequence 277616 BP; 84510 A; 49827 C; 49846 G; 93433 T; 0 U; 0 Other;
SQ
Query Match      16.1%; Score 67; DB 13; Length 277616;
Best Local Similarity 76.6%; Pred. No. 0.0002;
Matches 82; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY          166 TTATCTTTCTTTTTTTTTTTCCTTTCTTTCTTTCTTTGCTGTCT 225
DB          191133 TCCTTCTTTCTTTCTTTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTC
                226 TTCCTCTCTCTCTCTCTCTCTTTCTCTCTCTTTCTTTCTTTCTTTT 272
DB          191193 TTCCTCTTTCTTTCTCTCTCTCTCTCTCTCTCTCTTTTCTTTT 191239
RESULT 10
AADD62833
ID          AAD62833 standard; DNA; 170834 BP.
AC          AAD62833;
XX
XX          12-FEB-2004 (first entry)
DT
DE          Human BAC #2 containing formin (Fmn)-2 genomic DNA.
XX
XX          Recurrent pregnancy loss; RPL; formin-2; Fmn-2; diagnosis; therapy;
KM          human; ds.
XX
XX          Homo sapiens.
OS
PN          US2003170683-A1.
PF
PD          11-SEP-2003.
XX
XX          03-DEC-2002; 2002US-00308485.
XX
PR          13-APR-2000; 2000US-0196811P.
PR          12-APR-2001; 2001US-00852522.
XX
XX          (LEDE/) LEDER P.
PA

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XX	(LEAD// LEADER B.
PA	Leder P, Leder B;
P1	WPI, 2003-830607/77.
DR	
XX	
PT	Diagnosing recurrent pregnancy loss comprises examining formin-2 gene for
PT	a mutation and measuring biological activity and expression of formin-2
PT	identified to play a role in oocyte development.
XX	
PS	Example 11; Fig 13B; Opp; English.
XX	
CC	The invention relates to a method of diagnosing recurrent pregnancy loss
CC	(RPL). The method involves examining formin (Fmn)-2 gene for a mutation
CC	and measuring biological activity and expression of Fmn-2, in which
CC	decreased levels indicates an increased risk for RPL; or examining the
CC	person's formin-2 gene for polymorphisms, in which the presence of a
CC	polymorphism indicates an altered risk for RPL. The method is used for
CC	diagnosing and treating RPL e.g. in humans. The present sequence is human
CC	BAC containing formin (Fmn)-2 genomic DNA
SQ	Sequence 170834 BP; 49010 A; 35790 C; 34251 G; 48977 T; 0 U; 2806 Other;
Query Match	16.0%; Score 66.8; DB 10; Length 170834;
Best Local Similarity	75.5%; Pred. No. 0.00021;
Matches	83; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Oy	165 CTTATCTTTCTTTTTTTTTTTTTTTTTTTTTCTTTCTTCGCTTTGTCTTCTGC 224
Dd	117826 CTTTCTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTCGCTTTCTTTGTG 117885
Oy	225 TTTCCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTTTC 274
Dd	117886 TTGCCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTCC 117935
RESULT 11	
ID	ADL13761/c
AC	ADL13761 standard; DNA; 180821 BP.
XX	
AC	ADL13761;
DT	06-MAY-2004 (first entry)
DE	Osteoarthritis-associated polymorphic nucleotide #293.
XX	
KM	ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KM	joint space narrowing; osteophyte development; joint pain;
KM	osteoarthritis; SNP; single nucleotide polymorphism.
XX	
OS	Homo sapiens.
PN	WO2003054166-A2.
PD	03-JUL-2003.
PF	19-DEC-2002; 2002WO-US041225.
PR	20-DEC-2001; 2001US-0342603P.
PA	(INCY-) INCYTE GENOMICS INC.
PI	Jones KA, Schafer A;
WP1	WPI, 2003-559141/52.
XX	
PT	Determining susceptibility of an individual to joint space narrowing,
PT	osteophyte development and/or joint pain comprises identifying whether
PT	the individual has at least one polymorphism in a polynucleotide encoding
PT	a protein.
PS	Disclosure, SEQ ID NO 293; 297pp; English.
XX	

	CC	The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polynucleotide encoding at least one of the protein listed in the specification. The methods, composition and agent are useful for modulating the susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarthritis. The cell line and the non-human animal are useful for screening for an agent for diagnosing an individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint pain. This sequence corresponds to the polynucleotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcc_sequences).
XX	CC	fip.wipo.int/pub/published_pcc_sequences).
XX	CC	
SQ	Sequence	180821 BP; 59926 A; 31181 C; 31322 G; 58392 T; 0 U; 0 Other;
XX		
Query Match	15.84;	Score 66; DB 10; Length 180821;
Beat Local Similarity	73.74;	Pred. No. 0.00011;
Matches	84; Conservative	0; Mismatches 30; Indels 0; Gaps 0;
Dd	166	TTTATCTTCTTTTTTTTTTTTTCTTTTCCTTTTCCTTTTCCTTTGCTGTCT 225
Oy	66343	TCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 66284
Dd	226	TTCTCTCTCTCTCTCTGTCTTTCTTTCTCTCTCTTTCTTTCTTTTCTACT 279
Oy	66283	CTTCCCTTTCTTCTCTTCTTCTTTTCTTTCTTCTTCTTCTTGCGCTGCCTGCT 66230
RESULT 12		
ID	ADQ23651/C	ADQ23651 standard; DNA; 3583 BP.
XX	ADQ23651;	
AC	ADQ23651;	
XX		
DT	26-AUG-2004	(first entry)
XX		
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 6471.	
XX		
KW	soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004048938-A2.	
XX		
PD	10-JUN-2004.	
XX		
PF	26-NOV-2003; 2003WO-US038193.	
XX		
PR	26-NOV-2002; 2002US-0429739P.	
XX		
PA	(PROT.-) PROTEIN DESIGN LABS INC.	
XX		
PI	Aziz N, Ginsburg WM, Zlotnik A;	
XX		
DR	WPI; 2004-441208/41.	
XX		
PT	Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.	
XX		
PS	Example 2; SEQ ID NO 6471; 210pp; English.	
XX		
CC	The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual, and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the	

	The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene.
	The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-
	-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents a maize oil- associated gene.
SQ	Sequence 1073 BP; 358 A; 259 C; 232 G; 224 T; 0 U; 0 Other;
Query Match	15.7%; Score 65.4; DB 12; Length 1073;
Best Local Similarity	65.3%; Pred.No.0.00018;
Matches	96; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
Dn	166 TTAACTTTTCTTTTTTTTCCTTCTCCTTGCTGCTCGTCT 225 713 TT 654
Oy	226 TTCCTCTCTCTCTCTGTGCCTTCTTCCCTCTTTCTTCTCAATGGACAAG 285 653 TTGATAAAGAAGAAC 594
Oy	286 ATCTCTCATGGACGAATTAATCTGCC 312 Db 593 TTGTTTATTGTTAATAATGAAGATC 567
RESULT 15	
AAK69400	
ID	AAK69400 standard; DNA; 11456 BP.
XX AC	AAK69400;
XX DT	06-NOV-2001 (first entry)
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24212.
XX XX	Human; immune; haematopoeitic; immune/haematopoietic antigen; cancer; cytostatic gene therapy; vaccine; metastasis; ds. Homo sapiens.
OS	Homo sapiens.
PN	WO200157182-AZ.
PD	09-AUG-2001.
XX PF	17-JAN-2001; 2001WO-US001354.
PR	31-JUN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
PR	14-VUL-2000; 2000US-0218290P.
PR	26-VUL-2000; 2000US-0220963P.
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PR	14-AUG-2000; 2000US-0224518P.
PR	14-AUG-2000; 2000US-0224519P.
PR	14-AUG-2000; 2000US-0225213P.
PR	14-AUG-2000; 2000US-0225214P.

PR	14-AUG-2000	2000US-0225266P
PR	14-AUG-2000	2000US-0225267P
PR	14-AUG-2000	2000US-0225268P
PR	14-AUG-2000	2000US-0225270P
PR	14-AUG-2000	2000US-0225271P
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PR	18-AUG-2000	2000US-0226271P
PR	18-AUG-2000	2000US-0226681P
PR	22-AUG-2000	2000US-0226868P
PR	22-AUG-2000	2000US-0227182P
PR	23-AUG-2000	2000US-0227009P
PR	30-AUG-2000	2000US-0228924P
PR	01-SEP-2000	2000US-0229287P
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PR	01-SEP-2000	2000US-0229344P
PR	01-SEP-2000	2000US-0229345P
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PR	05-SEP-2000	2000US-0229513P
PR	06-SEP-2000	2000US-0230437P
PR	06-SEP-2000	2000US-0230438P
PR	08-SEP-2000	2000US-0231242P
PR	08-SEP-2000	2000US-0231243P
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PR	08-SEP-2000	2000US-0232080P
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PR	25-SEP-2000	2000US-0235027P
PR	25-SEP-2000	2000US-0235028P
PR	25-SEP-2000	2000US-0235029P
PR		

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 / Search time 2887.54 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133

Perfect score: 417
Sequence: 1 gccacgggggacatttctgg.....gctctggtccctcagctgt 417

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_est7:
7: gb_est8:
8: gb_est9:
9: gb_est10:
10: gb_est11:
11: gb_est12:
12: gb_est13:
13: gb_est14:
14: gb_est15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276.4	66.3	941	2	BG720951 602692616
2	227	54.4	314	2	AA903751 OK64C05.8
3	75.8	18.2	574	12	CE084870 tigr-gss-
4	72.8	17.5	831	11	AQ748216 HS_5536_A
5	72.8	17.4	558	10	DT851628
6	72.6	17.4	285	1	AA267532 m272h06.x
7	72.6	17.4	477	12	CE462296
8	72.4	17.4	712	12	CE389737 tigr-gss-
9	72.4	17.4	659	10	DT850178 LB00490.C
10	72.2	17.3	997	14	CNS0057E
11	71.8	17.2	1611	14	AG381869 Mus muscu
12	71.6	17.2	610	12	CE430482 tigr-gss-
13	71.6	17.2	618	12	CE616821 tigr-gss-
14	71.4	17.1	468	2	BI466468 i23b03.Y
15	71.2	17.1	819	10	DM258451 ur-s-GGI-
16	71	17.0	480	3	BU950798 i174d06.Y
17	71	17.0	1786	12	CL082766 CH216-171
18	70.6	16.9	305	10	DV439322 davisf000
19	70.6	16.9	354	12	CE136219 tigr-gss-

C 20	70.4	16.9	355	11	B2235143	B2235143 CH230-251
C 21	70.4	16.9	428	11	AQ557186	AQ557186 HS_2081_A
C 22	70	16.8	401	2	BM354761	BM354761 r1r16e10.Y
C 23	70	16.8	688	8	CV664201	CV664201 LCP604EX0
C 24	70	16.8	781	8	CX013225	CX013225 i064a07.b
C 25	70	16.8	1387	12	CL019342	CL019342 CH216-5B7
C 26	69.8	16.7	226	12	CE033446	CE033446 t1gr-gss-
C 27	69.8	16.7	764	12	CE543174	CE543174 t1gr-gss-
C 28	69.8	16.7	1344	14	AG332055	AG332055 Mus muscu
C 29	69.6	16.7	646	10	DV850851	DV850851 LB0222.CR
C 30	69.6	16.7	1210	14	AG340857	AG340857 Mus muscu
C 31	69.6	16.7	1322	12	CL078946	CL078946 CH216-154
C 32	69.4	16.6	513	12	CE495836	CE495836 t1gr-gss-
C 33	69.4	16.6	532	12	CE199619	CE199619 t1gr-gss-
C 34	69.4	16.6	533	12	CE182651	CE182651 t1gr-gss-
C 35	69.4	16.6	610	10	DT459589	DT459589 GH_ON3701
C 36	69.4	16.6	845	7	BF616304	BF616304 HVMHC000
C 37	69.4	16.6	885	3	BU957927	BU957927 AGENCOURT
C 38	69.4	16.6	1239	14	AG280281	AG280281 Mus muscu
C 39	69.2	16.6	435	1	A1753542	A1753542 cr12a04.X
C 40	69.2	16.6	554	12	CE427799	CE427799 t1gr-gss-
C 41	69	16.5	344	12	CE790240	CE790240 t1gr-gss-
C 42	69	16.5	501	12	CE738683	CE738683 t1gr-gss-
C 43	69	16.5	697	14	AG047727	AG047727 Pan trogl
C 44	68.8	16.5	387	12	CE571324	CE571324 t1gr-gss-
C 45	68.8	16.5	429	5	CF123422	CF123422 UI-HF-CHO

ALIGNMENTS

RESULT 1
BG720951/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BG720951 941 bp mRNA linear EST 08-MAY-2001
602692616F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825178 5',
mRNA sequence.
BG720951.1 GI:14000138
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 941)
NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM10737 row: 0 column: 03
High quality sequence stop: 666.
Location/Qualifiers
1. 941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4825178"
/lab_host="DH10B"
/clone_1lb="NIH MGC 97"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-xhoI
(gtagag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a

ORIGIN

primary library enriched for full-length clones and constructed using the Cap-trapper method (Garnick, in preparation). Library constructed by M. Brownstein (NIMH/NIHRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 66.3%; Score 276.4; DB 2; Length 941;
Best Local Similarity 91.8%; Pred. No. 4.5e-49;
Matches 349; Conservative 0; Mismatches 21; Indels 10; Gaps 5;

QY 47 TGTTCCTCAGCATTCACAGAAATTTGCCGAGCCCTCCGGAATGACACAGCCAGAG 106
DB 702 TGTTCCTCAGCATTCACAGC-AAATTTGCCGAGCCCTCCGGAATGACACAGCCAGAG 644
QY 107 AGCTCAGCGCAAGTAGAGAACTGGCGAGGAGACTCAGAGTCCCAAAAAAACT 166
DB 643 AGCTCAGCGCAAGTAGAGAACTGGCGAGGAGACTCAGAGTCCCAAAAAAACT 564
QY 167 TTAATC--TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTG 222
DB 583 TTAATCAGTTCCGAGTGGTTGTTCTGTTCTTTCTTTCTTTCTTTCTTTCTTTCTG 524
QY 223 TCTTTCT 278
DB 523 TCTTTCT 464
QY 279 TGGCAAGATCT 338
DB 463 TGGCAAGATCT 404
QY 339 GCCAGAGCATGCGCTCGCGCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 397
DB 403 GCCAGAGCATGCGCTCGCGCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 344
QY 398 GCTCTGCTCCCTTCAGCTGT 417
DB 343 GCTCTGCTCCCTTCAGCTGT 324

RESULT 2 314 bp mRNA linear EST 09-JUN-1998
LOCUS AA903751
DEFINITION ok6405..a1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518728 3'
similar to gb:X17360_fna1 HOMEOBOX PROTEIN HOX-D4 (HUMAN); mRNA
sequence.

ACCESSION AA903751 GI:3038874
VERSION AA903751
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 314)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdnp/image/image.html
Insert Length: 521 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 297.
Location/Qualifiers

FEATURES

source

1. 314
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1518728"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: pT73D-Pac1; 1st strand cDNA was prepared
from 3 pooled germ cell tumors, and was then primed with a
Not I - oligo (dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 54.4%; Score 227; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TTTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 250
DB 1 TTTCTTCTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 60
QY 251 TTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 310
DB 61 TTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 120
QY 311 CCTTGACTTGTGTTTCAGAGCTGCTTCTGCGAGACATGAGCTCGGCGTGTCTTTCTTT 370
DB 121 CCTTGACTTGTGTTTCAGAGCTGCTTCTGCGAGACATGAGCTCGGCGTGTCTTTCTTT 180
QY 371 CCGCTAATTAATTCAGAGCCCATCCAGCTGTGCTCCCTCAGCTGT 417
DB 181 CCGCTAATTAATTCAGAGCCCATCCAGCTGTGCTCCCTCAGCTGT 227

RESULT 3 574 bp DNA linear GSS 24-SEP-2003
LOCUS CE084870
DEFINITION tigr-gss-dog-1700035898436 Dog Library Canis familiaris genomic,
genomic survey sequence.

ACCESSION CE084870
VERSION CE084870.1 GI:35151716
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 574)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, D.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun
Location/Qualifiers

FEATURES

1. 574
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"

QY 310 GCCTGACCTTCCTTCACAGCTGCTTCACAGAACATGCGCTGGCTGTTTCTT 369
DB 342 TTAATGGCTCATGTACTGAGAAATCTGTTGGGGGACAAATGGCTTCGGGTCTCAAA 283
QY 370 TCCGCTATATATATCCAGGCCCATCCAGCTTCGTGCTCCCTCAGCTCT 417
DB 282 TGTAGTGTACAGATCTGATTTCTCCCACTTCAGCTCCTCTGCTGT 235

RESULT 6
AA267532/c 285 bp mRNA linear EST 21-MAR-1997
LOCUS m272h06.r1 Soares mouse lymph node NbMUN Mus musculus cDNA clone
DEFINITION IMAGE:719003 5' similar to gb:X75947 M.musculus mCBP mRNA (MOUSE);,
mRNA sequence.
AA267532
ACCESSION AA267532.1 GI:1904267
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
REFERENCE 1 (bases 1 to 285)
Maire, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Theissenberg, K., Stepec, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNC; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:444499
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 204.
Location/Qualifiers
1..285
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="IMAGE:719003"
/sex="male"
/tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_id="Soares mouse lymph node NbMUN"
/note="Organ: lymph node; Vector: pUT73-PacI; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I
- oligo(dT) primer (5',
TGTTCATATCTGATGAGGAGGAGCGCCGACATCTTTTCTTTTCTTTTCTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pUT73 vector. RNA
provided by Dr. Bertrand Jordan. Library constructed and
normalized by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 17.4%; Score 72.6; DB 1; Length 285;
Best Local Similarity 62.3%; Pred. No. 3.1e-05;
Matches 114; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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DB 111 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT

DB 279 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 220
QY 226 TTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTACATGGCAAG 285
DB 219 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 160
QY 286 ATCTCTCATGGAGAAATATCTGCTTGAATCTTTCTTTCTTTCTTTCTTTCTTT 345
DB 159 TTCCTGACATTCAGCAACTAACTGAATGTATTAATTAATCACTTTACATTTCCATGA 100
QY 346 CCA 348
DB 99 CAA 97

RESULT 7
CE462296
LOCUS tigr-gss-dog-17000309531079 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE462296
ACCESSION CE462296.1 GI:36762471
VERSION
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 477)
Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, M., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
Location/Qualifiers
1..477
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 17.4%; Score 72.6; DB 12; Length 477;
Best Local Similarity 59.4%; Pred. No. 3.2e-05;
Matches 123; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 165 CTTATCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTCTGCT 224
DB 230 CTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 289
QY 225 TTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 284
DB 290 TTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 349
QY 285 GATCTCTCATGGAGAAATATCTGCTTGAATCTTTCTTTCTTTCTTTCTTTCTTT 344
DB 350 CTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 409
QY 345 ACCATGGCGTGGGGGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 371
DB 410 TCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 436

[illegible]

REFERENCE
AUTHORS
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 659)
 Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y.,
 Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shemen, C.,
 Wagner, L., Bala, M., Barabazuk, S., Barber, S., Babakoff, R.,
 Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R.,
 Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R., Scott, J.,
 Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.
 Bovine Genome Sequencing Program: Full-length cDNA Sequencing
 Unpublished (2005)
TITLE
JOURNAL
COMMENT
 Contact: Robert Kirkpatrick
 Canada's Michael Smith Genome Sciences Centre
 BC Cancer Agency
 Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
 Canada, V5Z 4S6
 Tel: 1-604-707-5900 x5406
 Fax: 1-604-876-3561
 Email: robertk@bcgsc.ca
 Plate: LB00490 row: E column: 3
 High quality sequence, stop: 659.
FEATURES
 source
 1..659
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Crosbred x Angus"
 /db_xref="taxon:9913"
 /clone="IMAGE:8061773"
 /sex="female"
 /tissue_type="Liver"
 /dev_stage="Calv, 6 months old"
 /lab_host="ElectroMAX DH10 TI Phage-Resistant Cells"
 /clone_id="GC-BGC-04"
 /note="Organ: Liver; Vector: pCMV SPORT 6.0; site_1: SalI
 (5' end of cDNA); site_2: NotI (3' end of cDNA)"
ORIGIN
 Query Match 17.4%; Score 72.4; DB 10; Length 659;
 Best Local Similarity 60.8%; Pred. No. 3.6e-05;
 Matches 118; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
 QY 99 CCAGACAGAGCTGACGCCAAAGCTAAGAAACCTGGGGAGGAGACTCAGAGCCACA 158
 DB 646 CCAAAAAAGGGGGGGGGGTAACTTTGGCCCCCGGGGAAATTAAAGGGGCCCA 587
 QY 159 AAAAAGCTTATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 218
 DB 586 AAAACCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 527
 QY 219 TCTGTCTTCT 278
 DB 526 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 467
 QY 279 TGGCAAGATCTCCT 292
 DB 466 CAGGAGGTCTGCT 453
RESULT 10
CNS005TE
LOCUS
DEFINITION
 Drosophila melanogaster genome survey sequence TBT3 end of BAC #
 BACR12K22 of RPECI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 997)

[illegible][illegible]

Not 1: Site 2: Sal 1: The library was prepared by Catherine S. Lee and has not been published. The pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,

[illegible]

```

RESULT 2
US-09-949-016-14689
; Sequence 14689, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14689
; LENGTH: 39754
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(39754)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689

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Query Match	Similarity	100.0%	Score 417	DB 3	Length 39754
Beet Local	Similarity	100.0%	Pred. No. 8,9e-92		
Matches 417	Conservative	0	Mismatches	0	Indels 0
					Gaps 0
QY	1	GCACGGGGGACAAATTTTGTGCTCGACAGCCCTTTCATCTGTCGTGTTCTCAGCAAT	60		
Db	28400	GCCAGGGGGGACAAATTTTGTGCTCGACAGCCCTTTCATCTGTCGTGTTCTCAGCAAT	28459		
QY	61	CTCACAGAAATTTTGGCCGAGCCTCTCCGGAAATGACACGCCACACAGCTCAGCGGAAAA	120		
Db	28460	CTCACAGAAATTTTGGCCGAGCCTCTCCGGAAATGACACGCCACAGGCTCAGCGGAAAA	28519		
QY	181	GCTAGAGAACTGGCGGAGGAGAGACTACAGATGCGACAAAAAAACTTTATCTTTCTTTT	180		
Db	28520	GCTAGAGAACTGGCGGAGGAGAGACTACAGATGCGACAAAAAAACTTTATCTTTCTTTT	28579		
QY	181	TTTTTTCTTTCTTTCTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	240		
Db	28580	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	28635		
QY	241	CTGCTCTTCTTTCCGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	300		
Db	28640	CTGCTCTTCTTTCCGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	28695		
QY	301	AAATATATGCGCTTGACTTCTGTTTTCACGCTGTGCTTGCACAGACCATCGCTGGAGCT	360		
Db	28700	AAATATATGCGCTTGACTTCTGTTTTCACGCTGTGCTTGCACAGACCATCGCTGGAGCT	28755		
QY	361	GTTTTCTTTTCCGCTATATATATATACAGGCCCATCCAGCTGTGATCCCTCCACTGT	417		
Db	28760	GTTTTCTTTTCCGCTATATATATATACAGGCCCATCCAGCTGTGATCCCTCCACTGT	28816		

```

1      RESULT 3
2      US-08-232-463-14
3      ; Sequence 14, Application US/08232463
4      ; Patent No. 5670367
5      ; GENERAL INFORMATION:
6      ; APPLICANT: DORNER, F.
7      ; APPLICANT: SCHEIFLINGER, F.
8      ; APPLICANT: FALKNER, F. G.
9      ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
10     ; NUMBER OF SEQUENCES: 52
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: Foley & Lardner
13     ; STREET: 1800 Diagonal Road, Suite 500
14     ; CITY: Alexandria
15     ; STATE: VA
16     ; COUNTRY: USA
17     ; ZIP: 22313-0299
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: Patent Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/232,463
25     ; FILING DATE:
26     ; CLASSIFICATION: 435
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: US/07/935,313
29     ; FILING DATE:
30     ; APPLICATION NUMBER: EP 91 114 300.6
31     ; FILING DATE: 26-AUG-1991
32     ; ATTORNEY/AGENT INFORMATION:
33     ; NAME: BENT, Stephen A.
34     ; REGISTRATION NUMBER: 29,768
35     ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
36     ; TELECOMMUNICATION INFORMATION:
37     ; TELEPHONE: (703)836-9300
38     ; TELEFAX: (703)683-4109
39     ; TELEX: 899149
40     ; INFORMATION FOR SEQ ID NO: 14:
41     ; SEQUENCE CHARACTERISTICS:
42     ; LENGTH: 7218 base pairs
43     ; TYPE: nucleic acid
44     ; STRANDEDNESS: single
45     ; TOPOLOGY: linear
46     ; IMMEDIATE SOURCE:
47     ; CLONE: pTZspc-F18
48     ; US-08-232-463-14

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Query Match	20.9%	Score 87	DB 2	Length 7218
Best Local Similarity	4.3%	Pred. No. 1.3e-11		
Matches	12	Conservative 197	Mismatches 72	Indels 0
			Gaps	0
QY	131	CTGGCGAGGAGACTCACAGTGCACAAAAAATTATCTTTCTTTTCTTTCTT	190	
		: : :	: : : : : : : : : : : :	
Db	1046	CAGGTCCAGGAGCTGCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1105	
QY	191	TTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	250	
	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	: : : : : : : : : : : :	: : : : : : : : : : : :	
Db	1106	TT	1165	
	TT	: : : : : : : : : : : :	: : : : : : : : : : : :	
QY	251	TTCTCTCTTTCTTTCTTTTCTTCTACATGGCAAGATCTCTCATGCGAATAATCTG	310	
	TTTTTTCTTTCTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	: : : : : : : : : : : :	: : : : : : : : : : : :	
Db	1166	TT	1225	
	TT	: : : : : : : : : : : :	: : : : : : : : : : : :	
QY	311	CCTGACTCTGTCTTCCAGCTGCTTCGCCAGACATGGGCTCGGGCTTTTCTT	370	
	: :	: : : : : : : : : : : :	: : : : : : : : : : : :	
Db	1226	TT	1285	
	TT	: : : : : : : : : : : :	: : : : : : : : : : : :	
QY	371	CGGCTAATATATCAGGCGCATCCAGCTCGGCGCCTC	411	
	TT	: : : : : : : : : : : :	: : : : : : : : : : : :	
Db	1286	TT	1326	
	TT	: : : : : : : : : : : :	: : : : : : : : : : : :	

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Query Match Similarity      16.9%; Score 70.6; DB 3; Length 65745;
Beat Local Similarity       78.0%; Pred. No. 2.3e-07;
Matches      85; Conservative    0; Mismatches   24; Indels     0; Gaps     0;

QY      167 TTATCTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTGTCGTCTTCT 226
DB      4944 TTTCTTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 5003

QY      227 TTCCTCTCTCTCTCTGTCCTTTTCTTCCCTCTTTCTTTCTTTTCCCT 275
DB      5004 TCCTTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCT 5052

RESULT 6
US-09-949-016-13358
; Sequence 13358, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13358
; LENGTH: 260247
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13358

Query Match      16.1%; Score 67; DB 3; Length 260247;
Beat Local Similarity 76.6%; Pred. No. 2.5e-06;
Matches      82; Conservative    0; Mismatches   25; Indels     0; Gaps     0;

QY      166 TTATCTTTCCTTTTCTTTTCTTTTCTTTTCTTTCTTTCTTTCTTTCTTCT 225
DB      182931 TCTTCTTTTCTTTCTTTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTCT 182990

QY      226 TTCCTCTCTCTCTGTCCTTTTCTTCTCTCTTTCTTTCTTTCTTTCTTTT 272
DB      182991 TTCCTCTTTCTTTCTTTCTCTCTCTCTCTCTTCTTTCTTTCTTTT 183037

RESULT 7
US-09-949-016-12014/c
; Sequence 12014, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12014
; LENGTH: 39433
; TYPE: DNA

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US-09-949-002-678/c
; Sequence 678, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 678
; LENGTH: 56399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(56399)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-678

Query Match 15.6%; Score 65.2; DB 3; Length 56399;
Best Local Similarity 67.9%; Pred. No. 4.6e-06;
Matches 106; Conservative 0; Mismatches 48; Indels 2; Gaps 1;

QY 139 GGGAGACTCAGTCAGTCACAAAAAAGCTTATCTTTTCTTTTCTTTCTTTCTTCT 198
DB 46588 GAGAAATCTCCAAATACATTAAGAAACCTTCTTCTTCTTCTTCTTCTTCTCA 46529
QY 199 TTCTCTCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 256
DB 46528 CACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46469
QY 257 TCTTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 292
DB 46468 TCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46433

RESULT 12
US-09-949-002-839/c
; Sequence 839, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 839
; LENGTH: 56399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(56399)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-839

Query Match 15.6%; Score 65.2; DB 3; Length 56399;
Best Local Similarity 67.9%; Pred. No. 4.6e-06;
Matches 106; Conservative 0; Mismatches 48; Indels 2; Gaps 1;

QY 139 GGGAGACTCAGTCAGTCACAAAAAAGCTTATCTTTTCTTTTCTTTCTTTCTTCT 198
DB 46588 GAGAAATCTCCAAATACATTAAGAAACCTTCTTCTTCTTCTTCTTCTTCTCA 46529
QY 199 TTCTCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 256
DB 46528 CACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46469
QY 257 TCTTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 292
DB 46468 TCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46433

DB 46588 GAGAAATCTCCAAATACATTAAGAAACCTTCTTCTTCTTCTTCTTCTTCTCA 46529
QY 199 TTCTCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 256
DB 46528 CACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46469
QY 257 TCTTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 292
DB 46468 TCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46433

RESULT 13
US-09-949-016-12871
; Sequence 12871, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12871
; LENGTH: 100836
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(100836)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12871

Query Match 15.5%; Score 64.8; DB 3; Length 100836;
Best Local Similarity 75.0%; Pred. No. 6.7e-06;
Matches 81; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 166 TTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 225
DB 87889 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 87948
QY 226 TTCTCTCTCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 273
DB 87949 TTCTCTCTCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 87996

RESULT 14
US-09-949-016-17063
; Sequence 17063, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

[illegible]

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RESULT 2
US-09-925-065A-566754
; Sequence 566754, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 566754
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-566754

```

[illegible]

RESULT3
US-10-437-963-95688/C
: Sequence 95688, Application US/104379633
: Publication No. US2004012343A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: APPLICANT: Wu, Wei
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Barbazuk, Brad
: APPLICANT: Li, Ping

```

1  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
2  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
3  FILE REFERENCE: 38-21(53221)B
4  CURRENT APPLICATION NUMBER: US/10/437,963
5  CURRENT FILING DATE: 2003-05-14
6  NUMBER OF SEQ ID NOS: 204966
7  SEQ ID NO 95688
8  LENGTH: 1678
9  TYPE: DNA
10 ORGANISM: Oryza sativa
11 FEATURE:
12 OTHER INFORMATION: Clone ID: PAT_MRT4530_93858C.1
13 US-10-437-963-95688

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	Query Match	Best Local Similarity	Matches	Conservative	Score 71.2;	DB 8;	Length 1678;	Pred. No. 1.3e-06;	Mismatches 53;	Indels 0;	Gaps 0;
Oy	166	TTATCTTTCCTTTTTTTTTTTCTTTCTTCTCTCTTCTTGCTGTGCTCT	225								
Dd	1517	TT	1458								
Oy	226	TTCCTC	285								
Dd	1457	TTGGAGTTAAA	1398								
Oy	286	ATTCTCTCATGGCAGAATAATCGCTGACTTCT	321								
Dd	1397	ATGGCAACATTTTAGGCTCAAATGGCCCTTGCTTCT	1362								

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: RESULT 4
: US-09-925-065A-164899
: Sequence 164899, Application US/09925065A
: Publication No. US2040181046A1
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single
: FILE REFERENCE: 108827.135
: CURRENT APPLICATION NUMBER: US/09/925, 065A
: PRIOR FILING DATE: 2001-08-08
: PRIOR APPLICATION NUMBER: US 60/243, 096
: PRIOR FILING DATE: 2000-10-24
: PRIOR APPLICATION NUMBER: US 60/252, 147
: PRIOR FILING DATE: 2000-11-20
: PRIOR APPLICATION NUMBER: US 60/250, 092
: PRIOR FILING DATE: 2000-11-30
: PRIOR APPLICATION NUMBER: US 60/261, 766
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/289, 846
: PRIOR FILING DATE: 2001-05-09
: NUMBER OF SEQ ID NOS: 957086
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 164899
: LENGTH: 501
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-925-065A-164899

```

	Query Match	16.9%	Score 70.4;	DB 4;	Length 501;
	Best Local Similarity	78.2%	Pred. No. 1.4e-06;		
	Matches	97;	Conservative	0; Mismatches	26; Indels
				1; Gaps	1;
OY	168 TATCTTTTCTTTTTTTTTTCCTTTCTCTCTCTCTCTGCTCTTCTT	227			
Dd	111 TCTCTTTCTTTTAATTTTCTTCTCTCTCTCTCTCTCTCTCTC-TCTTCTTTCTTC	169			
OY	228 CCTCTCTCTCTGTCTCTTCTTCCCTCTCTCTTCTTTTCCACATGGCAAGAT	287			
Dd	170 TTCTCTTCTCTCTCTCTCTTCTCTCTCTCTCTGCTCTCTTCTCTCTTCCCTCC	229			
OY	288 CTCCTC	291			


```

? SEO ID NO 417
? LENGTH: 1548
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1548)
? FEATURE:
? NAME/KEY: modified base
? LOCATION: (896)..(935)
? OTHER INFORMATION: a, t, c, g, other or unknown
? US-10-343-650A-417

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Query Match	16.9%	Score 70.4;	DB 8;	Length 1548;
Best Local Similarity	78.2%;	Pred. No. 2e-06;		
Matches 97; Conservative	0;	Mismatches 26;	Indels 1;	Gaps 1;

Oy	168	TATCTTTTCCTTATTTCCTTTCTTTCCTTTCCTTGACCTTGCCTT	227
Ddb	1148	TCTCTTTTCTTTTAATTTTCCTTCTTTCCTTTCCTTCGCTC-TCTTTCTTCTTC	1099

Oy **228** CCGCTGCTGTCTCAGTGCCTTTTCCTTCCTTTCTTTCTTTTTCCTTAACATGGCAAGAT 287
Ddb **1089** TTCTCTTCTCTCTCTCTCTTTCTCTCTCTCTCTCTCTTTCTCTCTTTCTCTTCTTCCCTCC 1033

Qy	288	CTCC	291
Db	1029	CTCC	1026

RESULT 9
US-10-741-600-33383/C
33383
US-10-741-600-33383/C

Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OR INVENTION: GENETIC POLYMERIZING ASSOCIATED WITH

;; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001499
;; CURRENT APPLICATION NUMBER: US/10/741,600
;; CURRENT FILING DATE: 2003.12.22

```

;
;   NUMBER OF SEQ ID NOS: 73997
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 33383
;   FASTA:
;   201

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!
! TYPE: DNA
!
! ORGANISM: Homo sapiens
US-10-741-600-33383

```

Query Match	16.8%	Score 70.2	DB 9	Length 201
Best Local Similarity	78.5%	Pred. No. 1.2e-06		
Matches 84; Conservative		Mismatches 23	Indels 0	Gaps 0

Oy		165	CCTTACCTTTCTTTTTTCCTTTCCGTCGTGC	224
Db		190	CTCTTCTTTCTTCTTGCTTCTCTGCCCTTCTTCTTCTCCTC	131

[illegible]

RESULT 10
US-10-741-600-33385/C
Sequence 33385 Protocol: ITSC/10741600

Publication NO. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYOMYRISMS ASSOCIATED WITH

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; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22

```

```

; NUMBER OF SEQ ID NOS: 7397
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3385
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; OS=10-741-600-3385

```

Query Match	16.84;	Score	70.2;	DB	9;	Length	201;
Best Local Similarity	78.54;	Pred.	No.	1.2e-06;			
Matches	84;	Conservative	0;	Mismatches	23;	Indels	0;
						Gaps	0;

Dy 165 CTTTACCTTCCTTTTTTCTTTCTTTCTCCTTCCTTGCTGTC 224

Db 192 CTCCTTCTTTTCTTTCTGGCTTCTTCTCCCTTCTTTCTTCTCTGC 133

[illegible]

RESULT 11
US-10-741-600-33386/C
92222
3737456400 WU/10721600

Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OR INVENTION: GENETIC POLYNUCLEOTIDES ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22

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; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33386
; length 201
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-33386

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Query Match      16.8%;   Score 70.2;   DB 9;   Length 201;
Best Local Similarity 78.5%;   Pred. No. 1.2e-06;
Matches 84; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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[illegible][illegible]

RESULT 12
US-10-741-600-3338/c
Sequence 3338 Application IIS/10741600

;
 ; PUBLICATION NO. US20050026169A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: CARGILL, Michele et al.
 ;
 ; TITLE OR INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CL001499
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-32

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;
;      NUMBER OF SEQ ID NOS: 73997
;
;      SOFTWARE: FastSeq for Windows Version 4.0
;      SEQ ID NO 33388
;      LENGTH: 201

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!
! TYPE: DNA
!
! ORGANISM: Homo sapiens
US-10-741-600-3338
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Query Match	16.8%	Score 70.2%	DB 5%	Length 20%
-------------	-------	-------------	-------	------------

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:44:48 ; Search time 12.1553 Seconds
(without alignments)
4040.340 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133

Perfect score: 417
Sequence: 1 gccacgggggacatttctg.....gtctgtccctcagctgt 417

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:
1: /EMC_Celerra_SIDS3/prodata/1/pubpna/US09_NEW_PUB.seq:
2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:
3: /EMC_Celerra_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq:
4: /EMC_Celerra_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq:
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7: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:
8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	65.2	15.6	42999	7	US-11-284-877-17	Sequence 17, Appl
2	63.6	15.3	1292	6	US-10-953-349-10307	Sequence 10307, A
3	63	15.1	2442	6	US-10-953-349-35802	Sequence 35802, A
4	62.2	14.9	1985	6	US-10-196-749-27	Sequence 27, Appl
5	61.4	14.7	1999	6	US-10-505-928-758	Sequence 758, App
6	60.8	14.6	2773	6	US-10-196-749-149	Sequence 149, App
7	60.8	14.6	2773	7	US-11-101-316-33	Sequence 33, Appl
8	60	14.4	4600	7	US-11-301-554-1797	Sequence 1797, Ap
9	59	14.1	4640	6	US-10-196-749-75	Sequence 75, Appl
10	58.8	14.1	2272	6	US-10-953-349-37381	Sequence 37381, A
11	58.6	14.1	2163	6	US-10-953-349-37514	Sequence 37514, A
12	58.2	14.0	1628	6	US-10-953-349-28506	Sequence 28506, A
13	58.2	14.0	2378	7	US-11-293-697-1075	Sequence 1075, Ap
14	58	13.9	1843	6	US-10-511-937-620	Sequence 620, App
15	58	13.9	4670	7	US-11-145-307A-29	Sequence 29, Appl
16	57.8	13.9	2861	6	US-10-953-349-7328	Sequence 7328, Ap
17	57.6	13.8	2846	6	US-10-196-749-169	Sequence 169, Appl
18	57.6	13.8	2846	6	US-11-101-316-37	Sequence 37, Appl
19	57.4	13.8	2261	6	US-10-511-937-415	Sequence 415, App
20	57.2	13.7	1734	6	US-10-196-749-201	Sequence 201, App
21	57.2	13.7	1734	7	US-11-101-316-51	Sequence 51, Appl
22	56.2	13.5	2040	6	US-10-953-349-37996	Sequence 37996, A
23	56.2	13.5	1771	6	US-10-196-749-17	Sequence 17, Appl
24	56.2	13.5	1771	6	US-11-296-092-36	Sequence 36, Appl
25	56	13.4	2541	7	US-11-293-697-2275	Sequence 2275, Ap

C	26	55.6	13.3	1820	7	US-11-316-907-14	Sequence 14, Appl
	27	55.6	13.3	2111	7	US-11-293-697-379	Sequence 379, App
	28	55.6	13.3	6065	6	US-10-528-659-3	Sequence 3, Appl1
C	29	55.4	13.3	762	6	US-10-953-349-30826	Sequence 30826, A
C	30	54.8	13.1	641	6	US-10-488-619-1577	Sequence 1577, Ap
	31	54.6	13.1	1395	6	US-10-953-349-36407	Sequence 36407, A
	32	54.4	13.0	2059	7	US-11-293-697-1623	Sequence 1623, Ap
C	33	54.2	13.0	431	6	US-10-488-619-1226	Sequence 1244, Ap
	34	54	12.9	2059	7	US-11-293-697-1244	Sequence 1244, Ap
C	35	53.8	12.9	1761	6	US-10-953-349-38337	Sequence 38337, A
	36	53.8	12.9	70655	6	US-10-505-928-596	Sequence 596, App
C	37	53.6	12.9	56580	6	US-10-553-298-1	Sequence 1, Appl1
C	38	53.4	12.8	2278	7	US-11-293-697-164	Sequence 164, Appl
C	39	53.2	12.8	2205	6	US-10-953-349-9921	Sequence 9921, Ap
C	40	52.8	12.7	807	6	US-10-953-349-36144	Sequence 36144, A
C	41	52.8	12.7	1234	6	US-10-196-749-237	Sequence 237, App
C	42	52.8	12.7	1234	7	US-11-101-316-63	Sequence 63, Appl
C	43	52.8	12.7	2379	6	US-10-196-749-483	Sequence 483, App
C	44	52.6	12.6	1456	6	US-10-953-349-30078	Sequence 30078, A
C	45	52.2	12.5	1570	6	US-10-196-749-335	Sequence 335, App

ALIGNMENTS

RESULT 1
US-11-284-877-17
; Sequence 17, Application US/11284877
; Publication No. US20060095984A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson
; STREET: 12390 El Camino Real
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/284,877
; FILING DATE: 21-Nov-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/808,689
; FILING DATE: 24-MAR-2004
; APPLICATION NUMBER: 10/219,694
; FILING DATE: 14-AUG-2002
; APPLICATION NUMBER: 10/151,081
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/151,078
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/125,767
; FILING DATE: 17-APR-2002
; APPLICATION NUMBER: 10/287,313
; FILING DATE: 01-NOV-2002
; APPLICATION NUMBER: 09/799,462
; FILING DATE: 05-MAR-2001
; APPLICATION NUMBER: 09/724,872
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,726
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,693
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 08/835,682

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1      FILING DATE: 10-APR-1997
2      APPLICATION NUMBER: 08/695,191
3      FILING DATE: 07-AUG-1996
4      APPLICATION NUMBER: 08/682,080
5      FILING DATE: 15-JUL-1996
6      APPLICATION NUMBER: 08/629,822
7      FILING DATE: 10-APR-1996
8
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Seidman, Stephanie L
11     REGISTRATION NUMBER: 33,779
12     REFERENCE/DOCKET NUMBER: 17084-004018/402QC
13
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: 858-678-4777
16     TELEFAX: 202-626-7796
17
18     TELEX: <Unknown>
19
20     INFORMATION FOR SEQ ID NO: 17:
21     SEQUENCE CHARACTERISTICS:
22         LENGTH: 42399 base pairs
23         TYPE: nucleic acid
24         STRANDEDNESS: single
25         TOPOLOGY: linear
26     MOLECULE TYPE: Genomic DNA
27     HYPOTHEetical: NO
28
29     ANTI-SENSE: NO
30     FRAGMENT TYPE: <Unknown>
31     ORIGINAL SOURCE:
32     SEQUENCE DESCRIPTION: SEQ ID NO: 17:
33
34     US-11-284-877-17

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Query Match	15.6%;	Score 65.2;	DB 7;	Length 42999
Best Local Similarity	74.5%;	Pred. No. 4.4e-05;		
Matches 82;	Conservative	0;	Mismatches 28;	Indels 0;

[illegible]

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RESULT 2
US-10-953-349-10307/c
; Sequence 10307, Application US/10953349
; Publication No. US20060107345A1
;
GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10307
;
; LENGTH: 1292
; TYPE: DNA
;
; ORGANISM: Arabidopsis thaliana
;
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (874)..(875)
; OTHER INFORMATION: n is a, c, g, or t
;
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (877)..(877)
; OTHER INFORMATION: n is a, c, g, or t
;
US-10-953-349-10307

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Query Match	15.3%	Score 63.6;	DB 6;	Length 1292;
Best Local Similarity	62.7%;	Pred. No. 5.4e-05;		
Matches	96;	Conservative	0;	Mismatches 57;
			Indels	0;
			Gaps	0;

OY	166	TTATCTTTTCCTTTTTTTCTGCTGTGCCTCCTGGTGCCGCT	228
Dδ	984	TT	928
OY	226	TTCTCGCTCTCTGTGCTTTCTTCCTCTCTTCTTCTCATGGCAAG	288
Dδ	924	TTNNNTAAGAATA	868
OY	286	ATTCTCTCATGGACAATAATCTGCTGACT	318
Dδ	864	CACAGTTCCTTAATCTTAATAAACTGCTTTGCT	832

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RESULT 3
US-10-953-349-35802/c
; Sequence 35802, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35802
; LENGTH: 2442

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/ NAME/KEY: misc_feature
/ LOCATION: (539)..(539)
/ OTHER INFORMATION: n is a, c, g, or t
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (659)..(660)
/ OTHER INFORMATION: n is a, c, g, or t
/
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (2405)..(2411)
/ OTHER INFORMATION: n is a, c, g, or t
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (2432)..(2433)
/ OTHER INFORMATION: n is a, c, g, or t
/
US-10-953-349-35802

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Query Match	15.1%	Score 63;	DB 6;	Length 2442;
Best Local Similarity	68.9%	Pred. No. 7.8e-05;		
Matches 84; Conservative	0;	Mismatches 38;	Indels 0;	Gaps 0

[illegible]

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US-10-196-749-27/c
RESULT 4
; Sequence 27, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc

```

[illegible]

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; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-758

Query Match      14.7%; Score 61.4; DB 6; Length 1999;
Best Local Similarity 62.9%; Pred. No. 0.00016;
Matches 95; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

OY    166 TTATACCTTTCTTTTTTCTTTCTTTCTTTCTTTCTTTCTTTGTCCTTGCTGT 225
DB    1961 TTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1902

OY    226 TTCCTCCTCCGCCTGCTTCTTCTTCCCTCTTCTTCTTTCTTTCTTCAAGCGAAG 285
DB    1901 TTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCTCAAAC 1842

OY    286 ATCTCCATGCGAGAAATAATCTGCCCTGA 316
DB    1841 ATTTCCTTTATTATATAAAGCTTACTTA 1811

RESULT 6
US-10-196-749-149/c
; Sequence 149, Application US//10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US//10/196,749
PRIOR FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 149
LENGTH: 2773
TYPE: DNA
ORGANISM: Homo Sapien
US-10-196-749-149

Query Match      14.6%; Score 60.8; DB 6; Length 2773;
Best Local Similarity 62.5%; Pred. No. 0.00022;

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misc_feature      96130..104791
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misc_feature      117013..131368
                  /note="assembly_name:Contig44"
gap              131369..131468
                  /estimated_length=unknown
misc_feature      131469..142993
                  /note="assembly_name:Contig45"
gap              142994..143093
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misc_feature      143094..154361
                  /note="assembly_name:Contig46"
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gap              154362..154461
                  /estimated_length=unknown
misc_feature      154462..173802
                  /note="assembly_name:Contig47"
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gap              173803..173902
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misc_feature      173903..197031
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                  clone_end:SP6
                  vector_side:right"

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Best Local Similarity 100.0%; Pred. No. 4.5e-75;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY              1 TTCCTGCGAGTCCCTCTTCTGCTGGTGAACACATATGCGCGGCTGACAGGGTGA 60
Db              164235 TTCCTGCGAGTCCCTCTGCTGGTGAACACATATGCGCGGCTGACAGGGTGA 164294

QY              61 AGTGTGTGAATATCAGGAAGATGACTGACAGTCTTTGGGACTCCGTTTCTCATTTGTAAA 120
Db              164295 AGTGTGTGAATATCAGGAAGATGACTGACAGTCTTTGGGACTCCGTTTCTCATTTGTAAA 164354

QY              121 ATGAGGTTAATACAGACCTCTTCTACTCCCAACGACGTTGTCGCCGCGCAGAG 180
Db              164355 ATGAGGTTAATACAGACCTCTTCTACTCCCAACGACGTTGTCGCCGCGCAGAG 164414

QY              181 GGCCCAATTGTGTGCTGCTTCACGCATCAGTTAACCCCAAGACGGGTCAAGCCATTAAA 240
Db              164415 GGCCCAATTGTGTGCTGCTTCACGCATCAGTTAACCCCAAGACGGGTCAAGCCATTAAA 164474

QY              241 GGCGAACACGAGCCCGGT 257
Db              164475 GGCGAACACGAGCCCGGT 164491

RESULT 3
AP003531/c      199384 bp      DNA      linear      PRI 27-APR-2002
LOCUS           Homo sapiens genomic DNA, chromosome 11q clone:RP11-535C12,
DEFINITION      complete sequences.
ACCESSION       AP003531
VERSION         AP003531.2 GI:20334341
KEYWORDS        HTG.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE       1
AUTHORS         Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                  Fujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.
TITLE           Published Only in Database (2001)
JOURNAL         2 (bases 1 to 199384)
AUTHORS         Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                  Fujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.
TITLE           Direct Submission
JOURNAL         Submitted (18-APR-2001) Masahira Hattori, The Institute of Physical
                  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                  1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
                  (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                  Tel:81-45-503-9111, Fax:81-45-503-9170)
                  On Apr 26, 2002 this sequence version replaced gi:13699094.
FEATURES         location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.5e-75;
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Db	181417	ATGAGAGTTAATACCAAGCTTCTTCTTACTCCCCAAACGACGCTGTTGTGTCCCGGCACAG	181358						
QY	181	GGCCCAATTGTTGGCTGTTTCACGCATCAGTTACCCCCACAGACGGGTCAACCAATTAAA	240						
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DEFINITION	AF306570	Human sapiens uncoupling protein 2 gene, promoter region and exon 1;							
ACCESSION	AF306570								
VERSION	AF306570.1	GI:11037742							
KEYWORDS									
SOURCE	Human sapiens (human)								
ORGANISM	Human sapiens								
REFERENCE	Schneitler, C., Oberkofler, H., Esterbauer, H. and Patlach, W.								
AUTHORS	Schneitler, C., Oberkofler, H., Esterbauer, H. and Patlach, W.								
TITLE	UCP2 promoter region and exon 1								
JOURNAL	Unpublished								
REFERENCE	2 (bases 1 to 3270)								
AUTHORS	Schneitler, C., Oberkofler, H., Esterbauer, H. and Patlach, W.								
TITLE	Direct Subsequence								
JOURNAL	Submitted (18-SEP-2000) Laboratory Medicine, Landeslinken								
FEATURES	Salzburg, Mueller Hauptstr. 48, Salzburg A-5020, Austria								
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	/note="UCP2"								
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	Best Local Similarity	99.6%;	Pred. No. 1.1e-74;						
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QY	61	AGTGTGTGAATATCAAGGAAGATGATCGTAACGCTTCTTGGACTCCGTTCTCTATTGTAAA	120						
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QY	121	ATGAGAGTTAATACCAAGCTTCTTCTTACTCCCCAAACGACGCTGTTGTCCCGGCACAG	180						

Dn		2168	ATGAGGTATTATACGAGCCTTCTTTACTCCCAAAAGCAGCGTGTGTGCCGGCCAG	2227
QY		181	GCCCCAATTGTTGAGCTGTTACGCATCATGTTACCACACGAGCGGTCAGCCAATTAAA	240
Dn		2228	GGCCCAATTGTTGGCTGTTTCACGCGTCATGTTACCCACACGAGCGGTCAGCCAATTAAA	2287
OY		241	GGCGAACCCAGCGCCGGT	257
Dn		2288	GGCGAACCCAGCGCCGGT	2304
RESULT_5				
D0087219				
LOCUS			12177 bp DNA linear PRI 18-JUN-2005	
DEFINITION			Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier).	
ACCESSION			(UCP2) gene, complete cds; nuclear gene for mitochondrial product.	
VERSION			D0087219	
KEYWORDS			D0087219.1 GI:67515418	
SOURCE				
ORGANISM			Homo sapiens (human)	
AUTHORS			Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 12177) Livingston,R.U., Rieder,M.J., Shaffer,T., Bertucci,C., Baier,C.N., Rajkumar,N., Wills,H.T., Daniels,M., Downing,T.K., Stanaway,I.B., Nguyen,C.P., Gildersleeve,H., Cassidy,C.M., Johnson,B.U., Swenson,J.E., McFarland,I., YooI,B., Park,C. and Nickerson,D.A. Direct Submission Submitted (07-JUN-2005) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu). location/Qualifiers	
TITLE				
JOURNAL				
COMMENT				
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variation				/replace="t"
variation			2089	

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QY 61 AGGTGTGAATATCAGGAAGATGACGTAAGCTTTGGGACCTCCGTTCTCTCAATTGTAA 120
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QY 121 ATGAGAGTTAATACAGACCTCTTCTTACTCTCCCAACGACGCTGTGTCTCCGCGCAGAG 180
DB 1051 ATGAGAGTTAATACAGACCTCTTCTTACTCTCCCAACGACGCTGTGTCTCCGCGCAGAG 1110
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DB 1111 GGGCCCAATTGGTGGCTGTTCACGATCATGTTACCCCAACAGAGCGGCTCAGCCCAATTAA 1170
QY 241 GGGGAACCAAGCCCGGT 257
DB 1171 GGGGAACCAAGCCCGGT 1187

RESULT 6
AP003717/c 156370 bp DNA linear PRI 27-APR-2002
LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-167N4, complete
DEFINITION sequences.

ACCESSION AP003717
VERSION AP003717.3 GI:20334343
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Torok, Y., Watanabe, H. and Sakaki, Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 156370)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Torok, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2002 this sequence version replaced gi:16904692.

FEATURES
Location/Qualifiers
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Query Match 99.4%; Score 255.4; DB 5; Length 156370;
Best Local Similarity 99.6%; Pred. No. 1.5e-74;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCCTGCGAGTCCTCTTCTGCTGTGTAACACATATGCGCGCCGCTTACACAGGCTGTA 60
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QY 61 AGGTGTGAATATCAGGAAGATGACGTAAGCTTTGGGACCTCCGTTCTCTCAATTGTAA 120
DB 43935 AGGTGTGAATATCAGGAAGATGACGTAAGCTTTGGGACCTCCGTTCTCTCAATTGTAA 43876
QY 121 ATGAGAGTTAATACAGACCTCTTCTTACTCTCCCAACGACGCTGTGTCTCCGCGCAGAG 180

DB 43875 ATGAGAGTTAATACAGACCTCTTCTTACTCTCCCAACGACGCTGTGTCTCCGCGCAGAG 43816
QY 181 GGGCCCAATTGGTGGCTGTTCACGATCATGTTACCCCAACAGAGCGGCTCAGCCCAATTAA 240
DB 43815 GGGCCCAATTGGTGGCTGTTCACGATCATGTTACCCCAACAGAGCGGCTCAGCCCAATTAA 43756
QY 241 GGGGAACCAAGCCCGGT 257
DB 43755 GGGGAACCAAGCCCGGT 43739

RESULT 7
AC024029/c 155668 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
DEFINITION SEQUENCE, 15 unordered pieces.

ACCESSION AC024029.3 GI:7230916
VERSION AC024029
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 155668)
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 155668)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT On Mar 13, 2000 this sequence version replaced gi:7109555.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0167N04
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing strategy: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.38 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
* 11378 14368: contig of 2991 bp in length

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* 14369 14468: gap of unknown length
* 14469 20130: contig of 5662 bp in length
* 20131 20230: gap of unknown length
* 20231 25513: contig of 5283 bp in length
* 25514 25613: gap of unknown length
* 25614 30765: contig of 5152 bp in length
* 30766 30865: gap of unknown length
* 30866 37337: contig of 6472 bp in length
* 37338 37437: gap of unknown length
* 37438 45571: contig of 8134 bp in length
* 45572 45671: gap of unknown length
* 45672 60199: contig of 14528 bp in length
* 60200 60299: gap of unknown length
* 60300 71424: contig of 11125 bp in length
* 71425 71524: gap of unknown length
* 71525 86218: contig of 14694 bp in length
* 86219 86318: gap of unknown length
* 86319 104104: contig of 17786 bp in length
* 104105 104204: gap of unknown length
* 104205 155668: contig of 51464 bp in length.
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Best Local Similarity 99.2%; Pred. No. 1.de-70;
Matches 255; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 1 TTCCCTGGCAGTCCCTTCCTGCTGTGAACACATATGGCGCCGCTGACCAAGGTGTA 60
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QY 61 AGTGTGTAATATCAGAGATGACTGACGCTCTTGGGACTCCGTTTCCATTTGTA 120
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Db 69221 AGTGTGTAATATCAGAGATGACTGACGCTCTTGGGACTCCGTTTCCATTTGTA 69162

QY 121 ATGAGGTTAATACACAGCTTCTTCTAATCCCAACGACGCTTTGTCGGCCAGAG 180
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Db 69161 ATGAGGTTAATACACAGCTTCTTCTAATCCCAACGACGCTTTGTCGGCCAGAG 69102

QY 181 GGCCCAATTTGTGCTGTTTACGCATGATTACCCCAAGAGGGTACGCCAATTAA 240
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QY 241 GGGCAACACAGCCCGGT 257
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Db 69042 GGGCAACACAGCCCGGT 69026
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RESULT 8
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LOCUS Homo sapiens uncoupling protein 2 (UCP2) gene, promoter and exon 1.
DEFINITION AF208500
VERSION AF208500.1 GI:6684000
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
            1 (bases 1 to 3301)
REFERENCE 1
AUTHORS Tu,N., Chen,H., Winnikes,U., Reinert,I., Marmann,G., Pirke,K.M. and
            Lenters,K.U.
TITLE Molecular cloning and functional characterization of the promoter
            region of the human uncoupling protein-2 gene
JOURNAL Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)
PUBMED 10558866
REFERENCE 2 (bases 1 to 3301)
AUTHORS Tu,N., Chen,H., Winnikes,U., Reinert,I., Pirke,K.M. and
            Lenters,K.-U.
TITLE Functional characterization of the 5'-flanking and promoter regions
            of the human UCP3 gene
JOURNAL Biochem. Biophys. Res. Commun. (2000) In press
REFERENCE 3 (bases 1 to 3301)
AUTHORS Lenters,K.-U., Tu,N. and Chen,H.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics,
            Center for Psychobiological and Psychosomatic Research, University
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Db 146 TCCCTGTGCTTTGAAGCCACACAGGCAATGGGCTTGAACAGGGCTCAGCTGTG-AC 88
Qy 72 ATCAGGAAGATGACTGAACGCTTTGGAGACTCCGTTTCTCATTTGTAAGAGAGTTAA 131
Db 87 CTGGGAGAGTTACTGAACCTTTTGAGGCTCAGCTTTCTCATCTGGAACAGAGCTAA 28
Qy 132 TACC 135
Db 27 CAAC 24

RESULT 11
AK647079/c 16256 bp DNA linear PAT 04-MAR-2003
LOCUS Sequence 1271 from Patent EP1270724.
DEFINITION AK647079
ACCESSION AK647079 GI:28800062
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
AUTHORS Guanidine triphosphate-binding protein coupled receptors
TITLE Patent: EP 1270724-A 1271 02-JAN-2003;
JOURNAL National Institute of Advanced Industrial Science and Technology
(JIP) ; Center for Advanced Science and Technology Incubation, Ltd.
(JIP)

FEATURES
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8742..8932,14104..14223,14326..14487,14579..14707,
15950..16056)
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CRRLVSPHQCCPLTTLRLTROLCCSVGAKMARCORCTDSTARFKELCPKGYH
ILTSHTLTIQESDPSFLHPDGPPEPQOLPESPSQAPPEDTEERKGVTTDS
ERSVQSHPTATTPAPRPVLDLSQAGVRAKTEVERASVNIYSDSALPADI
SRSPPTMFLPDLPPSRSAVIAITOVTAAGQDVNAVQAMPPTMAADPADE
EKSLCPRLVSPHQCCPLTTLRLTROLCCSVGAKMARCORCTDSTARFKELCPG
KGYHILTSHTLTIQESDPSFLHPDGPPEPQOLPESPSQAPPEDTEERKGVTTDS
PVSERSVQSHPTATTPAPRPVLDLSQAGVRAKTEVERASVNIYSDSALPADI
WPLPDLPPSRSAVIAITOVTAAGQDVNAVQAMPPTMAADPADE
DCLNPPGSRVCVCPGHSIGSPRTQCIADKPEKSLCPRLVSPHQCCPLTTLRL
LCCSVGAKMARCORCTDSTARFKELCPKGYHILTSHTLTIQESDPSFLHPD
DGPPEPQOLPESPSQAPPEDTEERKGVTTDSVSMKQVRRGGRGGAHVATSR
QAGVGRATTEVERASVNIYSDSALPADIILTSHTLTIQESDPSFLHPD
PQVYRTDECRNLNONTGHEGCTVGPPTDVSCHNRPPTSPALILVNECEAPCPG
RGICMNTGSSYNCHNRYRLHVGAGRSVGRQGGGLDNECAKPLCGDGFC
INPFGYKNCYPGYRLKASRPVCEVQAAVSYDYTAFOQGOQSKPPIQLSQNTK
LAG"

ORIGIN
Query Match 16.2%; Score 41.6; DB 2; Length 16256;
Best Local Similarity 63.7%; P-Value 0.028;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Qy 12 TCCCTGTGCTTTGAAGCCACACAGGCAATGGGCTTGAACAGGGCTCAGCTGTG-AC 71
Db 13196 TCCCTGTGCTTTGAAGCCACACAGGCAATGGGCTTGAACAGGGCTCAGCTGTG-AC 13138
Qy 72 ATCAGGAAGATGACTGAACGCTTTGGAGACTCCGTTTCTCATTTGTAAGAGAGTTAA 131

Db 13137 CTGGGAGAGTTACTGAACCTTTTGAGGCTCAGCTTTCTCATCTGGAACAGAGCTAA 13078
Qy 132 TACC 135
Db 13077 CAAC 13074

RESULT 12
AP000579 70975 bp DNA linear HTG 30-MAY-2000
LOCUS Homo sapiens chromosome 11 clone Xkp1-110a10 map 11q13, WORKING
DEFINITION DRAFT SEQUENCE, 15 unordered pieces.
AP000579
ACCESSION AP000579 GI:8118786
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1 (bases 1 to 70975)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
AUTHORS Fujiyama, A., Yada, T., Toroki, Y., Watanabe, H. and Sakaki, Y.
TITLE Homo sapiens 70,975 genomic DNA of 11q13
JOURNAL Published Only in Database (1999)
2 (bases 1 to 70975)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
AUTHORS Fujiyama, A., Yada, T., Toroki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitaato Univ., 1-15-1 Kitaato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsr.riken.go.jp, Tel:01-42-778-9923,
Fax:01-42-778-9924)
URL: http://hgp.gsc.riken.go.jp/, Tel:01-42-778-9923.

COMMENT
On May 31, 2000 this sequence version replaced gi:6997470.
----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsr.riken.go.jp
----- Project Information
Center project name: HumDra11
Center clone name: Xkp1-110a10
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 64047 bases at least Q40
Consensus quality: 6606 bases at least Q30
Consensus quality: 68080 bases at least Q20
Insert size: 69575; sum-of-contigs
Quality coverage: 5.40x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
15 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 24733 24632 contig of 24632 bp in length
2 34535 contig of 9803 bp in length
3 34536 40636 contig of 6001 bp in length
4 40737 45581 contig of 4845 bp in length
5 45682 49888 contig of 4207 bp in length
6 49989 53496 contig of 3508 bp in length
7 53597 56066 contig of 2470 bp in length
8 56167 58948 contig of 2782 bp in length
9 59049 60647 contig of 1599 bp in length
10 60748 62804 contig of 2157 bp in length
11 63005 64533 contig of 1529 bp in length
12 64634 66654 contig of 2021 bp in length

66755 68335 contig of 1581 bp in length
68436 69753 contig of 1318 bp in length
69854 70975 contig of 1122 bp in length
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 24632: contig of 24632 bp in length
* 24732: gap of 100 bp
* 24733 24732: contig of 9803 bp in length
* 34535 34535: gap of 100 bp
* 34536 34535: contig of 6001 bp in length
* 40636 40636: gap of 100 bp
* 40736 40736: contig of 4845 bp in length
* 45581 45581: gap of 100 bp
* 45681 45681: contig of 4207 bp in length
* 49889 49889: gap of 100 bp
* 53496 53496: gap of 100 bp
* 53597 53597: gap of 100 bp
* 56067 56067: gap of 100 bp
* 56167 56167: gap of 100 bp
* 58948 58948: gap of 100 bp
* 59048 59048: gap of 100 bp
* 60647 60647: gap of 100 bp
* 60748 60748: gap of 100 bp
* 62905 62905: gap of 100 bp
* 63005 63005: gap of 100 bp
* 64534 64534: gap of 100 bp
* 64534 64534: contig of 2021 bp in length
* 66555 66555: gap of 100 bp
* 66755 66755: gap of 100 bp
* 68336 68336: gap of 100 bp
* 68436 68436: gap of 100 bp
* 69754 69754: gap of 100 bp
* 69854 69854: gap of 100 bp
* 70975 70975: contig of 1122 bp in length.

FEATURES

source

1. .70975
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/clone="XXP1-110A10"
1. .24632
/note="assembly_fragment"
24733. 34535
/note="assembly_fragment"
34536. 40636
/note="assembly_fragment"
40737. 45581
/note="assembly_fragment"
45682. 49889
/note="assembly_fragment"
49989. 53496
/note="assembly_fragment"
53597. 56066
/note="assembly_fragment"
56167. 58948
/note="assembly_fragment"
59049. 60647
/note="assembly_fragment"
60748. 62904
/note="assembly_fragment"
63005. 64533
/note="assembly_fragment"
64634. 66654
/note="assembly_fragment"

misc_feature 66755..68335
/note="assembly_fragment"
misc_feature 68436..69753
/note="assembly_fragment"
misc_feature 69854..70975
/note="assembly_fragment"

ORIGIN

Query Match 16.2%; Score 41.6; DB 12; Length 70975;
Best Local Similarity 63.7%; Pred. No. 0.031;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCCTTCCTGCTGATAAACAATATGCGCGCGCTGACACAGGCTGTAGTGTGAT 71
|||||
Db 49210 TCCCTTCCTGCTTGTGAAGCCACACAGCATGGCTTGAACACGCTCAGCTGTG-AC 49268
|||||
QY 72 ATCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 131
|||||
Db 49269 CTGGGCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 49328
|||||
QY 132 TACC 135
Db 49329 CAAC 49332

RESULT 13

AP000803

LOCUS

Homo sapiens chromosome 11 clone RP11-642F7 map 11q13, WORKING

DEFINITION DRAFT SEQUENCE. 39 unordered pieces.

ACCESSION

AP000803.2 GI:8118958

HTG; HTGS PHASE1; HTGS_DRAFT.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 140356)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens 140,356 genomic DNA of 11q13

2 (bases 1 to 140356)

Published Only in Database (1999)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (30-NOV-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)

On May 31, 2000 this sequence version replaced gi:6997640.

----- Genome Center

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp

----- Project Information

Center project name: Humdrat11

Center clone name: RP11-642F7

----- Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 11753 bases at least Q40

Consensus quality: 12814 bases at least Q30

Consensus quality: 13785 bases at least Q20

Insert size: 13656; sum-of-contigs

Quality coverage: 4.30x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of

39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

```
1 13642 contig of 13642 bp in length
13743 21060 contig of 7318 bp in length
21161 30193 contig of 9033 bp in length
30294 38592 contig of 8299 bp in length
38683 45688 contig of 6996 bp in length
45789 53108 contig of 7320 bp in length
53209 58558 contig of 5350 bp in length
58659 63503 contig of 4845 bp in length
63604 69634 contig of 6031 bp in length
69735 75598 contig of 5864 bp in length
75699 80624 contig of 4926 bp in length
80725 84015 contig of 3291 bp in length
84116 88588 contig of 4473 bp in length
88689 91909 contig of 3221 bp in length
91910 92009 contig of 100 bp in length
92010 95029 contig of 3020 bp in length
95129 95129 contig of 100 bp in length
95130 99186 contig of 4057 bp in length
99187 99286 contig of 100 bp in length
99287 102612 contig of 3326 bp in length
102613 102712 contig of 3326 bp in length
102713 104341 contig of 1629 bp in length
104342 106114 contig of 1673 bp in length
106215 108067 contig of 1853 bp in length
108168 111125 contig of 2958 bp in length
111226 114483 contig of 3258 bp in length
114584 116915 contig of 2232 bp in length
116916 119429 contig of 2513 bp in length
119430 121748 contig of 2219 bp in length
121749 121848 contig of 1031 bp in length
121849 122878 contig of 1031 bp in length
122879 122978 contig of 1410 bp in length
122979 124388 contig of 1421 bp in length
124389 124488 contig of 100 bp in length
124489 125909 contig of 1421 bp in length
125910 127923 contig of 1914 bp in length
127924 129208 contig of 1185 bp in length
129209 130851 contig of 1543 bp in length
130852 131540 contig of 589 bp in length
131541 133056 contig of 1416 bp in length
133057 133157 contig of 1131 bp in length
133158 134287 contig of 1057 bp in length
134288 135444 contig of 1200 bp in length
135445 136745 contig of 1154 bp in length
136746 137998 contig of 1154 bp in length
137999 138098 contig of 1097 bp in length
138099 139195 contig of 1097 bp in length
139196 139295 contig of 1061 bp in length
139296 140356 contig of 1061 bp in length

Sequence updated (26-May-2000).
NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
```

FEATURES

source

```
* 75599 75699: gap of 100 bp
* 75699 80624: contig of 4926 bp in length
* 80625 80724: gap of 100 bp
* 80725 84015: contig of 3291 bp in length
* 84016 84115: gap of 100 bp
* 84116 88588: contig of 4473 bp in length
* 88589 88688: gap of 100 bp
* 88689 91909: contig of 3221 bp in length
* 91910 92009: gap of 100 bp
* 92010 95029: contig of 3020 bp in length
* 95030 95129: gap of 100 bp
* 95130 99186: contig of 4057 bp in length
* 99187 99286: gap of 100 bp
* 99287 102612: contig of 3326 bp in length
* 102613 102712: gap of 100 bp
* 102713 104341: contig of 1629 bp in length
* 104342 106114: gap of 100 bp
* 106115 106214: gap of 100 bp
* 106215 108067: contig of 1853 bp in length
* 108068 108167: gap of 100 bp
* 108168 111125: contig of 2958 bp in length
* 111126 111225: gap of 100 bp
* 111226 114483: contig of 3258 bp in length
* 114484 114583: gap of 100 bp
* 114584 116915: contig of 2232 bp in length
* 116916 119429: gap of 100 bp
* 119430 119428: contig of 2513 bp in length
* 119429 119528: gap of 100 bp
* 119529 121747: contig of 2219 bp in length
* 121748 121847: gap of 100 bp
* 121848 122878: contig of 1031 bp in length
* 122879 122978: gap of 100 bp
* 122979 124388: contig of 1410 bp in length
* 124389 124488: gap of 100 bp
* 124489 125909: contig of 1421 bp in length
* 125910 126009: gap of 100 bp
* 126010 127923: contig of 1914 bp in length
* 127924 128023: gap of 100 bp
* 128024 129208: contig of 1185 bp in length
* 129209 129308: gap of 100 bp
* 129309 130851: contig of 1543 bp in length
* 130852 130951: gap of 100 bp
* 130952 131540: contig of 589 bp in length
* 131541 131640: gap of 100 bp
* 131641 133056: contig of 1416 bp in length
* 133057 133156: gap of 100 bp
* 133157 134287: contig of 1131 bp in length
* 134288 134387: gap of 100 bp
* 134388 135444: contig of 1057 bp in length
* 135445 135544: gap of 100 bp
* 135545 136744: contig of 1200 bp in length
* 136745 136844: gap of 100 bp
* 136845 137998: contig of 1154 bp in length
* 137999 138098: gap of 100 bp
* 138099 139195: contig of 1097 bp in length
* 139196 139295: gap of 100 bp
* 139296 140356: contig of 1061 bp in length.
```

Location/Qualifiers

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1. 140356
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source

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/clone="RP11-642F7"
1. 13642
/misc_feature
/feature="assembly_fragment"
13743..21060
/misc_feature
/feature="assembly_fragment"
21161..30193
/misc_feature
/feature="assembly_fragment"
30294..38592
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38693..45688
/note="assembly_fragment clone_end:SP6 vector_side:right"
misc_feature 45789..53108
/note="assembly_fragment"
misc_feature 53209..58558
/note="assembly_fragment"
misc_feature 58659..63503

Query Match 16.2%; Score 41.6; DB 12; Length 140356;
Best Local Similarity 63.7%; Pred. No. 0.033;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCTCTCTGCTGTAACACATATGCGCCGCGCTGACGAGGTGTAGTGTGAAT 71
107409 TCCTCTCTGCTTGTGAAGCCACACAGGATGGCTTGAACAGGCTCAGCTGTGTG-AC 107467

QY 72 ATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 131
107468 CTGGGCGAGGTACTGAACTCTTTGAGGCTTTCATCTGTAAGAAACGAGGCTTA 107527

QY 132 TACC 135
107528 CAACT 107531

RESULT 14
AP001459/ 150694 bp DNA linear HTG 30-MAY-2000
AP001459/ Homo sapiens chromosome 11 clone RP11-856C23 map 11q13, WORKING
DEFINITION DRAFT SEQUENCE, 44 unordered pieces.
ACCESSION AP001459
VERSION AP001459.2 GI:8117333
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 150694)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y.
TITLE Homo sapiens 150,694 genomic DNA of 11q13
JOURNAL Published Only in DataBase (2000)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitsato Univ., 1-15-1 Kitsato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
COMMENT On May 30, 2000 this sequence version replaced gi:7262592.
----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center Project name: HumDrat11
Center Clone name: RP11-856C23
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 123414 bases at least Q40
Consensus quality: 135962 bases at least Q30
Consensus quality: 142087 bases at least Q20
Insert size: 146394; sum-of-contigs
Quality coverage: 4.08x in Q20 bases; sum-of-contigs
-----
```

NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```
1 11401 contig of 11401 bp in length
11502 23078 contig of 11577 bp in length
23179 32309 contig of 9131 bp in length
32410 38694 contig of 6285 bp in length
38795 45338 contig of 6544 bp in length
45439 53500 contig of 8062 bp in length
53601 57891 contig of 4291 bp in length
57992 62254 contig of 4263 bp in length
62355 68449 contig of 6095 bp in length
68550 74597 contig of 6048 bp in length
74698 79320 contig of 4623 bp in length
79421 84028 contig of 4608 bp in length
84129 89011 contig of 4883 bp in length
89112 92481 contig of 3370 bp in length
92582 96064 contig of 3483 bp in length
96165 99717 contig of 3553 bp in length
99818 102767 contig of 2950 bp in length
102868 104437 contig of 1570 bp in length
104538 107049 contig of 2512 bp in length
107150 109447 contig of 2298 bp in length
109548 112354 contig of 2807 bp in length
112455 114620 contig of 2166 bp in length
114721 118139 contig of 3419 bp in length
118240 120002 contig of 1763 bp in length
120103 122301 contig of 2199 bp in length
122402 124473 contig of 2072 bp in length
124574 126352 contig of 1779 bp in length
126453 128696 contig of 2244 bp in length
128797 130034 contig of 1238 bp in length
130135 130639 contig of 505 bp in length
130740 131925 contig of 1186 bp in length
132026 134015 contig of 1990 bp in length
134116 135860 contig of 1745 bp in length
135961 137276 contig of 1316 bp in length
137377 138486 contig of 1110 bp in length
138587 140068 contig of 1482 bp in length
140169 141262 contig of 1094 bp in length
141363 142808 contig of 1446 bp in length
142909 144345 contig of 1437 bp in length
144446 145547 contig of 1102 bp in length
145548 146594 contig of 1047 bp in length
146795 147949 contig of 1155 bp in length
148050 149156 contig of 1107 bp in length
149257 150694 contig of 1438 bp in length
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 11401: contig of 11401 bp in length
11402 11501: gap of 100 bp
11502 23078: contig of 11577 bp in length
23079 23179: gap of 100 bp
23179 32309: contig of 9131 bp in length
32310 32409: gap of 100 bp
32410 38694: contig of 6285 bp in length
38695 45338: gap of 100 bp
45339 45438: contig of 6544 bp in length
45439 45539: gap of 100 bp
45540 53500: contig of 8062 bp in length
53501 53600: gap of 100 bp
53601 57891: contig of 4291 bp in length
```

```

* 57892 57991: gap of 100 bp
* 57992 62254: contig of 4263 bp in length
* 62255 62354: gap of 100 bp
* 62355 68449: contig of 6095 bp in length
* 68450 68549: gap of 100 bp
* 68550 74597: contig of 6048 bp in length
* 74598 74697: gap of 100 bp
* 74698 79320: contig of 4623 bp in length
* 79321 79421 84028: contig of 4608 bp in length
* 84029 84128: gap of 100 bp
* 84129 89011: contig of 4883 bp in length
* 89012 89111: gap of 100 bp
* 89112 92481: contig of 3370 bp in length
* 92482 92581: gap of 100 bp
* 92582 96064: contig of 3483 bp in length
* 96065 96164: gap of 100 bp
* 96165 99717: contig of 3553 bp in length
* 99718 99817: gap of 100 bp
* 99818 102767: contig of 2950 bp in length
* 102768 102867: gap of 100 bp
* 102868 104437: contig of 1570 bp in length
* 104438 104537: gap of 100 bp
* 104538 107049: contig of 2512 bp in length
* 107050 107149: gap of 100 bp
* 107150 109447: contig of 2298 bp in length
* 109448 109547: gap of 100 bp
* 109548 112354: contig of 2807 bp in length
* 112355 112454: gap of 100 bp
* 112455 114620: contig of 2166 bp in length
* 114621 114720: gap of 100 bp
* 114721 118139: contig of 3419 bp in length
* 118140 118239: gap of 100 bp
* 118240 120002: contig of 1763 bp in length
* 120003 120102: gap of 100 bp
* 120103 122301: contig of 2199 bp in length
* 122302 122401: gap of 100 bp
* 122402 124473: contig of 2072 bp in length
* 124474 124573: gap of 100 bp
* 124574 126452: contig of 1779 bp in length
* 126453 126452: gap of 100 bp
* 126453 128696: contig of 2244 bp in length
* 128697 128796: gap of 100 bp
* 128797 130034: contig of 1238 bp in length
* 130035 130133: gap of 100 bp
* 130133 130639: contig of 505 bp in length
* 130640 130739: gap of 100 bp
* 130740 131925: contig of 1186 bp in length
* 131926 132025: gap of 100 bp
* 132026 134015: contig of 1990 bp in length
* 134016 134115: gap of 100 bp
* 134116 135860: contig of 1745 bp in length
* 135861 135960: gap of 100 bp
* 135961 137276: contig of 1316 bp in length
* 137277 137376: gap of 100 bp
* 137377 138486: contig of 1110 bp in length
* 138487 138586: gap of 100 bp
* 138587 140068: contig of 1482 bp in length
* 140069 140168: gap of 100 bp
* 140169 141262: contig of 1094 bp in length
* 141263 141362: gap of 100 bp
* 141363 142808: contig of 1446 bp in length
* 142809 142908: gap of 100 bp
* 142909 144345: contig of 1437 bp in length
* 144346 144445: gap of 100 bp
* 144446 145447: contig of 1102 bp in length
* 145448 145647: gap of 100 bp
* 145649 146694: contig of 1047 bp in length
* 146695 146794: gap of 100 bp
* 146795 147949: contig of 1155 bp in length
* 147950 148049: gap of 100 bp
* 148050 149156: contig of 1107 bp in length
* 149157 149256: gap of 100 bp

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* 149257 150694: contig of 1438 bp in length.
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Best Local Similarity 63.7%; Pred. No. 0.033;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
QY 12 TCCCTTCTGCTGTGAACACATATGCGCCGCGCTGACAGGCTTAAGTGTGAAT 71
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Db 109272 TCCCTTGTCTTTTGAAGCCACACAGGATGAGGCTTGAACAGGCTCAGCTGTG-AC 109214
  |||||
QY 72 ATCAGGAAGATGACGTCGCTTTGGGACTCCGTTTCTCATTTGTAATAATGAGATTAA 131
  |||||
Db 109213 CTGGGAGAGTTACTGAACCTTTTGAAGCTTTCATCTGGAACAGAGCTTAA 109154
  |||||
QY 132 TACC 135
  |||||
Db 109153 CAAC 109150
  |||||
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LOCUS
DEFINITION
  Homo sapiens genomic DNA, chromosome 11, clone:RP11-856B14,
  complete sequence.
ACCESSION
  AP001362.5 GI:21327925
VERSION
  HTG.
KEYWORDS
  SOURCE
    Homo sapiens (human)
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    Homo sapiens
      Chordata; Craniata; Vertebrata; Euteleostomi;
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      Homnidae; Homo.
  REFERENCE
    1 Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
      Totoki,Y., Watanabe,H. and Sakaki,Y.
      Homo sapiens genomic DNA
      Published Only in Database (2000)
  TITLE
    JOURNAL
      2 (bases 1 to 211382)
  AUTHORS
    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
    Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
    Direct Submission
  JOURNAL
    Submitted (06-MAR-2000) Masahira Hattori, The Institute of Physical
    and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
    1-7-22 Suenho-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
    (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
    Tel:81-45-503-9111, Fax:81-45-503-9170)
    On Jun 6, 2002 this sequence version replaced gi:20334322.
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      /chromosome="11"
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Best Local Similarity 63.7%; Pred. No. 0.034;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
QY 12 TCCCTTCTGCTGTGAACACATATGCGCCGCGCTGACAGGCTTAAGTGTGAAT 71
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QY 72 ATCAGGAAGATGACTGAACGCTTTGGGACTCCGTTTCTCATTTGTAATAATGAGGTTAA 131
Db 29623 CTGGGGCAGGTTACTGAACCTCTTTGAGGCTCAGCTTCTCATCTGAAAAACGAGGCTAA 29682
QY 132 TACC 135
Db 29683 CAACT 29686

Search completed: June 5, 2006, 22:27:17
Job time : 1745.95 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 223.597 Seconds
(without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

Perfect score: 257
Sequence: 1 ttcctcgcagtcctcctcgc.....aaagcgcaaccagcccgct 257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	257	100.0	3505	3	AAA62932	AAA62932 DNA conta
2	41.6	16.2	3506	12	AD062971	AD062971 Novel hum
3	41.6	16.2	16256	10	AD068618	AD068618 Human GPC
4	37.6	14.6	332	4	AAK64094	AAK64094 Human imm
5	37	14.4	1510	5	AAK84317	AAK84317 DNA encod
6	36.8	14.3	57013	11	ACN45046	ACN45046 Human gen
7	36.8	14.3	149612	11	ACN45154	ACN45154 Human gen
8	35.6	13.9	2425	10	ABZ56972	ABZ56972 Lipocyte
9	35.4	13.8	4673	5	AAK30048	AAK30048 Human lun
10	35.4	13.8	4673	10	ADB33385	ADB33385 Human nov
11	35.4	13.8	7220	4	AAK84030	AAK84030 Human imm
12	35.4	13.8	143306	6	ABK49586	ABK49586 Human tra
13	35.4	13.8	152037	15	AEF74705	AEF74705 Human pol
14	35	13.6	100000	14	ADZ04285	ADZ04285 Human leu
15	35	13.6	100001	15	AEF72834	AEF72834 Human leu
16	34.8	13.5	110000	11	ACN43998_3	ACN43998_3
17	34.6	13.5	327	14	ACU59982	ACU59982 Human col
18	34.6	13.5	612	6	ABN61814	ABN61814 Human can

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C	22	34.4	13.4	113000	9	ABT44365
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C	24	34.4	13.4	325791	4	AAK43104
C	25	34.4	13.4	337022	12	ADQ59416
C	26	34.4	13.4	338780	14	ADZ13691
C	27	34	13.2	98606	11	ACN43868
C	28	33.8	13.2	13010	4	AAK72395
C	29	33.8	13.2	13012	4	AAK72396
C	30	33.6	13.1	33112	10	ACC85730
C	31	33.6	13.1	39001	12	AD138715
C	32	33.6	13.1	65608	6	ABL62910
C	33	33.6	13.1	65608	6	ABL64414
C	34	33.6	13.1	65608	6	ABL67668
C	35	33.6	13.1	109646	14	ABD18286
C	36	33.4	13.0	5691	4	AAK55423
C	37	33.4	13.0	5691	4	AAK84439
C	38	33.2	12.9	27499	13	ABD32620
C	39	33.2	12.9	36568	6	ABK50980
C	40	33.2	12.9	62118	11	ACN44566
C	41	33.2	12.9	85121	14	ADZ13027
C	42	33.2	12.9	133787	13	ABD33624
C	43	33.2	12.9	147463	15	AEF80127
C	44	32.8	12.8	127145	13	ADQ80254
C	45	32.6	12.7	110000	8	AAD53224_3

ALIGNMENTS

RESULT 1

ID AAA62932 standard; DNA; 3505 BP.

AC AAA62932;

DT 02-NOV-2000 (first entry)

XX DNA containing human uncoupling protein-2 (UCP-2) promoter region.

XX Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;

XX KW hypotension; hyperlipidaemia; anti-pyretic; de.

XX OS Homo sapiens.

XX PN WO200039315-A1.

XX PD 06-JUL-2000.

XX PF 22-DEC-1999; 99NO-JP007198.

XX PR 24-DEC-1998; 98JP-00366719.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Toyoda Y, Kobayashi M, Igaki S;

XX DR WPI; 2000-452407/39.

XX PT DNA with promoter region containing regulator sequence of uncoupling

XX PT protein-2 (UCP-2); applicable in screening anti-obesity, anti-diabetic,

XX PT hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in

XX PT therapy.

XX PS Claim 4; Fig 1-6; 43p; Japanese.

XX CC This invention relates to DNA comprising a promoter region containing the

Aal05930 Human rep
Ab198494 Human tes
Ad889097 Human ESR
Abt44365 Partial g
Acn45170 Human gen
Aas43104 Human Oes
Adq59416 Human can
Adz13691 Human can
Acn43868 Mouse gen
Aak72395 Human imm
Aak72396 Human imm
Acc85730 Human kin
Ad18715 Human ltm
Ab162910 Breast ca
Ab164414 Stomach c
Ab167668 Oesophagu
Aed18286 Fibroblc
Aak65423 Human imm
Aak84439 Human imm
Abk50980 Human bol
Acn44566 Human gen
Adz13027 Human can
Abd33624 Human can
Aef80127 Cancer-as
Adq80254 Hermansky
Continuation (4 of

CC transformants. The DNA and cells transformed using it can be used to
CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic
CC and anti-pyretic drugs. The present sequence represents DNA containing
CC the UCP-2 promoter sequences

CC SQ Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 257; DB 3; Length 3505;

Best Local Similarity 100.0%; Pred. No. 1.2e-80;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCTCGCAGTCCCTTCTGCTGTGTAACATATGCGCGCGCTGACCGGCTGTA 60

DB 1133 TTCCTCGCAGTCCCTTCTGCTGTGTAACATATGCGCGCGCTGACCGGCTGTA 1192

QY 61 AGTGTGATATACAGAAAGATGACTGAAGCTCTTGGGAGCTCGTTTCTCATTTGAAA 120

DB 1193 AGTGTGATATACAGAAAGATGACTGAAGCTCTTGGGAGCTCGTTTCTCATTTGAAA 1252

QY 121 ATGGAAGTTAATACAGACCTTCTTCTACTCCCAAGCGACGTTTGTCCCGGCAAG 180

DB 1253 ATGGAAGTTAATACAGACCTTCTTCTACTCCCAAGCGACGTTTGTCCCGGCAAG 1312

QY 181 GGGCCATTGTGGCTGTTCAAGCATCAGTACCCCAAGAGCGGGTCAAGCAATTAAA 240

DB 1313 GGGCCATTGTGGCTGTTCAAGCATCAGTACCCCAAGAGCGGGTCAAGCAATTAAA 1372

QY 241 GGGCAACAGAGCCCGGT 257

DB 1373 GGGCAACAGAGCCCGGT 1389

RESULT 2

ADQ62971/c

ID ADQ62971 standard; cDNA; 3506 BP.

AC ADQ62971;

DT 07-OCT-2004 (first entry)

XX Novel human cDNA sequence #132.

XX ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
XX cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
XX neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
XX cancer.

XX Homo sapiens.

XX BP1440981-A2.

XX PD 28-JUL-2004.

XX PF 21-JAN-2004; 2004BP-00001196.

XX PR 21-JAN-2003; 2003JP-00102206.

XX PR 09-MAY-2003; 2003JP-00131392.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PT Tsogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX PI Yamamoto J, Isono Y, Negai K, Irie R;

XX DR WPI; 2004-535376/52.

XX DR P-PSDB; ADQ65159.

XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX PS Claim 1; SEQ ID NO 132; 2449bp; English.

CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences

CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.

CC SQ Sequence 3506 BP; 647 A; 1039 C; 1184 G; 636 T; 0 U; 0 Other;

Query Match 16.2%; Score 41.6; DB 12; Length 3506;

Best Local Similarity 63.7%; Pred. No. 0.0013; Indels 1; Gaps 1;

Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TTCCTTCTGCTGTGTAACATATGCGCGCGCTGACCAAGGCTGTAAGTGTGAAT 71

DB 146 TTCCTTGTGCTTTTGAAGCCACAGGCGATGGCTTGAACAGGCTGAGCTGTG-AC 88

QY 72 ATCAGGAAGATGACTGAAGCTCTTGGGACTCGCTTCTCATTTGTAATAAGAGTTAA 131

DB 87 CTGGGCGAAGTTACTGAACCTCTTGAAGGCTCAGCTTCTCATTTGTAATAAGAGTTAA 28

QY 132 TACC 135

DB 27 CAAC 24

RESULT 3

ADC6818/c

ID ADC6818 standard; DNA; 16256 BP.

AC ADC6818;

DT 01-JAN-2004 (first entry)

XX Human GPCR gene SEQ ID NO:1271.

XX ds; gene; human; GPCR;

XX KW guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX OS Homo sapiens.

XX PN BP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002BP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX DR WPI; 2003-315783/31.

XX DR P-PSDB; ADC6819.

XX PT New polynucleotide, useful for preparing a composition for treating a

XX patient in need of increased or suppressed activity or expression of the

XX guanosine triphosphate-binding protein coupled receptor.

XX Claim 1; SEQ ID NO 1271; 28pp; English.

CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC68548-ADC687616 encode GPCR's of the
CC invention.

Sequence 16256 BP; 3574 A; 4360 C; 4175 G; 3847 T; 0 U; 300 Other;
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Best Local Similarity 63.7%; Pred. No. 0.0025;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
QY 12 TCCCTTCTGCTGTGAACAACATATGCGCGGCTGACAGGCTGTATGTGTGAAT 71
DB 13196 TCCCTTGTGCTTTGAAGCCACACAGGCATGGGCTTGAACACGGCTCAGCTGTGTG-AC 13138
QY 72 ATCAGGAAGATGACTGACGCTTTGGGACTCCGCTTCCATCTGTAATAATGAGGTTAA 131
DB 13137 CTGGGGACGGTACTGTAACCTTTGAGGCTCAGCTTTCATCTGGAACACGAGGCTAA 13078
QY 132 TACC 135
DB 13077 CAAAC 13074
RESULT 4
AAK64094/c
ID AAK64094 standard; cDNA; 332 BP.
XX AAK64094;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:9154.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WC000157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WC-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198133P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX DR P-PSDB; AAM91313.
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX
PS Claim 1; SEQ ID NO 9154; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (II)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
XX
SQ Sequence 332 BP; 62 A; 81 C; 94 G; 91 T; 0 U; 4 Other;

Query Match 14.6%; Score 37.6; DB 4; Length 332;
Best Local Similarity 68.1%; Pred. No. 0.012;
Matches 49; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

QY 70 AATATCAGGAAAGTAAAGCTCTTGGACTCCGTTCTCTAATGTAATAAGAGGTT 129
DB 141 ATTTGGGGRRAAATAACTTAACCTCTGAGCCTCAGTTCTCATCGCAAAAGAGAT 82
QY 130 AATACGACGCTT 141
: | | | | |

DB 81 MACAACACTTT 70
RESULT 5
AAS84317/c
ID AAS84317 standard; cDNA; 1510 BP.
XX AAS84317/
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #20121.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
PN WO200175067-A2.
XX
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US008631.
PF
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX DR P-PSDB; ABG20130.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX
XX Claim 1; SEQ ID NO 20121; 103bp; English.
XX
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1510 BP; 335 A; 414 C; 432 G; 329 T; 0 U; 0 Other;

Query Match 14.4%; Score 37; DB 5; Length 1510;
Best Local Similarity 57.3%; Pred. No. 0.039;
Matches 67; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 21 CTGTGTAAACACATATGCGCGCGCTGACCAAGGTGTAAGTGTGTAATATCAGGAAG 80
DB 1395 CAGGAGGACAGCACTAGGGGCTGTGGCAGAGCAAGGCTTAGCTGTGTGACCTTGGGACGG 1336
: | | | | |

FT	Key	Location/Qualifiers
FT	CDS	2032..2274
FT		/*tag= "a"
FT		/product= "8.8"
XX		
PN	CN1355192-A.	
XX		
PD	26-JUN-2002.	
XX		
PB	01-DEC-2000; 2000CN-00127648.	
XX		
PR	01-DEC-2000; 2000CN-00127648.	
XX		
PA	(UHFU-) UNIV FUDAN.	
PI	Mao Y, Xie Y;	
XX		
DR	WPI; 2003-000129/01.	
DR	P-PDB; ABP60159.	
XX		
PT	Polypeptide-lipocyte differentiation associated protein 8.8 and polynucleotide for coding it.	
XX		
PS	Claim 6; Page 26-27 (disclosure); 34pp; Chinese.	
CC	The invention relates to a lipocyte differentiation associated protein designated 8.8. Also disclosed are the polynucleotide encoding the polypeptide, and the process for preparing this polypeptide using DNA recombination techniques. The application of the polypeptide is in treating diseases such as obesity and Alexander disease. The current sequence represents the lipocyte differentiation associated protein 8.8 encoding cDNA	
CC		
SQ	Sequence 2425 BP; 910 A; 361 C; 439 G; 715 T; 0 U; 0 Other;	
XX		
XX		
Query Match	13.9%; Score 35.6; DB 10; Length 2425;	
Best Local Similarity	58.5%; Pred No. 0.15;	
Matches	62; Conservative 0; Mismatches 44; Indels 0; Gaps 0	
OY	35 TATGCGCGCGCCTGACCGAGGTGAAGTGTGTAATATCAGGAAGACTGAACGCTCT 94 	
Db	903 TAGAGCCCGTGCTGTGCCACTTACTTCGGGTGAATGAAACAAGTTGCACATTCTT 962 	
OY	95 TTGGGACTCCGTTTCTCTCATTTGTAATAAGAGCTTAATACCAGCCT 140 	
Db	963 ATTTCCTCAGTTTCTTCATTATATAAAGAGATAAATATGCACT 1008 	
RESULT 9		
AAS30048/c		
ID	AAS30048 standard; DNA; 4673 BP.	
XX		
AC	AAS30048;	
XX		
DT	21-NOV-2001 (first entry)	
XX		
DE	Human lung antigen genomic DNA #118.	
XX		
KM	Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; immunosuppressive; antiathritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardian; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerrary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; de; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.	
OS	Homo sapiens.	
XX		
PN	WO200155303-A2.	

XX	02-AUG-2001.	
PD		
XX	17-JAN-2001,	200IMO-US01301.
XX		
PR	31-JAN-2000,	2000US-01790653P
PR	04-FEB-2000,	2000US-01806282P
PR	24-FEB-2000,	2000US-01846649P
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PR	14-AUG-2000,	2000US-02209646P
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PR	14-AUG-2000,	2000US-02245199P
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PR	14-AUG-2000,	2000US-02252143P
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PR	27-SEP-2000,	2000US-02358349P
PR	29-SEP-2000,	2000US-02363379P

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PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
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PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254057P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX

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DR WPI; 2001-457723/49.
XX
XX Isolated polypeptide for treating, preventing and/or diagnosing
PT respiratory disorders related to the lung including lung cancers and also
PT for testing and detection e.g. diagnosis.
XX
XX Claim 1; SEQ ID NO 312; 507bp; English.
XX
CC Sequences AAS29931-AS30164 represent genomic DNA molecules, which encode
CC the lung antigen polypeptides of the invention. Lung antigen polypeptides
CC and their associated polynucleotides are useful in the diagnosis,
CC treatment and prevention of various types of disorders in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by detecting the presence or
CC absence of a mutation in a lung antigen polynucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischaemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma and pleurisy. The polypeptides can
CC also be used to aid wound healing, to prevent skin aging due to sunburn,
CC to maintain organs before transplantation, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 13.8%; Score 35.4; DB 5; Length 4673;
Best Local Similarity 55.2%; Pred. No. 0.24;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 59 TAAAGTGTGATATGACGAAGATGACTGAACGCTTTGGACCTCGTTCCATTGTA 118
Db 141 TAAACGTTAACTTTGGAATGTGCTTAAACGTGTGTGCTCACTTCCATCTTT 82
QY 119 AAATGAGCTTATACCAAGCTTCTTACTCCCAACGACGCTTTGTCCGGCAG 178
Db 81 AAAGAAAGGATATGACACTGTATGATTAATCATATACATATGGACACTTTCAC 22
QY 179 AGGAC 183
Db 21 AGTGC 17

RESULT 10
ADB33385/c
ADB33385 standard; DNA; 4673 BP.
XX
AC ADB33385;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human novel lung related polypeptide DNA SEQ ID NO 312.
XX
XX gene therapy; lung antigen; neoplasia; acute myelogenous leukemia;
XX adenocarcinoma; respiratory disorder; chronic rhinitis; sinusitis;
XX immunodeficiency; X-linked agammaglobulinemia; inflammatory
XX X-linked infantile agammaglobulinemia; inflammatory disorder;
XX adrenallitis; alveolitis; immune complex disease; serum sickness;
XX polyarteritis nodosa; bleeding disorder; thrombocytopenia;
XX Von Willebrand's disease; acquired platelet dysfunction; kidney failure;
XX multiple myeloma; macropneumonia related disorder; Gaucher's disease;
XX Niemann-Pick disease; tumour; colon cancer; pancreatic cancer;
XX renal disorder; nephritis; bone disorder; Albers-Schönberg disease;
XX bowleg; muscle disorder; Becker's muscular dystrophy;
XX Duchenne's muscular dystrophy; nervous disorder; ischaemic lesion;
XX traumatic lesion; endocrine disorder; Cushing's syndrome;
XX corticosteroid deficiency; gastrointestinal disorder; dysphagia;

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KW gastric reflux; human; da.
XX
OS Homo sapiens.
XX
PN US2003054368-A1.
XX
PD 20-MAR-2003.
XX
PF 22-FEB-2002; 2002US-00079854.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
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(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM, Barash SC;
WPI, 2003-695900/66.
Novel isolated lung antigen polypeptides useful for treating, preventing,
diagnosing acute myelogenous leukemias, adenocarcinoma, thrombocytopenia,
Von Willebrand's disease.
Disclosure; SEQ ID NO 312; 178pp; English.

Query Match 13.8%; Score 35.4; DB 10; Length 4673;

QY 59 TAACTGTGTGAATATCAGGAACATGACTGAACGCTCTTTGGGACTCCGTTTCCATTTGA 118
 Db 141 TAAACGCTGTAAACCTTTTGGAAATGTTGCTTAAACTGCTGTGTTCTAGTTTCCATCTTT 82
 QY 119 AAATGAGGTTAATATACACACCTTTCTTACTCCCAAACGCAAGTGTGTTGTCGGGCGAG 178
 Db 81 AAAGAAAGGATATATGACACTGTTATGATTAATTACATTAATACATATGGAACACTTTCAAC 22
 QY 179 AGGCG 183
 Db 21 AGTGC 17

	RESULT 11
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ID	AAK84030 standard; DNA; 7220 BP.
XX	
AC	AAK84030;
XX	
DT	07-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38842
XX	
KM	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer
KW	cytostatic; gene therapy; vaccine; metaclasis; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200157182-A2.
XX	
PD	09-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US0001354.
XX	
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.

PR	24-FEB-2000	2000US-01846340
PR	02-MAR-2000	2000US-01863540
PR	16-MAR-2000	2000US-01898740
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PR	18-APR-2000	2000US-01981230
PR	19-MAY-2000	2000US-02055150
PR	07-JUN-2000	2000US-02094670
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PR	08-SEP-2000	2000US-02312420
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PR	08-SEP-2000	2000US-02312440
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PR	08-SEP-2000	2000US-02314140
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PR	02-OCT-2000	2000US-02370370
PR	02-OCT-2000	2000US-02370380

XX	02-OCT-2000;	2000US-0237039P.
PR	02-OCT-2000;	2000US-0237040P.
PR	13-OCT-2000;	2000US-0239935P.
PR	13-OCT-2000;	2000US-0239937P.
PR	20-OCT-2000;	2000US-0240960P.
PR	20-OCT-2000;	2000US-0241221P.
PR	20-OCT-2000;	2000US-0241785P.
PR	20-OCT-2000;	2000US-0241786P.
PR	20-OCT-2000;	2000US-0241787P.
PR	20-OCT-2000;	2000US-0241808P.
PR	20-OCT-2000;	2000US-0241809P.
PR	01-NOV-2000;	2000US-0241826P.
PR	08-NOV-2000;	2000US-0244617P.
PR	08-NOV-2000;	2000US-0246474P.
PR	08-NOV-2000;	2000US-0246475P.
PR	08-NOV-2000;	2000US-0246476P.
PR	08-NOV-2000;	2000US-0246477P.
PR	08-NOV-2000;	2000US-0246478P.
PR	08-NOV-2000;	2000US-0246523P.
PR	08-NOV-2000;	2000US-0246524P.
PR	08-NOV-2000;	2000US-0246525P.
PR	08-NOV-2000;	2000US-0246526P.
PR	08-NOV-2000;	2000US-0246527P.
PR	08-NOV-2000;	2000US-0246528P.
PR	08-NOV-2000;	2000US-0246532P.
PR	08-NOV-2000;	2000US-0246609P.
PR	08-NOV-2000;	2000US-0246610P.
PR	08-NOV-2000;	2000US-0246611P.
PR	08-NOV-2000;	2000US-0246613P.
PR	17-NOV-2000;	2000US-0249207P.
PR	17-NOV-2000;	2000US-0249208P.
PR	17-NOV-2000;	2000US-0249209P.
PR	17-NOV-2000;	2000US-0249210P.
PR	17-NOV-2000;	2000US-0249211P.
PR	17-NOV-2000;	2000US-0249212P.
PR	17-NOV-2000;	2000US-0249213P.
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PR	17-NOV-2000;	2000US-0249215P.
PR	17-NOV-2000;	2000US-0249216P.
PR	17-NOV-2000;	2000US-0249217P.
PR	17-NOV-2000;	2000US-0249218P.
PR	17-NOV-2000;	2000US-0249244P.
PR	17-NOV-2000;	2000US-0249245P.
PR	17-NOV-2000;	2000US-0249246P.
PR	17-NOV-2000;	2000US-0249265P.
PR	17-NOV-2000;	2000US-0249297P.
PR	17-NOV-2000;	2000US-0249299P.
PR	17-NOV-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0259678P.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SM;	
XX	WPI; 2001-483426/52.	
DR		
XX	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and metastasis	
XX		
PS	Disclosure; SEQ ID NO 38842; 3071pp + Sequence Listing; English.	
XX		

CC	AAG54951.	to AAK64702 encode the human immune/haematopoietic antigen (I)
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytotoxic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting the	
CC	nucleic acids into a host cell and culturing the cell to express the	
CC	protein. (I) proteins and polynucleotides may be used to prevent,	
CC	diagnose and treat immune/haematopoietic-related diseases, especially	
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703	
CC	to AAK87694 represent human immune/haematopoietic antigen genomic	
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169	
CC	represent sequences used in the exemplification of the present invention	
XX		
SQ	Sequence 7220 BP; 2177 A; 1230 C; 1433 G; 2380 T; 0 U; 0 Other;	
Query Match	13.8%; Score 35.4; DB 4; Length 7220;	
Best Local Similarity	55.2%; Pred. No. 0.29;	
Matches	69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;	
OY	59 TAAGTGTGTAATATACGAAAGATGACTGAACGCTTTGGGACCTCGTTTCATTGTGA 118	
Dd	4869 TTACCCTGTATACCTTTTGGAATGTGTCTTAAACGCTTGCTGCACCTTTCCTCATCTTT 4810	
OY	119 AAATGGAGGTTAATATACGAGCCTTCTTACTGCCCAAGACAGCTGTTTGCCGGGACAG 178	
Dd	4809 AAAAGAAGGATTAATGACACGTTTATGATAATTACATATATACATATGAGGACACTTTAAC 4750	
OY	179 AGGCG 183	
Dd	4749 AGTGC 4745	
RESULT 12		
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ID	ABK49586 standard; DNA; 143306 BP.	
XX		
AC	ABK49586;	
XX		
DT	15-JUN-2002 (first entry)	
XX		
DE	Human transporter protein gene.	
XX		
KM	Human, ds; gene; transporter; transgenic; transporter mediated disease;	
KM	drug screening; pharmacogenomic analysis; chromosome 18; SNP;	
KM	single nucleotide polymorphism.	
XX		
OS	Homo sapiens.	
XX		
FH		
Key	Location/Qualifiers	
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FT	/tag= o	
FT	/standard_name= "Single-nucleotide polymorphism"	
FT	variation	
FT	replace(1012,T)	
FT	/tag= p	
FT	/standard_name= "Single-nucleotide polymorphism"	
FT	variation	
FT	replace(1990,G)	
FT	/tag= q	
FT	/standard_name= "Single-nucleotide polymorphism"	
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FT	3000..3051	
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FT	variation	
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FT replace(25321,G)
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FT replace(27280,T)
FT /tag= br
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FT /standard_name= "Single-nucleotide polymorphism"
FT replace(29303,C)
FT /tag= bc
FT /standard_name= "Single-nucleotide polymorphism"
FT replace(29302..29303,T)
FT /tag= bu

Query Match 13.8%; Score 35.4; DB 6; Length 143306;
Best Local Similarity 69.6%; Pred. No. 1.1;
Matches 48; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Oy 69 AATATCAGAGATGACTGACGCTTTGGGACTCCGTTTCCATTGTAAATGAGGT 128
Db 95018 AATACGGGCAAGTTTAACTTCTCTGGCCTCACTTCCATGATTAATGAGGC 94959
|||
|||
|||

Oy 129 TAATACCAG 137
Db 94958 TAATACAG 94950
|||
|||
|||

RESULT 13
AEP74705
ID AEP74705 standard; DNA; 152037 BP.
XX
XX
AC AEP74705;
XX
DT 06-APR-2006 (first entry)
XX
DB Human polynucleotide #219.
XX
XX Diagnosis; gene regulation; gene expression;
XX post traumatic stress disorder; psychiatric disorder; tranquilizer; gene;
XX ds.
XX
XX Homo sapiens.
XX
XX OS
XX PN MO2006013561-A2.
XX
XX PD 09-FEB-2006.
XX
XX PF 02-AUG-2005; 2005MO-IL000824.
XX
XX PR 02-AUG-2004; 2004US-0592408P.
XX
XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
XX
XX PI Segman R, Shalev A, Goltser T, Friedman N, Shefi N, Kaminski N;
XX
XX DR WPI; 2006-145797/15.
XX
XX PT New kit comprising 10 and no more than 574 polynucleotides capable of
XX specifically binding at least one specific polynucleotide sequence,
XX useful for determining predisposition of a subject to develop PTSD, or
XX for diagnosing PTSD.
XX
XX PS Claim 1; SEQ ID NO 219; 157BP; English.
XX
XX CC The invention relates to a kit for determining predisposition of a
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CC subject to developing post-traumatic stress disorder (PTSD) comprising at
CC least 10 and no more than 574 polynucleotides, where each of the
CC polynucleotides is capable of specifically binding at least one specific
CC polynucleotide sequence. The invention also relates to a kit for
CC diagnosing PTSD in a subject, agents for the manufacture of the kit
CC cited comprising the polynucleotides cited, and a microarray comprising
CC at least 10 and no more than 904 oligonucleotides where each of the
CC oligonucleotides is capable of specifically binding at least one specific
CC polynucleotide sequence. The kit comprises each of the polynucleotides
CC selected from an oligonucleotide molecule, a cDNA molecule, a genomic
CC molecule and an RNA molecule. Each of the polynucleotides is at least 10
CC and no more than 50 nucleic acids in length. Each of the polynucleotides
CC is bound to a solid support. The kit also comprises at least one reagent
CC suitable for detecting hybridization of the polynucleotides and at least
CC one RNA transcript. The kit further comprises packaging materials
CC packaging the at least one reagent and instructions for using the kit in
CC determining predisposition of the subject to developing PTSD or for
CC diagnosing the disease. The microarray comprises oligonucleotides of at
CC least 10 and no more than 40 nucleic acids in length. The agent is
CC capable of regulating an expression level of at least one gene as a
CC pharmaceutical or for the manufacture of a medicament identified for
CC preventing PTSD. The kit is useful for determining predisposition of a
CC subject to developing PTSD or for diagnosing PTSD. This sequence
CC represents a human polynucleotide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
```

Sequence 152037 BP; 44112 A; 33269 C; 33124 G; 41532 T; 0 U; 0 Other;

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Query Match 13.8%; Score 35.4; DB 15; Length 152037;
Best Local Similarity 69.6%; Pred. No. 1.1;
Matches 48; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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Oy 69 AATATCAGAGATGACTGACGCTTTGGGACTCCGTTTCCATTGTAAATGAGGT 128
Db 22903 AATTCAGGCAAGTTACTGACCTCTGTGACTAGTGTCCATCTTAAATGAGGA 22962
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|||
|||
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Oy 129 TAATACCAG 137
Db 22963 TAATATAG 22971
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|||
|||
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RESULT 14
ADZ04285
ID ADZ04285 standard; DNA; 100000 BP.
XX
XX ADZ04285;
XX
XX 16-JUN-2005 (first entry)
XX
XX DB Human leukotriene A4 hydrolase (LTA4H) gene SegID1.
XX
XX myocardial infarction; cardiac; vasotropic; antianginal;
XX antiarteriosclerotic; antidiabetic; hypotensive; anlipenic; anorectic;
XX diabetes; hypertension; hypercholesterolemia; obesity; unstable angina;
XX blood; chromosome-12; gene; ds.
XX
XX OS Homo sapiens.
XX
XX PN MO2005027886-A2.
XX
XX PD 31-MAR-2005.
XX
XX PF 17-SEP-2004; 2004MO-US030582.
XX
XX PR 17-SEP-2003; 2003US-0503587P.
XX
XX PA (DECO-) DECODE GENETICS EHF.
XX
XX PI Helgadóttir A, Gurney ME, Hakonarson H, Gulcher JR;
XX
XX DR WPI; 2005-262656/27.
```


DR P-PSDB; AD204287.
XX Use of leukotriene inhibitor for preventing or treating myocardial
PT infarction or decreasing susceptibility to myocardial infarction and
PT acute coronary syndrome.
XX Example 1; SEQ ID NO 1; 201pp; English.
XX This invention relates to a novel method of preventing or treating
CC myocardial infarction (MI) or decreasing susceptibility to MI or acute
CC coronary syndrome (ACS) in an individual which comprises administration
CC of a leukotriene inhibitor. The invention may be useful for the
CC development of compounds with a cardiant, vasotropic, antianginal,
CC antiarteriosclerotic, antidiabetic, hypotensive, antilipemic or anorectic
CC activity acting as a leukotriene inhibitor. The invention is useful for
CC preventing or treating myocardial infarction or decreasing susceptibility
CC to myocardial infarction in an individual, who has at least one risk
CC factor of haplotype or other variant for myocardial infarction (MI) in
CC any MI disease gene, haplotype or variant in 5-lipoxygenase activating
CC protein (FLAP), haplotype or other variant in the leukotriene A4
CC hydroxylase (LTA4H) gene or a polymorphism in an LTA4H nucleic acid. The
CC method of the invention may also be useful for preventing or treating
CC diabetes, hypertension, hypercholesterolemia, elevated lip(a), obesity,
CC past/current smoker, acute coronary syndrome such as unstable angina, non
CC ST-elevation myocardial infarction (NSTEMI) or ST-elevation MI (STEMI)
CC in an individual who has atherosclerosis or who requires treatment (for
CC example angioplasty, stents, coronary artery bypass graft) to restore
CC blood flow in arteries, and for decreasing risk of a subsequent
CC myocardial infarction in an individual who has had at least one
CC myocardial infarction. The present sequence is that of the human
CC leukotriene A4 hydroxylase (LTA4H) gene, located on chromosome 12q23, which
CC was used during the development of the method of the invention. Note: The
CC present sequence contains introns, the number and location of which are
CC not provided in the specification.
XX
SQ Sequence 100000 BP; 29762 A; 21176 C; 20553 G; 28509 T; 0 U; 0 Other;
XX
Query Match 13.6%; Score 35; DB 14; Length 100000;
Best Local Similarity 61.5%; Pred. No. 1.3;
Matches 56; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 42 CCGGCTGACCGAGGTGTAAGTGTGAATATCAGGAAGTGAAGCTTTGGGAC 101
DB 22966 CTGGCTCTGCCATTGTGTAAGTGTATGACTTGTGGCAAGTATTGACTTCTGTGGCC 23025
QY 102 TCCGTTTCCTCATTTGTAATAATGAGGTTAAT 132
DB 23026 TCAGTTGCTCATCTCTGTAATAATGAAATTAAT 23056
RESULT 15
AEF72834
ID AEF72834 standard; DNA; 100001 BP.
XX
AC AEF72834;
XX
DT 06-APR-2006 (first entry)
XX
XX Human leukotriene A4 hydroxylase (LTA4H) gene - SEQ ID 718.
XX
XX propylaxis; SNP detection; myocardial infarction; cardiant;
KM leukotriene A4 hydroxylase; LTA4H; gene; ds.
XX
OS Homo sapiens.
XX
XX US2006019269-A1.
XX
XX 26-JAN-2006.
XX
XX 30-MAR-2005; 2005US-00096191.
XX
XX 17-OCT-2002; 2002US-0419433P.
XX
XX 21-FEB-2003; 2003US-0449331P.
XX
XX

PR 17-SEP-2003; 2003US-0503587P.
PR 16-OCT-2003; 2003WO-US032556.
PR 30-JAN-2004; 2004US-00769744.
PR 22-APR-2004; 2004US-00830477.
PR 17-SEP-2004; 2004WO-US030582.
PR 10-JAN-2005; 2005US-0642909P.
PR 31-JAN-2005; 2005WO-US003312.
XX
XX (DECO-) DECODE GENETICS INC.
XX
PI Helgadottir A, Hakonarson H, Gulcher JR, Gurney ME;
DR WPI; 2006-124282/13.
DR P-PSDB; AEF72836.
XX
XX
PT Prophylaxis therapy for myocardial infarction comprises selecting a human
PT by screening for genetic variation in e.g. 5-lipoxygenase activating
PT protein gene, administering a composition comprising a agent and
PT monitoring inflammatory marker.
XX
PS Disclosure; SEQ ID NO 718; 134pp; English.
XX
XX The invention comprises a method of prophylaxis therapy for myocardial
CC infarction. The method involves selecting a human subject susceptible to
CC myocardial infarction by screening for a genetic variation in either the
CC 5-lipoxygenase activating protein (FLAP) gene or the leukotriene A4
CC hydroxylase (LTA4H) gene. The method further involves administration of a
CC therapeutic agent and monitoring at least one inflammatory marker in the
CC subject before and during the prophylaxis treatment. The method of the
CC invention is useful for prophylaxis therapy for myocardial infarction.
CC The present DNA sequence represents the human LTA4H gene. NOTE: The
CC present sequence is not shown in the specification, but has been
CC retrieved from the USPTO website.
XX
SQ Sequence 100001 BP; 29763 A; 21176 C; 20553 G; 28509 T; 0 U; 0 Other;
XX
Query Match 13.6%; Score 35; DB 15; Length 100001;
Best Local Similarity 61.5%; Pred. No. 1.3;
Matches 56; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 42 CCGGCTGACCGAGGTGTAAGTGTGAATATCAGGAAGTGAAGCTTTGGGAC 101
DB 22966 CTGGCTCTGCCATTGTGTAAGTGTATGACTTGTGGCAAGTATTGACTTCTGTGGCC 23025
QY 102 TCCGTTTCCTCATTTGTAATAATGAGGTTAAT 132
DB 23026 TCAGTTGCTCATCTCTGTAATAATGAAATTAAT 23056

Search completed: June 5, 2006, 16:57:58
Job time : 227.597 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 ; Search time 1779.61 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

Perfect score: 257
Sequence: 1 ttcctcgagcagctccctcgcg.....aaagcgaccagcccgct 257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255.4	99.4	941	2	BG720951 602692616
2	77	30.0	314	2	AA903751 064C05.8
3	41.6	16.2	555	8	CN282871 170004245
4	41.6	16.2	558	9	DA094053 DA094053
5	40	15.6	855	1	AJ817111 AJ817111
6	38.6	15.0	444	8	CV402643 RCO-BN024
7	38.6	15.0	685	12	CE142616 tigr-g88-
8	37.6	14.6	777	12	CC004107 PUGJ51TB
9	36.8	14.3	641	13	DU383369 DU383369
10	36.8	14.3	749	14	DU516086 109860979
11	36.4	14.2	374	11	AQ024482 HS-2180_B
12	36.4	14.2	707	14	CR095999 Forward_B
13	36.2	14.1	571	11	AZ412085 IM015SH19
14	36	14.0	810	13	CL654603 PRI0121a
15	36	14.0	906	14	CT069763 Sus scrofa
16	35.8	13.9	614	12	CG745747 P038-4-A1
17	35.8	13.9	614	12	AQ315012 RBC111-94
18	35.6	13.9	268	14	CT256996 Sus scrofa
19	35.6	13.9	268	13	CZ414110 1009813 R

20	35.6	13.9	397	11	AQ428350	AQ428350	CITBI-E1-
21	35.6	13.9	516	11	AQ428343	AQ428343	CITBI-E1-
22	35.6	13.9	523	9	DA589393	DA589393	DA589393
23	35.4	13.8	760	14	CT184624	CT184624	Sus scrofa
24	35.4	13.8	792	14	CR795773	CR795773	GR0AA13C
25	35.4	13.8	810	1	AU119919	AU119919	AU119919
26	35	13.6	335	11	AQ018075	AQ018075	CITBI-E1-
27	35	13.6	417	11	AQ020685	AQ020685	CIT-HSP-2
28	35	13.6	572	14	DU513025	DU513025	109860962
29	35	13.6	644	14	AG158418	AG158418	Pan trogl
30	34.8	13.5	434	2	BG952217	BG952217	CM4-CT062
31	34.8	13.5	592	11	AQ423759	AQ423759	CITBI-E1-
32	34.8	13.5	655	14	DU481223	DU481223	109841594
33	34.8	13.5	676	13	DU233749	DU233749	109857402
34	34.8	13.5	680	14	AG092833	AG092833	Pan trogl
35	34.8	13.5	711	13	DU438587	DU438587	109842102
36	34.8	13.5	737	12	CE199080	CE199080	tigr-g88-
37	34.8	13.5	755	14	CT180346	CT180346	Sus scrofa
38	34.8	13.5	780	13	DU176408	DU176408	109853345
39	34.8	13.5	833	13	DU193469	DU193469	109855323
40	34.6	13.5	266	1	AA091849	AA091849	mm0333.se
41	34.6	13.5	327	12	CG891660	CG891660	Ymc130E3
42	34.6	13.5	480	11	AQ332789	AQ332789	HS 5008 A
43	34.6	13.5	589	11	AQ625001	AQ625001	CITBI-E1-
44	34.6	13.5	593	11	AQ628004	AQ628004	CITBI-E1-
45	34.6	13.5	727	11	AQ417175	AQ417175	RPCI-11-2

ALIGNMENTS

RESULT 1
BG720951/c
LOCUS
DEFINITION
602692616F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825178 5', mRNA sequence.
ACCESSION
BG720951.1 GI:14000138
VERSION
BG720951.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 941)
NIH-MGC <http://mgc.ncl.nih.gov/>
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshituki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: LHAM10737 row: O column: 03
High quality sequence stop: 666.
Location/Qualifiers
1. 941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4825178"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to R0T 5. This is a

FEATURES

source

ORIGIN

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NIHRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 99.4%; Score 255.4; DB 2; Length 941;

Best Local Similarity 99.6%; Pred. No. 8e-71;

Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCCTGGGAGTCCCTTCTGCTGTGAAAACATATGGGCGGCTTACACGGGTGA 60

DB 324 TTCCTGGGAGTCCCTTCTGCTGTGAAAACATATGGGCGGCTTACACGGGTGA 265

QY 61 AGTGTGAATATCAGGAAGATGACTGAAGCTCTTGGAGCTCCGTTTCTCAATTGTA 120

DB 264 AGTGTGAATATCAGGAAGATGACTGAAGCTCTTGGAGCTCCGTTTCTCAATTGTA 205

QY 121 ATGAGGTTAATACCAAGCTTCTTCTTACTCCCAAAAGCAGTGTGTCGGGCGGAG 180

DB 204 ATGAGGTTAATACCAAGCTTCTTCTTACTCCCAAAAGCAGTGTGTCGGGCGGAG 145

QY 181 GGGCCAAATGTTGGCTGTTACGACATGTTACCCCAAGAGCGGTGACCAATTAA 240

DB 144 GGGCCAAATGTTGGCTGTTACGACATGTTACCCCAAGAGCGGTGACCAATTAA 85

QY 241 GGGCAACACAGCGCGGT 257

DB 84 GGGCAACACAGCGCGGT 68

RESULT 2
LOCUS AA903751 314 bp mRNA linear EST 09-JUN-1998

DEFINITION OK6405.81 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518728.3, similar to gb:U17360.1_mal HOMBOX PROTEIN HOX-D4 (HUMAN);, mRNA sequence.

ACCESSION AA903751

VERSION AA903751.1 GI:3038874

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgabs-remail.nih.gov

TISSUE Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Sequencing by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.dio.llnl.gov/bdrp/image/image.html

Insert length: 521 Std Error: 0.00

Seq primer: -40ml3 fwd. ST from Amerisham

High quality sequence stop: 297.

Location/Qualifiers

1. 314

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1518728"

/issue_type="pooled germ cell tumors"

/lab_host="DH10B"

/clone_id="NCI_CGAP_GC4"

ORIGIN

/note="Vector: pT773D-Pac1; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 30.0%; Score 77; DB 1; Length 314;

Best Local Similarity 98.9%; Pred. No. 2e-13;

Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCTGGGAGTCCCTTCTGCTGTGAAAACATATGGGCGGCTTACACGGGTGA 60

DB 227 TTCCTGGGAGTCCCTTCTGCTGTGAAAACATATGGGCGGCTTACACGGGTGA 285

QY 61 AGTGTGAATATCAGGAAGATGACTGA 89

DB 286 AGTGTGAATATCAGGAAGATGACTGA 314

RESULT 3
LOCUS CN282871 555 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000424523059 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN282871

VERSION CN282871.1 GI:47299285

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 (bases 1 to 555)

Bradenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fiek, G., J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

JOURNAL 15146197

COMMENT Contact: Bradenberger R

Regenerative Medicine

Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbradenberger@genon.com

Insert length: 555 Std Error: 0.00.

Location/Qualifiers

1. 555

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/issue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"

/clone_id="GRN_EB"

/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowth derived from h9s cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

Query Match 16.2%; Score 41.6; DB 8; Length 555;

Best Local Similarity 63.7%; Pred. No. 0.061;

Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TTCCTTGTGCTGTGAAAACATATGGGCGGCTTACACGGGTGTAAGTGAAT 71

DB 176 TTCCTTGTGCTGTGAAAACATATGGGCGGCTTACACGGGTGTAAGTGAAT 118

QY 72 ATCAGGAAGATGACTGAAGCTTTGGGACTCCGTTTCTCATTTGAAATGAGGTAA 131

Db 117 CTGGGGAGGTTACTGAACCTTTGAGGCTTTCATCTGTGAAAAACGAGGCTAA 58
QY 132 TACC 135
Db 57 CAAC 54

RESULT 4
DA094053/c
LOCUS DA094053 558 bp mRNA linear EST 31-OCT-2005
DEFINITION DA094053 BRACE3 Homo sapiens cDNA clone BRACE3003192 5', mRNA
sequence.
ACCESSION DA094053
VERSION DA094053.1 GI:78418757
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 558)

REFERENCE
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuna,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanabe,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560

JOURNAL
PUBMED
COMMENT Contact: Takao Isogai
PLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
1. 558
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRACE3003192"
/issue_type="cerebellum"
/clone_lib="BRACE3"
/note="Vector: PME18SFL3"

ORIGIN
Query Match 16.2%; Score 41.6; DB 9; Length 558;
Best Local Similarity 63.7%; Pred. No. 0.061;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Db 12 TCCCTCTGCTGGTGAACACATATGCGCGCCCTGACACAGGCGTAAAGTGAAT 71
QY 146 TCCCTCTGCTGGTGAACACACAGGCGCATGGCTTGAACAGGCTCAGCTGTGTG-AC 88
Db 72 ATCAGGAAGATGACTGAACCTTTGGAGCTCCGTTTCTCATTTGTAATAATGAGGTTAA 131
QY 87 CTGGGGAGGTTACTGAACCTTTGAGGCTCAGCTTTCATCTGTGAAAAACGAGGCTAA 28
Db 132 TACC 135
QY 27 CAAC 24

RESULT 5
AJ817111
LOCUS AJ817111 855 bp mRNA linear EST 12-MAY-2005
DEFINITION AJ817111 KN206 Bos sp. cDNA clone C0006007111, mRNA sequence.
ACCESSION AJ817111
VERSION AJ817111.1 GI:51884587
KEYWORDS EST.
SOURCE Bos sp.
ORGANISM Bos sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 855)
McGuire,K. and Glass,E.J.
The expanding role of microarrays in the investigation of
macrophage responses to pathogens
Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
Contact: McGuire K
Genomics and Genetics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -mismc 20
and -mismatch 12 options. Vector:pluescriptII(SK+) R. Site
1:EcoRV(lost) R. Site 2:NotI Seg Primer: T7 Normalised library
constructed from pooled monocytes from Bos taurus (Holstein) and
Bos indicus (Sahiwal) cattle subjected to various stimuli,
including infection with the protozoan parasite Theileria annulata.
Location/Qualifiers
1. 855
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/mol_type="mRNA"
/db_xref="taxon:29061"
/clone="C0006007111"
/issue_type="blood"
/cell_type="bovine monocyte"
/clone_lib="KN206"
/note="Vector: pBluescriptII(SK+); Site 1: EcoRV(lost);
Site 2: NotI; Normalised library constructed from pooled
monocytes from Bos taurus (Holstein) and Bos indicus
(Sahiwal) cattle subjected to various stimuli, including
infection with the protozoan parasite Theileria annulata"

ORIGIN
Query Match 15.6%; Score 40; DB 1; Length 855;
Best Local Similarity 57.0%; Pred. No. 0.22;
Matches 73; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Db 4 CCTGGAGTCCCTTGTGCTGGTGAACACATATGCGCGCCCTGACACAGGCGTAAAGT 63
QY 416 CTTAGCAGTCTTCGACACCCAGCTCAATGCTAAAAAGTTAGTTTATACAGTAGTACGT 475
Db 64 GTGTGAATATCAGGAAGATGACTGAACGTTTGGAGCTCCGTTTCTCATTTGTAATAATG 123
QY 476 GTGCGAACCTTCAGGACATGCTTAATCTCTAGGCGCTCAACTTCTCATCTATAAAGT 535
Db 124 GAGGTTAA 131
QY 536 GGGAGTTAA 543

RESULT 6
CV402643
LOCUS CV402643 444 bp mRNA linear EST 28-SEP-2004
DEFINITION RC0-BN0248-310700-025-a04 BN0248 Homo sapiens cDNA, mRNA sequence.
ACCESSION CV402643
VERSION CV402643.1 GI:52798116
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS
Hominidae; Homo.
1 (bases 1 to 444)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brennan,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
PROC. NACL. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
1073800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. <http://www.ludwig.org.br>.
location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="BN0248"
/note="Organ: breast normal; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 15.0%; Score 38.6; DB 8; Length 444;
Best Local Similarity 59.6%; Pred. No. 0.53;
Matches 65; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 38 GGGCCGCGCTGACCGAGGTGAAGTGTGAATATGAGAAGTACGACTCTTTG 97
DB 66 GACTCCCTGCTTCCATATACCAAGTGCCTGACCCCTGTGCAGATGCTTTAAATCCTTCT 125
QY 98 GGACTCCGCTTCCATTTAAATGAGGTTAATACCACTTCTTCT 146
DB 126 GGCTCAGATTGTGATCTGAAAGTGGGTTAATGCCATCTGCTTCT 174
RESULT 7
CE142616/c 685 bp DNA linear GSS 25-SEP-2003
LOCUS CE142616
DEFINITION c1gr-gss-dog-17000371256164 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE142616
VERSION CE142616.1 GI:35254038
KEYWORDS GSS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 685)
REFERENCE
AUTHORS
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: Shotgun.
location/Qualifiers
1..685
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_1lb="dog library"
/note="Site_1: BstXI; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match 15.0%; Score 38.6; DB 12; Length 685;
Best Local Similarity 52.9%; Pred. No. 0.6; 74; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 18 CTGCTGTGAAAACATATAGCGCGCGCTGACCAAGGTGAAGTGTGAATATCAGG 77
DB 651 CTGACCTGAGAGCAATCTGCTGGGCTATGATCATTTGCTGTGTGATTTTGA 592
QY 78 AAGATGACTGAAACGTTTGGGACTCCGTTCTCATTTGAAATGAGTTAATACAG 137
DB 591 AAATTTATGAACTGCTATGAACCTCAGTTTCTCATAGGAAATGGGATATATACAG 532
QY 138 CTTTCTTACCTCCCAACGCGACGTGTTGTCGGG 174
DB 531 TACACTGTGTGAGGACACAGAGACTATTTCTGG 495
RESULT 8
CC004107/c 777 bp DNA linear GSS 31-MAR-2003
LOCUS CC004107
DEFINITION PUGUT51TB_ZM_0.6_1.0_KB Zea mays genomic clone ZMBR4400106,
genomic survey sequence.
ACCESSION CC004107
VERSION CC004107.1 GI:29382667
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 777)
REFERENCE
AUTHORS
Whitehead,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSes: PUGUT51TD
Contact: Cathy Whitehead
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitehead@tigr.org
Seq primer: TK
Class: sheared ends.
location/Qualifiers
1..777
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

Query Match 14.6%; Score 37.6; DB 12; Length 777;
Best Local Similarity 72.1%; Pred. No. 1.3;
Matches 49; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 54 GGGGTGAAGTGTGATATCAGGAAGTACGTCCTTTGGGACTCCGTTCTCA 113
DB 718 GGGGGAAGGGGTGAAATCAGGAACAGGTGATCATTTGTTACTCATTCACAA 659
QY 114 TTGTAAAA 121
DB 658 TTATPAAA 651

RESULT 9
DU383369/c 641 bp DNA linear GSS 05-OCT-2005
LOCUS 1098313087090 CHORI-243 Ovis aries genomic clone CH243-86D11,
DEFINITION genomic survey sequence.

ACCESSION DU383369
VERSION DU383369.1 GI:77113232
KEYWORDS GSS.

SOURCE Ovis aries (sheep)
ORGANISM Ovis aries

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 641)
Kirchner, E., Shetty, J., de Jong, P., McEwan, J.C., Oddy, H. and
Cockett, N.

AUTHORS Ovine BAC End Sequences from Library CHORI-243
TITLE Unpublished (2004)
JOURNAL Other GSSs: 1098313044849
COMMENT Contact: Ewen Kirchner
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirchner@tigr.org

Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVI/JTC; http://www.venterlinstitute.org/).
Original Trace: 1098313087090 Trace TI: gml|ti|918927275
Insert Length: 184000 Std Error: 0.00 row: D column: 11
Seq primer: T7
Class: BAC ends.

FEATURES
source location/Qualifiers

1..641
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-86D11"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-243"
/note="Vector: pPARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"

ORIGIN

Query Match 14.3%; Score 36.8; DB 13; Length 641;
Best Local Similarity 69.4%; Pred. No. 2.2;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGTGAACGCTTTGGGACTCCGTTCTCATTTGTAATGAGGCT 128
DB 324 AATATCAGGAAGTGAACGCTTTGGGACTCCGTTCTCATTTGTAATGAGGCT 265

QY 129 TAATACGAGCCT 140
DB 264 CAATPATAGCCT 253

RESULT 10
DU516086/c 749 bp DNA linear GSS 06-OCT-2005
LOCUS 1098609797641 CHORI-243 Ovis aries genomic clone CH243-514E4,
DEFINITION genomic survey sequence.

ACCESSION DU516086
VERSION DU516086.1 GI:77341805
KEYWORDS GSS.

SOURCE Ovis aries (sheep)
ORGANISM Ovis aries

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 749)
Kirchner, E., Shetty, J., de Jong, P., McEwan, J.C., Oddy, H. and
Cockett, N.

AUTHORS Ovine BAC End Sequences from Library CHORI-243
TITLE Unpublished (2004)
JOURNAL Other GSSs: 1098609881785
COMMENT Contact: Ewen Kirchner
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirchner@tigr.org

Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVI/JTC; http://www.venterlinstitute.org/).
Original Trace: 1098609797641 Trace TI: gml|ti|958319337
Insert Length: 184000 Std Error: 0.00 row: E column: 4
Seq primer: T7
Class: BAC ends.

FEATURES
source location/Qualifiers

1..749
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-514E4"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-243"
/note="Vector: pPARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"

ORIGIN

Query Match 14.3%; Score 36.8; DB 14; Length 749;
Best Local Similarity 69.4%; Pred. No. 2.3;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGTGAACGCTTTGGGACTCCGTTCTCATTTGTAATGAGGCT 128
DB 440 AATATCAGGAAGTGAACGCTTTGGGACTCCGTTCTCATTTGTAATGAGGCT 381

QY 129 TAATACGAGCCT 140
DB 380 CAATPATAGCCT 369

RESULT 11
A0024482/c 374 bp DNA linear GSS 23-JUN-1998
LOCUS HS_2180_B2_H07_MR_CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=2180 Col=14 Row=P, genomic survey
sequence.

ACCESSION A0024482
VERSION A0024482.1 GI:3243707
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 374)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2180 row: P column: 14
Class: BAC ends
High quality sequence stop: 374.

FEATURES
source
1..374
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2180 Col=14 Row=P"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBetaBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 14.2%; Score 36.4; DB 11; Length 374;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 49; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 76 GGAAGATGACTGAACGCTTTGGACTCCGTTCTCTATTGTAATGAGGTTAATACC 135
Db 133 GGAAGATTATGAACTCTCTGTCTCAGCTTCTTCAATTTGAAATGGAATATGTT 74
QY 136 AGCCTCTTC 145
Db 73 AACTCTCTCC 64

RESULT 12 707 bp DNA linear GSS 05-JUL-2004
CR095999/c Chromosome engineering clone MHPN181020, genomic survey sequence.
LOCUS CR095999
DEFINITION Forward strand read from insert in 5'HRT insertion targeting and
chromosome engineering clone MHPN181020, genomic survey sequence.
ACCESSION CR095999.1 GI:49833534
VERSION CR095999.1
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 707)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,T., Yu,Y., Rogers,J., and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
UK. http://www.sanger.ac.uk/MICR

FEATURES
source
1..707
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN181020"
/clone_lib="MHPN"

ORIGIN

Query Match 14.2%; Score 36.4; DB 14; Length 707;
Best Local Similarity 59.8%; Pred. No. 3.1;
Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 60 AAGTGTGAATATTCGGAAGATGACTGAACGCTTTGGAGCTCCGTTCTATTGTA 119
Db 504 AGGTGTGTACCTTTAGGAAGATTATGAACTTTTGAAGCTTCAGAAATCCCATGTAA 445
QY 120 AATGAGTTAATATACCGACCTTCTTCTACTCCCAACGAC 161
Db 444 AACCGAATATTAATAGGCTACTGCTAGTCTATTAACTATC 403

RESULT 13 571 bp DNA linear GSS 03-OCT-2000
AZ412085
LOCUS 1M0185H19F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0185H19 F, genomic survey sequence.
ACCESSION AZ412085
VERSION AZ412085.1 GI:10536098
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0185 row: H column: 19
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 571.

FEATURES
source
1..571
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0185H19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adapted mouse DNA was annealed to

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 14.1%; Score 36.2; DB 11; Length 571;
Best Local Similarity 53.1%; Pred. No. 3.4;
Matches 77; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 106 TTTCCTCATTTAAATGAGGTTAATACGACCTTCTTACCTCCCAAGCAGCTGT 165
DB 219 TCTCTCTTTCTTAAAAAGAAAAAACCACTATTATTATTTACATATATTTGCGT 278
QY 166 TTGTCCCGGCGCAGAGGGCCCAATTGTGGCTGTTCAGCATTCAGTTACCCCAAGAGC 225
DB 279 TTTTCCGCGCTGATATCTGTAGATGTGATTCACACAGCTGTAATCCACCATGTGG 338
QY 226 GGTACGCAATTAAGGCGAACCG 250
DB 339 GAGCAGGGAATTGAACGAGATCTG 363

RESULT 14
CL654603/c
LOCUS
DEFINITION
CL654603 810 bp DNA linear GSS 09-JUL-2004
PRI0121a.B01 - PRI0121a.B21 (810) Mixed stage fosmid library of *P. pacificus* var. *Californica* *Pristionchus pacificus* genomic, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CL654603.1 GI:50133560
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; *Pristionchus*.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 810)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
ApbADB: an Acedb database for the nematode satellite organism *Pristionchus pacificus*

JOURNAL
PUBMED
COMMENT
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..810
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="Californica"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of *P. pacificus*
var. *Californica*"
/note="Vector: pBplfos-5 Fosmid vector"

FEATURES

ORIGIN

Query Match 14.0%; Score 36; DB 13; Length 810;
Best Local Similarity 54.5%; Pred. No. 4.3;
Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 108 TCGTCATTTAAATGAGGTTAATACGACCTTCTTACCTCCCAAGCAGCTTT 167
DB 714 TTCCCATTTTACATTCAGGGAATACGGACATCTTCTCTCAATATCAAGGAAA 655
QY 168 GTCCCGGCGCAGAGGCCCAATTGTGGCTGTTCAGCATTCATCCCAAGAGCGG 227

DB 654 AGATGAGCAGCGTCCCGAATTTTACGCTCAAAATGAAGCCCGAAGCAGATAACTGT 595
QY 228 TCAGCCCAATTAA 239
DB 594 ACTTCTCAATTGA 583

RESULT 15
CT069763 906 bp DNA linear GSS 01-NOV-2005
LOCUS
DEFINITION
CT069763
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CT069763.1 GI:78627896
GSS.
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 906)
Humphray,S.J., Plumb,R.W. and Durham,J.L.
Direct Submission
Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 66B15. 66B15 is
part of the PigBAC BAC library created by Roslin Institute/RFCGR.
Further details: http://www.sanger.ac.uk/projects/S_scrofa/.

FEATURES
source
Location/Qualifiers
1..906
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone_lib="PigB-66B15"
/issue_type="Blood cells"
/note="vector pbelOBAC11
sex male"

ORIGIN

Query Match 14.0%; Score 36; DB 14; Length 906;
Best Local Similarity 62.0%; Pred. No. 4.5;
Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 42 CCGACCTGACGAGGTTAGTGTGTGAATATCAGAAATGACTGAACGCTTTGGGAC 101
DB 515 CTGGCCTTGCCATTTATCACTGTGTGACCTTTGGCAAGTATTTGATCTCTGGGTC 574
QY 102 TCGTTTCTCATTTGTAATGAGGTTAATA 133
DB 575 TTGGTTTCTCATTTAATGAGGATATA 606

Search completed: June 6, 2006, 00:08:50
Job time: 1782.61 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:58:22 / Search time 65.8364 Seconds
(without alignments)
7304.087 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

Perfect score: 257

Sequence: 1 ttccctggcagtcctctcg.....aaagcgcaaccagcccggt 257

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/prodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/prodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/prodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/prodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/prodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/prodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/prodata/2/ina/PP_COMB.seq:*
8: /EMC_Celerra_SIDS3/prodata/2/ina/RE_COMB.seq:*
9: /EMC_Celerra_SIDS3/prodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255.4	99.4	11808	3	US-09-949-016-15281 Sequence 15281, A
2	255.4	99.4	39754	3	US-09-949-016-14689 Sequence 14689, A
3	39.4	15.3	93920	3	US-09-949-016-12461 Sequence 12461, A
4	39.4	15.3	93920	3	US-09-949-016-16853 Sequence 16853, A
5	38.2	14.9	128470	3	US-09-949-016-13765 Sequence 13765, A
6	36.8	14.3	133613	3	US-09-949-016-16382 Sequence 16382, A
7	36.4	14.2	109038	3	US-09-949-016-12189 Sequence 12189, A
8	36.4	14.0	25166	3	US-09-949-016-16072 Sequence 16072, A
9	35.4	13.8	601	3	US-09-949-016-51777 Sequence 51777, A
10	35.4	13.8	21136	3	US-09-949-016-13748 Sequence 13748, A
11	35.4	13.8	146095	3	US-09-949-016-12872 Sequence 12872, A
12	35.4	13.8	146104	3	US-09-949-016-13239 Sequence 13239, A
13	35.4	13.6	601	3	US-09-949-016-17171 Sequence 17171, A
14	35.4	13.6	26933	3	US-09-949-016-12045 Sequence 12045, A
15	35.4	13.6	26933	3	US-09-949-016-15872 Sequence 15872, A
16	35.4	13.6	298336	3	US-09-949-016-16600 Sequence 16600, A
17	35.4	13.5	56131	3	US-09-949-016-12944 Sequence 12944, A
18	34.6	13.4	601	3	US-09-949-016-84988 Sequence 84988, A
19	34.4	13.4	601	3	US-09-949-016-85139 Sequence 85139, A
20	34.4	13.4	68452	3	US-09-949-016-13305 Sequence 13305, A
21	34.4	13.4	109159	3	US-09-949-016-14169 Sequence 14169, A
22	34.4	13.4	109159	3	US-09-949-016-14170 Sequence 14170, A
23	34.4	13.4	109159	3	US-09-949-016-14170 Sequence 14170, A

24	34.4	13.4	325791	3	US-09-768-185A-1 Sequence 1, Appli
25	34.2	13.3	601	3	US-09-949-016-127649 Sequence 127649, A
26	34.2	13.3	601	3	US-09-949-016-127650 Sequence 127650, A
27	34.2	13.3	601	3	US-09-949-016-127651 Sequence 127651, A
28	34.2	13.3	601	3	US-09-949-016-127985 Sequence 127985, A
29	34.2	13.3	601	3	US-09-949-016-127987 Sequence 127987, A
30	34.2	13.3	601	3	US-09-949-016-127988 Sequence 127988, A
31	34.2	13.3	304533	3	US-09-949-016-15371 Sequence 15371, A
32	34.2	13.3	304533	3	US-09-949-016-15372 Sequence 15372, A
33	33.6	13.1	33112	3	US-10-429-873A-3 Sequence 3, Appli
34	33.6	13.1	42633	3	US-09-949-016-17317 Sequence 17317, A
35	33.6	13.1	42633	3	US-09-949-016-17318 Sequence 17318, A
36	33.6	13.1	93894	3	US-09-949-016-13629 Sequence 13629, A
37	33.4	13.0	239527	3	US-09-949-016-15980 Sequence 15980, A
38	33.2	12.9	46118	3	US-09-949-016-15703 Sequence 17003, A
39	33	12.8	84916	3	US-09-949-016-14736 Sequence 14736, A
40	33	12.8	118136	3	US-09-949-016-12439 Sequence 12439, A
41	32.8	12.8	36016	3	US-09-949-016-14223 Sequence 14223, A
42	32.8	12.8	421491	3	US-09-949-016-12805 Sequence 12805, A
43	32.8	12.8	421494	3	US-09-949-016-14060 Sequence 14060, A
44	32.6	12.7	601	3	US-09-949-016-43267 Sequence 43267, A
45	32.6	12.7	601	3	US-09-949-016-43456 Sequence 43456, A

ALIGNMENTS

```
RESULT 1
US-09-949-016-15281
/ Sequence 15281, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTNER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C1001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15281
/ LENGTH: 11808
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-15281

Query Match 99.4%; Score 255.4; DB 3; Length 11808;
Best Local Similarity 99.6%; Pred. No. 5.3e-81;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCCCTGGCAGTCCTTCTGCTGCTGTAACATATATGCGCGGCTGACCGGGGTA 60
    |||||
DB 901 TTCCCTGGCAGTCCTTCTGCTGCTGTAACATATATGCGCGGCTGACCGGGGTA 960
    |||||

QY 61 AGTGTGATATATCAGGAAGATGATGACGCTTTGGAGCTCCGTTTCTCATTTGAA 120
    |||||
DB 961 AGTGTGATATATCAGGAAGATGATGACGCTTTGGAGCTCCGTTTCTCATTTGAA 1020
    |||||

QY 121 ATGAGGTTATATACGAGCTTTCTTACTCCCAACGACGCTTTGTCCTCCGCGAG 180
    |||||
DB 1021 ATGAGGTTATATACGAGCTTTCTTACTCCCAACGACGCTTTGTCCTCCGCGAG 1080
    |||||

QY 181 GGGCCATTGTTGGCTGTTTACGATCATGTTACCCCAAGAGGCTGACCAATTAA 240
    |||||
DB 1081 GGGCCATTGTTGGCTGTTTACGATCATGTTACCCCAAGAGGCTGACCAATTAA 1140
    |||||

QY 241 GGGCAACGAGCCCGGT 257
```

Db 1141 GCGGAACGAGCCCGGT 1157

RESULT 2

US-09-949-016-14689
Sequence 14689, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14689
LENGTH: 39754
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) - (39754)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689

Query Match 99.4%; Score 255.4; DB 3; Length 39754;
Best Local Similarity 99.6%; Pred. No. 9,4e-81;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCCTGGCAGTCCCTTCTGCTGTGAAAACACATATGCGCGGCTGACGAGGTGA 60
DB 28816 TTCCTGGCAGTCCCTTCTGCTGTGAAAACACATATGCGCGGCTGACGAGGTGA 28875
QY 61 AGTGTGAATATCAGGAAGATGACTGAACTGTTGGGACTCGTTTCTCAATTGAAA 120
DB 28876 AGTGTGAATATCAGGAAGATGACTGAACTGTTGGGACTCGTTTCTCAATTGAAA 28935
QY 121 ATGAGGTTAATACGAGCTTCTTCTACTCCCAAAAGCAGTGTGTCGCGGACAG 180
DB 28936 ATGAGGTTAATACGAGCTTCTTCTACTCCCAAAAGCAGTGTGTCGCGGACAG 28995
QY 181 GGGCCAAATTGCTGCTGTTCAAGCATGTTAAGCCCAAGAGCGGTCAAGCAATTAAA 240
DB 28996 GGGCCAAATTGCTGCTGTTCAAGCATGTTAAGCCCAAGAGCGGTCAAGCAATTAAA 29055
QY 241 GGGGAACGAGCGCGGT 257
DB 29056 GGGGAACGAGCGCGGT 29072

RESULT 3

US-09-949-016-12461/C
Sequence 12461, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12461
LENGTH: 93920
TYPE: DNA
ORGANISM: Human
US-09-949-016-12461

Query Match 15.3%; Score 39.4; DB 3; Length 93920;
Best Local Similarity 62.9%; Pred. No. 0.0087;
Matches 61; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 50 ACCAGGTTGAAGTGTGTAATATCAGGAAGTGAAGTCTTGGGACTCCGTTTC 109
DB 63793 ACCATTATTAAGCTGTGACTTGGAGAAAGTTACTTAACCTCTGTGATTCAATTTC 63734
QY 110 CTCATTGTAATGAGGTTAATACGACCTTCTCT 146
DB 63733 CTCATTGTAATGAGGTTAATACGACGCTATCTCT 63697

RESULT 4

US-09-949-016-16853/C
Sequence 16853, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16853
LENGTH: 93920
TYPE: DNA
ORGANISM: Human
US-09-949-016-16853

Query Match 15.3%; Score 39.4; DB 3; Length 93920;
Best Local Similarity 62.9%; Pred. No. 0.0087;
Matches 61; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 50 ACCAGGTTGAAGTGTGTAATATCAGGAAGTGAAGTCTTGGGACTCCGTTTC 109
DB 63793 ACCATTATTAAGCTGTGACTTGGAGAAAGTTACTTAACCTCTGTGATTCAATTTC 63734
QY 110 CTCATTGTAATGAGGTTAATACGACCTTCTCT 146
DB 63733 CTCATTGTAATGAGGTTAATACGACGCTATCTCT 63697

RESULT 5

US-09-949-016-13765/C
Sequence 13765, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13765
; LENGTH: 128470
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13765

Query Match 14.3%; Score 38.2; DB 3; Length 128470;
Best Local Similarity 73.1%; Pred. No. 0.027;
Matches 49; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 70 ATATCAGAGAGTGAACGCTTTGGAGCTCCGTTCTCTATGTAATAATGAGGCTT 129
DB 61211 ATCTGGGACATGACTTAACCTCTGAGCTCAGTTCTCATTTTAAAGAGATGAG 61152
QY 130 AATACCA 136
DB 61151 AATCCA 61145

RESULT 6
US-09-949-016-16382/c
; Sequence 16382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16382
; LENGTH: 36103
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16382

Query Match 14.3%; Score 36.8; DB 3; Length 36103;
Best Local Similarity 63.6%; Pred. No. 0.048;
Matches 56; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 59 TAAGTGTGAATATCAGGAAGTGAACGCTTTGGAGCTCCGTTCTCTATGTA 118
DB 3675 TAAAGATTACCTGCTCAGGCAATGTATTAATCTTTGGGCTCAGTTCTCATCTGT 3616
QY 119 AATGAGGTTAATACCAAGCTTCTCT 146
DB 3615 AAAAGTGGGATACAGAGCTGCTCT 3588

RESULT 7
US-09-949-016-15824/c
; Sequence 15824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15824
; LENGTH: 133613
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15824

Query Match 14.3%; Score 36.8; DB 3; Length 133613;
Best Local Similarity 69.4%; Pred. No. 0.088;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 70 ATATCAGAGAGTGAACGCTTTGGAGCTCCGTTCTCTATGTAATAATGAGGCTT 129
DB 83380 ATTCCAGAGAGTGAACCTTCTGATATCTCATTTCTCATTTAAATGGGATC 83321
QY 130 AATACCA 141
DB 83320 AGTATTACCTT 83309

RESULT 8
US-09-949-016-12199
; Sequence 12199, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12199
; LENGTH: 109038
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(109038)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12199

Query Match 14.2%; Score 36.4; DB 3; Length 109038;
Best Local Similarity 70.0%; Pred. No. 0.11;
Matches 49; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 67 TGAATATCAGAGAGTGAACGCTTTGGAGCTCCGTTCTCTATGTAATAATGAG 126
DB 79268 TGAACCTTGGAGGTTACTCACTCTGAGCCAGTTCTCATGTAATGAG 79327
QY 127 GTTAATACCA 136
DB 79328 GTTAAATCA 79337

RESULT 9
US-09-949-016-16072

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/ Sequence 16072, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16072
/ LENGTH: 25166
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(25166)
/ OTHER INFORMATION: n = A,T,C or G
/
/ US-09-949-016-16072
```

```
Query Match          14.0%; Score 36; DB 3; Length 25166;
Best Local Similarity 60.0%; Pred. No. 0.078;
Matches 60; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
```

```
QY 52 CAGGGGTGAAGTGTGATATATCAGGAAGTACGTAAGCTCTTTGGACTCCGTTTCT 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10238 CAGACTGCGCTGGCTTGATCTCAGCTCCATCTGTGACGTGTGGACTCCGTTTCT 10297
QY 112 CATTGTAATGAGGTATATACCAAGCTCTTCTTACTCC 151
DB 10298 CACCTGTAATGTGGGATATACCAATAGTTTCACTCC 10337
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RESULT 10
/ US-09-949-016-51777
/ Sequence 51777, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 51777
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
/
/ US-09-949-016-51777
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```
Query Match          13.8%; Score 35.4; DB 3; Length 601;
Best Local Similarity 69.6%; Pred. No. 0.022;
Matches 48; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```

```
QY 69 AATATCAGAAGATGATGTAAGCTCTTGGAGCTCCGTTTCCATTGTAATGAGGT 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 AATACCGGAGATTATTACTTCTGGGCTCAGTCTTTCATAGATTAATGAGGC 198
```

```
QY 129 TAATACCAG 137
    ||| ||| |||
DB 199 TATTAACAG 207
```

```
RESULT 11
/ US-09-949-016-13748/C
/ Sequence 13748, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13748
/ LENGTH: 21136
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(21136)
/ OTHER INFORMATION: n = A,T,C or G
/
/ US-09-949-016-13748
```

```
Query Match          13.8%; Score 35.4; DB 3; Length 21136;
Best Local Similarity 55.2%; Pred. No. 0.12;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
```

```
QY 59 TAAGTGTGAATATATCAGGAAGTACGTAAGCTCTTTGGACTCCGTTTCTCATTTGA 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 17934 TAACGCTGTACCTTTTGAATGTCTTAACTGCTGTGCTCAGTTTCTCATCTT 17875
QY 119 AATGAGGTATATACCAAGCTCTTCTACTCCCAAGCAGTGTGTCGGGCGAG 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 17874 AAGAAAGGATATGACCTGTTATGATATACATATACATATGAGGAGCACTTCAAC 17815
QY 179 AGGAGC 183
DB 17814 AGTGC 17810
```

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RESULT 12
/ US-09-949-016-12872/C
/ Sequence 12872, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12872
/ LENGTH: 146095
/ TYPE: DNA
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:40:12 ; Search time 511.092 Seconds
(without alignments)
6178.780 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	256.6	100.0	562	4	US-09-925-065A-566754 Sequence 566754, Ap
2	256.6	100.0	562	5	US-09-925-065A-566754 Sequence 566754, Ap
3	244.6	95.2	554	4	US-09-925-065A-177131 Sequence 177131, A
4	244.6	95.2	554	5	US-09-925-065A-177131 Sequence 177131, A
5	244.6	95.2	561	12	US-10-301-480-268288 Sequence 268288, A
6	244.6	95.2	561	12	US-10-301-480-268288 Sequence 268288, A
7	41.6	16.2	16256	7	US-10-017-161-1597 Sequence 1597, Ap
8	41.6	16.2	16256	7	US-10-017-161-1597 Sequence 1597, Ap
9	41.6	16.2	16256	7	US-10-017-161-1597 Sequence 1597, Ap
10	41.6	16.2	16256	7	US-10-017-161-1597 Sequence 1597, Ap
11	41.6	16.2	16256	7	US-10-017-161-1597 Sequence 1597, Ap
12	41.6	16.2	16256	7	US-10-017-161-1597 Sequence 1597, Ap
13	38.8	15.1	1664	10	US-10-750-185-50997 Sequence 50997, A
14	38.8	15.1	1664	10	US-10-750-185-50997 Sequence 50997, A
15	37.4	14.6	407	4	US-09-925-065A-496734 Sequence 496734, A
16	37.4	14.6	407	5	US-09-925-065A-496734 Sequence 496734, A
17	37.4	14.6	407	5	US-09-925-065A-496734 Sequence 496734, A

C 18	36.8	14.3	57013	6	US-10-087-192-1798 Sequence 1798, Ap
C 19	36.8	14.3	149612	6	US-10-087-192-1798 Sequence 1798, Ap
C 20	36.6	14.2	640	4	US-09-925-065A-501248 Sequence 501248, A
C 21	36.6	14.2	640	5	US-09-925-065A-501248 Sequence 501248, A
C 22	36.4	14.2	177175	15	US-11-121-086-79 Sequence 79, Appl
C 23	36.2	14.1	28499	9	US-10-741-600-17869 Sequence 17869, A
C 24	36.2	14.1	28499	10	US-10-995-561-13420 Sequence 13420, A
C 25	36.2	14.1	28499	10	US-10-995-561-13420 Sequence 13420, A
C 26	36.2	14.0	564	6	US-10-027-632-121496 Sequence 121496, A
C 27	36.2	14.0	35956	7	US-10-017-161-1597 Sequence 1597, Ap
C 28	36.2	14.0	167891	15	US-11-121-086-79 Sequence 79, Appl
C 29	35.6	13.9	627	6	US-10-027-632-1228402 Sequence 1228402, A
C 30	35.6	13.9	627	7	US-10-027-632-1228402 Sequence 1228402, A
C 31	35.4	13.8	4673	3	US-09-764-878-312 Sequence 312, App
C 32	35.4	13.8	4673	6	US-10-079-854-312 Sequence 312, App
C 33	35.4	13.8	143306	3	US-09-729-920-3 Sequence 3, Appl
C 34	35.4	13.8	143306	9	US-10-867-932-3 Sequence 3, Appl
C 35	35.4	13.8	152037	10	US-10-756-149-198 Sequence 198, App
C 36	35.2	13.7	524	6	US-10-027-632-273815 Sequence 273815, A
C 37	35.2	13.7	524	7	US-10-027-632-273815 Sequence 273815, A
C 38	35.2	13.7	691	12	US-10-301-480-571176 Sequence 571176, A
C 39	35.2	13.7	691	12	US-10-301-480-571176 Sequence 571176, A
C 40	35.2	13.7	849	6	US-10-027-632-169223 Sequence 169223, A
C 41	35.2	13.7	849	6	US-10-027-632-169223 Sequence 169223, A
C 42	35.2	13.7	849	7	US-10-027-632-169223 Sequence 169223, A
C 43	35.2	13.7	849	7	US-10-027-632-169223 Sequence 169223, A
C 44	35.2	13.7	996	12	US-10-301-480-581001 Sequence 581001, A
C 45	35.2	13.7	996	12	US-10-301-480-581001 Sequence 581001, A

ALIGNMENTS

RESULT 1
US-09-925-065A-566754
Sequence 566754, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Mang, David G.
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 566754
LENGTH: 562
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-566754

Query Match 100.0%; Score 257; DB 4; Length 562;
Best Local Similarity 99.6%; Pred. No. 1.7e-83;
Matches 256; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCTGAGCAGTCCCTTCTGCTGTAAGAAACATATAGCGCGGCTGACGAGGTGA 60
DB 228 TTCCTGAGCAGTCCCTTCTGCTGTAAGAAACATATAGCGCGGCTGACGAGGTGA 287
QY 61 AGTGTGTAATATACGAGAGATGACGAGCGCTTGGAGCTCCGTTTCTCATTTGAA 120
DB 288 AGTGTGTAATATACGAGAGATGACGAGCGCTTGGAGCTCCGTTTCTCATTTGAA 347

QY	121	ATGAGGGTTAAATACAGAGCTTCTCTACATCCCCAAAGGACGGTTGTCGCCGGCAGAG	180
Db	348	ATGGAGGTTAAATACAGAGCTTCTCTACATCCCCAAAGGACGGTTGTCGCCGGCAGAG	407
QY	181	GGCCCAATTGTTGGCTGTACAGCATCAGTTACCCACAGAGGGGTACGCCAATTAAA	240
Db	408	GGCCCAATTGTTGGCTGTACAGCATCAGTTACCCACAGAGGGGTACGCCAATTAAA	467
QY	241	GGCGAACACGAGCCCGGT	257
Db	468	GGCGAACACGAGCCCGGT	484

RESULT 2

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US-09-925-065A-566754
/ Sequence 566754, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.115
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 566754
/ LENGTH: 562
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-566754

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Query Match	100.0%	Score 257	DB 5	Length 562
Best Local Similarity	99.6%	Pred. No. 1.7e-83		
Matches 256; Conservative	1	Mismatches 0	Indels 0	Gaps 0

QY	1	TTCCCTGGGAGAGTCCCTTCTGCTGTGTAAAAACAATATGAGCGCCGGCTGACAGAGGGTGA	60
Db	228	TTCCCTGGGAGAGTCCCTTCTGCTGTGTAAAAACAATATGAGCGCCGGCTGACAGAGGGTGA	287
QY	61	AGTGTGTGATATCAGAAAGATGACTGAACGTCGCTTTGGAGCTCCGTTTCTCATTTGTAAA	120
Db	288	AGTGTGTGATATCAGAAAGATGACTGAACGTCGTTGGAGCTCCGTTTCTCATTTGTAAA	347
QY	121	ATGAGAGGTAAATACCAAGCCTCTCTTCACTCCCAAAAGCAAGGTTTGTCCGGCCAGAG	180
Db	348	ATGAGAGGTAAATACCAAGCCTCTCTTCTTCACTCCCAAAAGCAAGGTTTGTCCGGCCAGAG	407
QY	181	GGCCCAATTTGGTGGCTTTCACGCATCAGTTAACCCCAACAGAGCGGTCAGCCAAATTTAA	240
Db	408	GGCCCAATTTGGTGGCTTTCACGCATCAGTTAACCCCAACAGAGCGGTCAGCCAAATTTAA	467
QY	241	GGCGAACCAGGCCCGGT	257
Db	468	GGCGAACCAGGCCCGGT	484

RESULT 3

US-09-925-065A-177131/c
; Sequence 177131, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

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1  APPLICANT: Wang, David G.
2  TITLE OF INVENTION: Identification and Mapping of Single
3  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
4  FILE REFERENCE: 106827.135
5  CURRENT APPLICATION NUMBER: US/09/925,065A
6  CURRENT FILING DATE: 2001-08-08
7  PRIOR APPLICATION NUMBER: US 60/243,036
8  PRIOR FILING DATE: 2000-10-24
9  PRIOR APPLICATION NUMBER: US 60/252,147
10 PRIOR FILING DATE: 2000-11-20
11 PRIOR APPLICATION NUMBER: US 60/250,092
12 PRIOR FILING DATE: 2000-11-30
13 PRIOR APPLICATION NUMBER: US 60/261,766
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: US 60/289,846
16 PRIOR FILING DATE: 2001-05-09
17 NUMBER OF SEQ ID NOS: 957086
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO 171131
20 LENGTH: 554
21 TYPE: DNA
22 ORGANISM: Homo sapiens
23 US-09-925-065A-171131

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Query

Query Match	95.2%	Score 244.6	DB 4	Length 554
Best Local Similarity	99.2%	Pred. No. 4.6e-79		
Matches 255; Conservative	1	Mismatches 0	Indels 1	Gaps 1

QY	1	TTCCCTGGGAGAGTCCCTTCGTGGGTGAAAAACAATATGAGCGCGGCTGACACAGGGGTGA	60
Ds	552	TTCCCTGGGAGAGTCCCTTCGTGGGTGAAAAACAATATGAGCGCGGCTGACACAGGGGTGA	4333
QY	61	AGTGTGTGAATATCAGGAAGATGACTGAACGTTCTTGGGACTTCGCTTCTCATTTGTAAA	120
Ds	492	AGTGTGTGAATATCAGGAAGATGACTGAACGTTCTTGGGACTTCGCTTCTCATTTGTAAA	4333
QY	121	ATGAGAGTTAATATCCAGCGCTTCTTACTCTCCCCAAAGGCAAGTGTGTGTCGCCGGCCAGAG	180
Ds	432	ATGAGAGTTAATATCCAGCGCTTCTTACTCTCCCCAAAGGCAAGTGTGTGTCGCCGGCCAGAG	3737
QY	181	GGGCCAATTGTTGGCTGTTACGCAATCAGTTAACCCCAACAGAGCGGTCAGCCCAATTTAAA	240
Ds	372	GG-CAATTGTTGGCTGTTACGCAATCAGTTAACCCCAACAGAGCGGTCAGCCCAATTTAAA	3141
QY	241	GGCGAACACAGGCCCGGT	257
Ds	313	GGCGAACACAGGCCCGGT	297

RESULT 4

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US-09-925-065A-177131/c
? Sequence 177131, Application US/09925065A
? Publication No. US20050228172A9
? GENERAL INFORMATION:
? APPLICANT: Wang, David G.
? TITLE OF INVENTION: Identification and Mapping of Single
? Nucleotide Polymorphisms in the Human Genome
? FILE REFERENCE: 108427.135
? CURRENT APPLICATION NUMBER: US/09/925,065A
? CURRENT FILING DATE: 2001-08-08
? PRIOR APPLICATION NUMBER: US 60/743,096
? PRIOR FILING DATE: 2000-10-24
? PRIOR APPLICATION NUMBER: US 60/252,147
? PRIOR FILING DATE: 2000-11-20
? PRIOR APPLICATION NUMBER: US 60/250,092
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/261,766
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/289,846
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 177131

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LENGTH: 554
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-177131

Query Match 95.2%; Score 244.6; DB 5; Length 554;
Best Local Similarity 99.2%; Pred. No. 4.7e-79;
Matches 255; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCCTGGCAGTCCCTTCTGCTGTGTAACACATATAGGCGCGGCTGACCGAGGTGTA 60
DB 552 TTCCCTGGCAGTCCCTTCTGCTGTGTAACACATATAGGCGCGGCTGACCGAGGTGTA 493
QY 61 AGTGTGTAATATCAGAGATGACGTGACGCTTTGGGACTCCGTTTCTCATTTGTAA 120
DB 492 AGTGTGTAATATCAGAGATGACGTGACGCTTTGGGACTCCGTTTCTCATTTGTAA 433
QY 121 ATGAGAGTTAATACGAGCTTTCTTACTCCCAACGCGCTTTGTGTCGGCCAGAG 180
DB 432 ATGAGAGTTAATACGAGCTTTCTTACTCCCAACGCGCTTTGTGTCGGCCAGAG 373
QY 181 GGGCAATTGTTGGCTGTTCAGCATCAGTTACCCCAAGAGCGGGTCAGCCATTAA 240
DB 372 GG-CAATTGTTGGCTGTTCAGCATCAGTTACCCCAAGAGCGGGTCAGCCATTAA 314
QY 241 GGGCAACAGGCCCGGT 257
DB 313 GGGCAACAGGCCCGGT 297

RESULT 5
US-10-301-480-268288/c
Sequence 268288, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 268288
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-268288

Query Match 95.2%; Score 244.6; DB 12; Length 561;
Best Local Similarity 99.2%; Pred. No. 4.7e-79;
Matches 255; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCCTGGCAGTCCCTTCTGCTGTGTAACACATATAGGCGCGGCTGACCGAGGTGTA 60
DB 559 TTCCCTGGCAGTCCCTTCTGCTGTGTAACACATATAGGCGCGGCTGACCGAGGTGTA 500
QY 61 AGTGTGTAATATCAGAGATGACGTGACGCTTTGGGACTCCGTTTCTCATTTGTAA 120
DB 499 AGTGTGTAATATCAGAGATGACGTGACGCTTTGGGACTCCGTTTCTCATTTGTAA 440
QY 121 ATGAGAGTTAATACGAGCTTTCTTACTCCCAACGCGCTTTGTGTCGGCCAGAG 180
DB 439 ATGAGAGTTAATACGAGCTTTCTTACTCCCAACGCGCTTTGTGTCGGCCAGAG 380
QY 181 GGGCAATTGTTGGCTGTTCAGCATCAGTTACCCCAAGAGCGGGTCAGCCATTAA 240
DB 379 GG-CAATTGTTGGCTGTTCAGCATCAGTTACCCCAAGAGCGGGTCAGCCATTAA 321

QY 241 GGGCAACAGGCCCGGT 257
DB 320 GGGCAACAGGCCCGGT 304

RESULT 6
US-10-301-480-881697/c
Sequence 881697, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 881697
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-881697

Query Match 95.2%; Score 244.6; DB 12; Length 561;
Best Local Similarity 99.2%; Pred. No. 4.7e-79;
Matches 255; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCCTGGCAGTCCCTTCTGCTGTGTAACACATATAGGCGCGGCTGACCGAGGTGTA 60
DB 559 TTCCCTGGCAGTCCCTTCTGCTGTGTAACACATATAGGCGCGGCTGACCGAGGTGTA 500
QY 61 AGTGTGTAATATCAGAGATGACGTGACGCTTTGGGACTCCGTTTCTCATTTGTAA 120
DB 499 AGTGTGTAATATCAGAGATGACGTGACGCTTTGGGACTCCGTTTCTCATTTGTAA 440
QY 121 ATGAGAGTTAATACGAGCTTTCTTACTCCCAACGCGCTTTGTGTCGGCCAGAG 180
DB 439 ATGAGAGTTAATACGAGCTTTCTTACTCCCAACGCGCTTTGTGTCGGCCAGAG 380
QY 181 GGGCAATTGTTGGCTGTTCAGCATCAGTTACCCCAAGAGCGGGTCAGCCATTAA 240
DB 379 GG-CAATTGTTGGCTGTTCAGCATCAGTTACCCCAAGAGCGGGTCAGCCATTAA 321
QY 241 GGGCAACAGGCCCGGT 257
DB 320 GGGCAACAGGCCCGGT 304

RESULT 7
US-10-017-161-1597/c
Sequence 1597, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1597
LENGTH: 16256
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(16256)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(306)
FEATURE:
NAME/KEY: CDS
LOCATION: (760)..(918)
FEATURE:
NAME/KEY: CDS
LOCATION: (1009)..(1194)
FEATURE:
NAME/KEY: CDS
LOCATION: (1602)..(1618)
FEATURE:
NAME/KEY: CDS
LOCATION: (1692)..(1764)
FEATURE:
NAME/KEY: CDS
LOCATION: (1837)..(2040)
FEATURE:
NAME/KEY: CDS
LOCATION: (3954)..(4181)
FEATURE:
NAME/KEY: CDS
LOCATION: (4272)..(4457)
FEATURE:
NAME/KEY: CDS
LOCATION: (4863)..(4879)
FEATURE:
NAME/KEY: CDS
LOCATION: (4953)..(5072)
FEATURE:
NAME/KEY: CDS
LOCATION: (5184)..(5294)
FEATURE:
NAME/KEY: CDS
LOCATION: (6999)..(7197)
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NAME/KEY: CDS
LOCATION: (7651)..(7809)
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NAME/KEY: CDS
LOCATION: (7900)..(8085)
FEATURE:
NAME/KEY: CDS
LOCATION: (8493)..(8586)
FEATURE:
NAME/KEY: CDS
LOCATION: (8742)..(8932)
FEATURE:
NAME/KEY: CDS
LOCATION: (14104)..(14223)
FEATURE:
NAME/KEY: CDS
LOCATION: (14326)..(14487)
FEATURE:
NAME/KEY: CDS
LOCATION: (14579)..(14707)
FEATURE:
NAME/KEY: CDS
LOCATION: (15950)..(16056)
FEATURE:
NAME/KEY: modified_base
LOCATION: (3847)..(3946)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (6897)..(6996)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:

NAME/KEY: modified_base
LOCATION: (10323)..(10422)
OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1597

Query Match 16.2%; Score 41.6; DB 7; Length 16256;
Best Local Similarity 63.7%; Pred. No. 0.0015;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCTCTCTGCTGTAACACATATAGCGCCGCTGACCAAGGCTGTAAGTGTGAAT 71
DB 13196 TCCTCTCTGCTTGTGAAGCCACACAGGATGGCTTGAACACGCTCAGCTGTG-AC 13138
QY 72 ATCAGGAAGATGACTGAACGCTTTGGACCTCCGTTCTCATTTGAAATGAGGTTAA 131
DB 13137 CTGGGGCAGGTTACTGAACCTCTTTGAGGCTCAGCTTCTCATCTGAAACGAGGCTAA 13078
QY 132 TACC 135
DB 13077 CAAC 13074

RESULT 8

US-10-292-798-1271/c
Sequence 1271, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1271
LENGTH: 16256
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1)..(16256)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(306)
FEATURE:
NAME/KEY: CDS
LOCATION: (760)..(918)
FEATURE:
NAME/KEY: CDS
LOCATION: (1009)..(1194)
FEATURE:
NAME/KEY: CDS
LOCATION: (1602)..(1618)
FEATURE:
NAME/KEY: CDS
LOCATION: (1692)..(1764)
FEATURE:
NAME/KEY: CDS
LOCATION: (1837)..(2040)
FEATURE:
NAME/KEY: CDS
LOCATION: (3954)..(4181)
FEATURE:
NAME/KEY: CDS
LOCATION: (4272)..(4457)

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4863)..(4879)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4953)..(5072)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5184)..(5294)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6999)..(7197)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7651)..(7809)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7900)..(8085)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8493)..(8586)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8742)..(8932)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14104)..(14223)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14326)..(14487)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14579)..(14707)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15950)..(16056)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (3847)..(3946)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (10323)..(10422)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-1271
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Query Match      16.2%; Score 41.6; DB 7; Length 16256;
Best Local Similarity 63.7%; Pred. No. 0.0015;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCCTTCTGCTGTAACACATATGCGCGCTGACACAGGCTGTAGTGTGAAT 71
Db 13196 TCCCTTGTGTTTGAAGCCACACAGGCTGTAGGCTGACGCTGCTGTGTC-AC 13138

QY 72 ATCAGAAAGTGAAGTGAAGCTCTTTGGAGCTCCGTTTCTCATGTGTAATAATGAGGTTAA 131
Db 13137 CTGGGACAGGTTACTGAACCTCTTTGAGGCTCAGCTTTCATCTGGAACAGAGGCTAA 13078

QY 132 TACC 135
Db 13077 CAAC 13074
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RESULT 9
US-10-301-480-45633
; Sequence 45633; Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45633
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-45633

Query Match      16.0%; Score 41; DB 12; Length 459;
Best Local Similarity 61.9%; Pred. No. 0.00059;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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QY 26 GAAACACATATGCGCGCGCTGACACAGGCTGTAGTGTGAATATCAGAGATGAC 85
Db 76 GAAACAGCTCAGAGACGACACTGCCAGGTTGAACTCTTCCACGTAGGCAAGTTAC 135

QY 86 TGAACGCTTTGGGACTCCGTTTCTCATGTGTAATAATGAGGTTA 130
Db 136 TTAACCTTTTGAAGCTCAGTTTCTCTCTTAAATGAAATCA 180
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RESULT 10
US-10-301-480-659042
; Sequence 659042; Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 659042
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-659042
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Query Match      16.0%; Score 41; DB 12; Length 459;
Best Local Similarity 61.9%; Pred. No. 0.00059;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 26 GAAACACATATGCGCGCGCTGACACAGGCTGTAGTGTGAATATCAGAGATGAC 85
Db 76 GAAACAGCTCAGAGACGACACTGCCAGGTTGAACTCTTCCACGTAGGCAAGTTAC 135

QY 86 TGAACGCTTTGGGACTCCGTTTCTCATGTGTAATAATGAGGTTA 130
Db 136 TTAACCTTTTGAAGCTCAGTTTCTCTCTTAAATGAAATCA 180
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RESULT 11
US-10-027-632-187045/c
; Sequence 187045; Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 187045
/ LENGTH: 484
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-187045
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Query Match          16.0%; Score 41; DB 6; Length 484;
Best Local Similarity 61.9%; Pred. No. 0.0006;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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QY 26 GAAACACATATGCGCCGCTGACCGAGGTGTAAGTGTGAATATCAGGAATGAC 85
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QY 86 TGAACGCTTTGGAGCTCCGTTCTCATGTGTAATAATGAGGTTA 130
DB 349 TTAAGCTTTTGAAGCTCAGCTTCTCTCTTTAAATGAATCA 305
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RESULT 12
US-10-027-632-187045/c
/ Sequence 187045, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
/ FILE REFERENCE: 108827.129
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 187045
/ LENGTH: 484
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-187045
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Query Match 16.0%; Score 41; DB 7; Length 484;

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Best Local Similarity 61.9%; Pred. No. 0.0006;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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QY 26 GAAACACATATGCGCCGCTGACCGAGGTGTAAGTGTGAATATCAGGAATGAC 85
DB 409 GAAACACGCTCAGAGCGACAGCTGCGAGGTTGAATCCCTGCCAGTAGGAATTAC 350
QY 86 TGAACGCTTTGGAGCTCCGTTCTCATGTGTAATAATGAGGTTA 130
DB 349 TTAAGCTTTTGAAGCTCAGCTTCTCTCTTTAAATGAATCA 305
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RESULT 13
US-10-750-185-50997/c
/ Sequence 50997, Application US/10750185
/ Publication No. US200502603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 50997
/ LENGTH: 1664
/ TYPE: DNA
/ ORGANISM: Bovine
US-10-750-185-50997
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Query Match          15.1%; Score 38.8; DB 10; Length 1664;
Best Local Similarity 70.3%; Pred. No. 0.0065;
Matches 52; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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QY 73 TCAGGAAGATGACTGAACGCTTTGGAGCTCCGTTCTCATGTGTAATAATGAGGTTAAT 132
DB 439 TCAGGACGAGTCGATGAACCTTTGGCTCAGTTCTTAATGAAGAAATGCGATTAAT 380
QY 133 ACCAGCCTTCTTCT 146
DB 379 AATAGCCCTACCT 366
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RESULT 14
US-10-750-623-50997/c
/ Sequence 50997, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 50997
/ LENGTH: 1664
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TYPE: DNA
ORGANISM: Bovine 1986881425868
US-10-750-623-50997

Query Match 15.1%; Score 38.8; DB 10; Length 1664;
Best Local Similarity 70.3%; Pred. No. 0.0065;
Matches 52; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 73 TCAGAGATGATGACGTAAGCTTTGGGACTCCGTTTCCTCATTTGTAATAATGAGGTTAAT 132
DB 439 TCAGGAGGCTCGATGAACTCTTTGCTCCTCAGTTTCTTAATGAGAAATGCGGATAAT 380

QY 133 ACCAGCCTTCTCT 146
DB 379 AATAGCCCTACCT 366

RESULT 15

US-09-925-065A-496734/c
Sequence 496734, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 496734
LENGTH: 407
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-496734

Query Match 14.6%; Score 37.4; DB 4; Length 407;
Best Local Similarity 61.6%; Pred. No. 0.012;
Matches 77; Conservative 0; Mismatches 46; Indels 2; Gaps 1;

QY 47 CTGACCAAGGCTGTAAGTGTGAATATCAGAAAGATGTAACGCTTTGGGACTCCGT 106
DB 385 CTGACTTAAGCTATATATATATATGTAAGCAAAATGACTTAACCTTTCAGAGCTCAGT 326

QY 107 TTCCCTATTGTAATGAGGTTAATACCA--GGCTTCTCTACTCCCAAGCAAGCACTG 164
DB 325 TTCCCTATTGTAATGAGGATATATACAGTGCCTTCTTTCTCTTCAATGAATTA 266

QY 165 TTGTGT 169
DB 265 TGTGT 261

Search completed: June 6, 2006, 00:20:59
Job time: 513.092 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using SW model

Run on: June 5, 2006, 22:44:48 ; Search time 7.49143 Seconds
(without alignments)
4040.340 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

Perfect score: 257
Sequence: 1 ttcctcgcagtcctcctcg.....aaagcgaccagcccgct 257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications NA New:
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3: /EMC Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:
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7: /EMC Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:
8: /EMC Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.8	12.4	151830	6 US-10-519-335-37	Sequence 37, Appl
2	30.6	11.9	1780	7 US-11-293-697-1981	Sequence 1981, Ap
3	30.6	11.9	3719	6 US-10-529-452-49	Sequence 49, Appl
4	30	11.7	3646	6 US-10-511-937-358	Sequence 358, Appl
5	29.8	11.6	6035	7 US-11-293-383-12	Sequence 12, Appl
6	29.6	11.5	3646	7 US-11-293-697-1350	Sequence 150, Appl
7	29	11.3	258	7 US-11-304-129-58	Sequence 58, Appl
8	28	10.9	1458	6 US-10-511-937-598	Sequence 598, Appl
9	28	10.9	1830	7 US-11-293-697-1731	Sequence 1731, Appl
10	28	10.9	3252	7 US-11-293-697-604	Sequence 604, Appl
11	28	10.9	9973	6 US-10-857-260-29	Sequence 29, Appl
12	27.6	10.7	56580	6 US-10-553-298-1	Sequence 1, Appl1
13	27.4	10.7	3165	7 US-11-293-697-1501	Sequence 1501, Appl
14	27.2	10.6	591	6 US-10-488-619-1537	Sequence 1537, Appl
15	27.2	10.6	2788	7 US-11-293-697-1674	Sequence 1674, Appl
16	27	10.5	1389	7 US-11-217-529-75896	Sequence 75896, Appl
17	27	10.5	2940	7 US-11-302-678-13	Sequence 13, Appl1
18	26.8	10.4	1479	6 US-10-526-538-15	Sequence 15, Appl
19	26.6	10.4	256	7 US-11-301-554-423	Sequence 423, Appl
20	26.6	10.4	3500	6 US-10-525-126-89	Sequence 89, Appl
21	26.4	10.3	3106	7 US-11-293-697-565	Sequence 565, Appl
22	26.2	10.2	2190	7 US-11-293-697-2423	Sequence 2423, Appl
23	26.2	10.2	16125	7 US-11-236-238-1	Sequence 1, Appl1
24	26	10.1	454	7 US-11-301-554-1557	Sequence 1557, Appl
25	25.8	10.0	1491	7 US-11-217-529-81443	Sequence 81443, Appl

26	25.8	10.0	2378	7 US-11-293-697-1075	Sequence 1075, Appl
27	25.8	10.0	15314	6 US-10-501-834-218	Sequence 218, Appl
28	25.8	10.0	394191	6 US-10-506-549-3	Sequence 3, Appl1
29	25.6	10.0	1922	6 US-10-526-538-1	Sequence 1, Appl1
30	25.4	9.9	1703	6 US-10-953-349-11062	Sequence 11062, Appl
31	25.4	9.9	1813	7 US-11-293-697-1815	Sequence 1815, Appl
32	25.4	9.9	2256	6 US-10-505-928-657	Sequence 657, Appl
33	25.4	9.9	2646	7 US-11-293-697-1153	Sequence 1153, Appl
34	25.4	9.9	3524	6 US-10-511-937-390	Sequence 390, Appl
35	25.4	9.9	3541	6 US-10-505-928-113	Sequence 113, Appl
36	25.2	9.8	9730	6 US-10-501-834-219	Sequence 219, Appl
37	25	9.7	736	7 US-11-145-807A-33	Sequence 33, Appl
38	25	9.7	759	7 US-11-217-529-4431	Sequence 4431, Appl
39	25	9.7	824	6 US-10-488-619-1933	Sequence 1933, Appl
40	25	9.7	1321	6 US-10-196-749-371	Sequence 371, Appl
41	25	9.7	1587	7 US-11-293-697-1139	Sequence 1139, Appl
42	25	9.7	2892	7 US-11-293-697-235	Sequence 235, Appl
43	25	9.7	3486	7 US-11-302-678-25	Sequence 25, Appl
44	25	9.7	3934	6 US-10-196-749-349	Sequence 349, Appl
45	24.8	9.6	597	7 US-11-217-529-705	Sequence 705, Appl

ALIGNMENTS

RESULT 1
US-10-519-335-37/c
Sequence 37, Application US/10519335
Publication No. US20060099210A1
GENERAL INFORMATION:
APPLICANT: Cavarec, Laurent
APPLICANT: Chumakov, Ilya
APPLICANT: Destenaves, Benoit
APPLICANT: Gonthier, Catherine
APPLICANT: Elias, Isabelle
TITLE OF INVENTION: NOVEL KNOX POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN THE TREATMENT OF MENTAL DISORDERS
FILE REFERENCE: G-194US03PCT
CURRENT APPLICATION NUMBER: US/10/519,335
PRIOR FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 60/391,359
PRIOR FILING DATE: 2002-06-25
NUMBER OF SEQ IDS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 151830
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (10)..(110)
OTHER INFORMATION: n = a or c or g or t
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: 5' UTR
LOCATION: (1)..(54)
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
LOCATION: (55)..(124)
OTHER INFORMATION: exon 1
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NAME/KEY: exon
LOCATION: (91147)..(91244)
OTHER INFORMATION: exon 2
FEATURE:
NAME/KEY: exon
LOCATION: (93669)..(93834)
OTHER INFORMATION: exon 3
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NAME/KEY: exon
LOCATION: (96310)..(96422)
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OTHER INFORMATION: exon 4
FEATURE:
NAME/KEY: exon
LOCATION: (99546)..(99723)
OTHER INFORMATION: exon 5
FEATURE:
NAME/KEY: exon
LOCATION: (125441)..(125605)

Query Match 12.4%; Score 31.8; DB 6; Length 151830;
Best Local Similarity 58.3%; Pred. No. 0.43; Indels 1; Gaps 1;
Matches 74; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

QY 18 CTGCTGGTGAACACATATGCGCCGCTGACGAGGTGTATGTGTGAATATCAGG 77
DB 25888 CTCACCTGACGCGCAGAGGGGACGAGGCGCAGCGGGGGAACAGAGATCTTGCA 25829
QY 78 AAGATGACTGACAGCTCTTTGGGACTCCGTTTCTCAT-TGTAAATGGAGTTATACCA 136
DB 25828 AAGATCAGCTTGCTCTCCCTGAGCTTCAGTTTCTCATCTGTACAAAGAGATGAAATCA 25769
QY 137 GCCTCT 143
DB 25768 CTCTCT 25762

RESULT 2

US-11-293-697-1981
Sequence 1981, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1981
LENGTH: 1780
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-1981

Query Match 11.3%; Score 30.6; DB 7; Length 1780;
Best Local Similarity 65.2%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 62 GTGTGGAATATGAGAAATGACTGAACTCTTTGGGACTCCGTTTCTCATTTGTAA 121
DB 1415 GTGTCTTGACTGTGGGCAAGTACTTCACTCTGGGCGCTCAGTTTCTCACTAGAAA 1474
QY 122 TGGAGTTA 130
DB 1475 TAGGGTTA 1483

RESULT 3

US-10-529-452-49/C
Sequence 49, Application US/10529452
Publication No. US20060099218A1
GENERAL INFORMATION:
APPLICANT: Iwamoto, Aikichi
APPLICANT: Techikawa, Ai
TITLE OF INVENTION: Methods For Enhancing Exogenous Epitope
FILE REFERENCE: 50026/051001
CURRENT APPLICATION NUMBER: US/10/529,452
CURRENT FILING DATE: 2005-03-28
PRIOR APPLICATION NUMBER: PCT/JP03/12595
PRIOR FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: JP 2002-288394
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 3719
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (97)...(2205)
US-10-529-452-49

Query Match 11.3%; Score 30.6; DB 6; Length 3719;
Best Local Similarity 65.2%; Pred. No. 0.19; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 76 GGAAGTACTGACAGCTCTTTGGGACTCCGTTTCTCATTTGTAATGAGAGTTATACC 135
DB 2963 GGAAGTACTGACAGCTCTTTGGGACTCCGTTTCTCATTTGTAATGAGAGTTATACC 2904
QY 136 AGCTTCTT 144
DB 2903 CAACCTCAT 2895

RESULT 4

US-10-511-937-358
Sequence 358, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 358
LENGTH: 3646
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-358

Query Match 11.7%; Score 30; DB 6; Length 3646;
Best Local Similarity 64.3%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGTGTAGAGCTTTGGGACTCCGTTTCTCATTTGTAATGAGAGT 128
DB 3158 AACCTTGGGACATTAATATGTCTTTGAGCTTGTGTTTCTCATCTGTAAACAGGGA 3217
QY 129 TAATACAGC 138
DB 3218 TAATACAGC 3227

RESULT 5

US-11-297-383-12/C

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/ Sequence 12, Application US/11297383
/ Publication No. US20060110813A1
/ GENERAL INFORMATION:
/ APPLICANT: Ajinomoto Co., Inc.
/ TITLE OF INVENTION: Process for Producing L-Glutamic Acid
/ FILE REFERENCE: C210MOPC4045
/ CURRENT APPLICATION NUMBER: US/11/297,383
/ PRIOR FILING DATE: 2005-12-09
/ PRIOR APPLICATION NUMBER: 2003-165545
/ PRIOR FILING DATE: 2003-06-10
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 6035
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: plasmid pSTVCB
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (2129)..(3439)
US-11-297-383-12
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Query Match 11.6%; Score 29.8; DB 7; Length 6035;
Best Local Similarity 58.4%; Pred. No. 0.47;
Matches 52; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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```
QY 143 TTCTACCCCAAGCAGCGTGTTCCTCCGCGCAGAGCCCAATTGTTGCTTAC 202
DB 1834 TTCTGACCTTCAGGCGACCATTTCAACCCGCTAGAGGTGAAATGCTGCTTAAG 1775
QY 203 GCATCAGTTACCCCAAGCAGCGGTCTAG 231
DB 1774 GCATTAATAATCCACATATAGTGACTG 1746
```

```
RESULT 6
US-11-293-697-1350
/ Sequence 1350, Application US/11293697
/ Publication No. US20060105376A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ PRIOR FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1350
/ LENGTH: 3646
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-293-697-1350
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Query Match 11.5%; Score 29.6; DB 7; Length 3646;
Best Local Similarity 51.5%; Pred. No. 0.43;
Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
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```
QY 94 TTGGAGCTCCGTTCTCTCATTTGTAATGAGGTTAATCAAGCCTTCTTACCC 153
DB 774 TCTGGGCTCCAGTTTCCCATTTGTGATGAGGCACTTCCATGCTCTCTAGGCT 833
QY 154 AAAGCAGCGTTTGTCTCCGCGCAGAGGCCCAATTGTTGCTGTTACGCATCAGTTAC 213
DB 834 GCACGTAAAGTATTTTTCAGTTCAAGTCAAGCAGGTAAAGGCGCATTCATCTGTG 893
QY 214 CCCACAGAGAG 225
DB 894 CTCATATCAGG 905
```

```
RESULT 7
US-11-304-129-58/c
/ Sequence 58, Application US/11304129
/ Publication No. US20060088915A1
/ GENERAL INFORMATION:
/ APPLICANT: OHTAKI, Tetuya
/ APPLICANT: MASUDA, Yasuaki
/ APPLICANT: TAKATSU, Yoshihiro
/ APPLICANT: MATANABE, Takuya
/ APPLICANT: TERAU, Yasuko
/ APPLICANT: SHINTANI, Yasuaki
/ APPLICANT: HINUMA, Syuji
/ TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
/ FILE REFERENCE: 2762USOP
/ CURRENT APPLICATION NUMBER: US/11/304,129
/ PRIOR FILING DATE: 2005-12-15
/ PRIOR APPLICATION NUMBER: US/10/333,192
/ PRIOR FILING DATE: 2003-09-29
/ PRIOR APPLICATION NUMBER: JP 2000-217442
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: JP 2001-26779
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: PCT/JP01/06162
/ PRIOR FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 58
/ SEQ ID NO 58
/ LENGTH: 258
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic DNA
US-11-304-129-58
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Query Match 11.3%; Score 29; DB 7; Length 258;
Best Local Similarity 55.4%; Pred. No. 0.2;
Matches 56; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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```
QY 137 GCCTTCTTACTTCCCAAGCAGCGTGTTCCTCCGCGCAGAGGCCCAATTGTTGCT 196
DB 123 GCATCTTCACCTTCAGGACCCGCGGGTGCAATACGACGACGACGAGCCAGGCT 64
QY 197 GTTCAGCATCATGTTACCCCAAGCAGCGGTGAGCCAT 237
DB 63 AATCGCAGCAGGTATCCGACCGCATGTCATCATCAGTT 23
```

```
RESULT 8
US-10-511-937-598/c
/ Sequence 598, Application US/10511937
/ Publication No. US2006008836A1
/ GENERAL INFORMATION:
/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.
/ APPLICANT: Wohlgemuth, Jay
/ APPLICANT: Fry, Kirk
/ APPLICANT: Woodward, Robert
/ APPLICANT: Ly, Ngoc
/ APPLICANT: Prentice, James
/ APPLICANT: Morris, MacDonald
/ APPLICANT: Rosenberg, Steven
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
/ FILE REFERENCE: 50661200104
/ CURRENT APPLICATION NUMBER: US/10/511,937
/ PRIOR FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/012946
/ PRIOR FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 10/131,831
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 10/325,899
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 3117
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 598
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LENGTH: 1458
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-598

Query Match 10.9%; Score 28; DB 6; Length 1458;
Best Local Similarity 53.7%; Pred. No. 1.1;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 66 GTGAATATCAGGAAGATGATGACGCTTTGGACCTCCCTTCTCATTTGTAATGA 125
DB 380 GTGACATATCAGGAATGCTGCTGAAAGTTCTCTGTTCATTCCTTTAGCTCCACA 321
QY 126 GGTAAATACGAGCCTTCTTACTCCCAACGACGCTTTGTCGCG 173
DB 320 GAGTCTCTCCACGACACTTCTTAGCTTAATCCCAAGTTTGGTACAG 273

RESULT 9

US-11-293-697-1731/c
Sequence 1731, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1731
LENGTH: 1830
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-1731

Query Match 10.9%; Score 28; DB 7; Length 1830;
Best Local Similarity 53.7%; Pred. No. 1.2;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 66 GTGAATATCAGGAAGATGATGACGCTTTGGACCTCCCTTCTCATTTGTAATGA 125
DB 438 GTGACATATCAGGAATGCTGCTGAAAGTTCTCTGTTCATTCCTTTAGCTCCACA 379
QY 126 GGTAAATACGAGCCTTCTTACTCCCAACGACGCTTTGTCGCG 173
DB 378 GAGTCTCTCCACGACACTTCTTAGCTTAATCCCAAGTTTGGTACAG 331

RESULT 10

US-11-293-697-604/c
Sequence 604, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 604
LENGTH: 3252
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-604

Query Match 10.9%; Score 28; DB 7; Length 3252;
Best Local Similarity 63.2%; Pred. No. 1.6;

Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 70 ATATCAGAGATGATGATGACGCTTTGGACCTCCCTTCTCATTTGTAATGAGGTT 129
DB 877 ATCTTGGGCAATGTTACTTACTCTCTATGCTCTGTTCTCTCATTTGTAATGAGGAT 818
QY 130 AATACGAG 137
DB 817 AATACGAG 810

RESULT 11

US-10-857-260-29
Sequence 29, Application US/10857260
Publication No. US20060110742A1
GENERAL INFORMATION:
APPLICANT: Lyons, Leslie A.
APPLICANT: Graham, Robert
APPLICANT: Erdman, Carolyn
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-146800US
CURRENT APPLICATION NUMBER: US/10/857,260
CURRENT FILING DATE: 2004-05-28
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 9973
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
OTHER INFORMATION: Genbank Accession No. AC145332.28 genomic DNA for
OTHER INFORMATION: PKD1 9973 bp contig
NAME/KEY: modified base
LOCATION: (1)..(9973)
OTHER INFORMATION: n = g, a, c or t
US-10-857-260-29

Query Match 10.9%; Score 28; DB 6; Length 9973;
Best Local Similarity 60.5%; Pred. No. 2.7;
Matches 46; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 61 AGTGTGGAATATCAGAGATGATGACGCTTTGGACCTCCCTTCTCATTTGTAATGA 120
DB 8374 AGCTGTGATTTTGGACACCTCCCTTCCGCTCTGAGGCTCAGTTTCCATCTGAAC 8433
QY 121 ATGAGGTTAATACCA 136
DB 8434 ATTGGGATCATACGA 8449

RESULT 12

US-10-553-298-1
Sequence 1, Application US/10553298
Publication No. US20060110385A1
GENERAL INFORMATION:
APPLICANT: NeuroNova AG
TITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
FILE REFERENCE: XXX
CURRENT APPLICATION NUMBER: US/10/553,298
CURRENT FILING DATE: 2005-10-14
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 56580
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon1
LOCATION: (3000)..(3124)
OTHER INFORMATION:
FEATURE:

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; NAME/KEY: exon2
; LOCATION: (24841)..(25009)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon3
; LOCATION: (26134)..(26202)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon4
; LOCATION: (30958)..(31030)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon5
; LOCATION: (32481)..(32577)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon6
; LOCATION: (35416)..(35496)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon7
; LOCATION: (36113)..(36242)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon8
; LOCATION: (37541)..(37677)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon9
; LOCATION: (45470)..(45560)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon10
; LOCATION: (47229)..(47295)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon11
; LOCATION: (47380)..(47529)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon12
; LOCATION: (50438)..(50539)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon13
; LOCATION: (54392)..(54889)
; OTHER INFORMATION:
; US-10-553-298-1

Query Match          10.7%; Score 27.6; DB 6; Length 56580;
Best Local Similarity 67.2%; Pred. No. 8.7;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 76 GGAAGATGACTGAACGCTTGTGGACCTCCGTTTCCTATTGTAATAATGAGGTTAATA 133
Db 33237 GGAATAAGCTTAACCTCTCTGAGTTTCAGTGTCCTCACTGTAATAAGCAGAAATAATA 33234

RESULT 13
US-11-293-697-1501
; Sequence 1501, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1501
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; LENGTH: 3165
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1501

Query Match          10.7%; Score 27.4; DB 7; Length 3165;
Best Local Similarity 50.4%; Pred. No. 2.5;
Matches 67; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 69 AATATCAGGAGATGACTGAACGCTTTTGGACTCCGTTTCCTATTGTAATAATGAGGT 128
Db 1610 AAGATTACAGAGAGAGGAGCAACCCGAGAGCTGTCTCTCTGACTGTGACCCG 1669

QY 129 TAATACAGCCTTCTTCTACTCCCAACGACGTTGTCCTCCGCGCAGAGGCCCAAT 188
Db 1670 TCAGGGCATTCATCTTGCTCCCAATTTACCCCGTGATGATGCGGCAATGACATAC 1729

QY 189 TGTGGCTGTCA 201
Db 1730 CGCTGGCAGTGCA 1742

RESULT 14
US-10-488-619-1537/c
; Sequence 1537, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Wanner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1537
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1537

Query Match          10.6%; Score 27.2; DB 6; Length 591;
Best Local Similarity 48.7%; Pred. No. 1.3;
Matches 74; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 96 TGGAGCTCCGTTCCCTCATTTGAATAAGAGGTTAATACAGGCTTCTTACTCCCA 155
Db 213 TCGCCATAGCCCTGTTCACTTGAAGAAGTCTACAGACCATCCACAGGGCCGAG 154

QY 156 ACGCAGCTGTTTGTCCCGGCGAGAGGCCCAATGTTGCTGTTCACGATCAGTTACC 215
Db 153 GCACCCCTCTTCCCTGGCTGTCTCCCTGGGTGTGTGACTCGTACAGGGTCTT 94

QY 216 CCAAGAGCGGTCACGCAATTAAGCGCAAC 247
Db 93 GCCAGGGCGGGGTGGGCAAGCAGTGCACAC 62

RESULT 15
US-11-293-697-1674
; Sequence 1674, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1674
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LENGTH: 2788
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-293-697-1674

Query Match 10.6%; Score 27.2; DB 7; Length 2788;
 Best Local Similarity 61.1%; Pred. No. 2.8;
 Matches 44; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY	62	GTGTGGAATATCAGAGATGACTGACGCTTTGGGACTCCGTTCTTCATTGTAAA	121
Db	2031	GTATGAAACTTAGGTAATTAATTACTTAACCTCTGACCTCAGTTTCTTCATCTGTAAA	2090
QY	122	TGAGGTTAATA	133
Db	2091	ACAGGATTAACA	2102

Search completed: June 6, 2006, 00:22:30
 Job time : 8.49143 secs

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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:46 ; Search time 10852.7 Seconds
(without alignments)
9445.379 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_1857

Perfect score: 1603
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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10: gb_vl:*
11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1603	100.0	3505	2	ES4511 UCP-2, promo
2	1589.4	99.2	199384	5	AP003531 Homo sapi
3	1587.8	99.1	32270	5	AF306570 Homo sapi
4	1587.8	99.1	12177	5	DQ087219 Homo sapi
5	1575.8	98.3	156370	5	AP003717 Homo sapi
6	1563.8	97.6	155668	12	AC024029 Homo sapi
7	1547.4	96.5	197031	12	AC019121 Homo sapi
8	1251.6	78.1	3301	5	AF208500 Homo sapi
9	158.4	9.9	168721	5	AC136431 Homo sapi
10	158.4	9.9	173113	12	AC138962 Homo sapi
11	158.4	9.9	175069	12	AC140895 Homo sapi
12	158.4	9.9	175785	12	AC138897 Homo sapi
13	158.4	9.9	189911	12	AC138897 Homo sapi
14	158.4	9.9	211419	5	AC136434 Homo sapi
15	158.4	9.9	235330	12	AC140522 Homo sapi
16	158.2	9.9	66188	5	AL391136 Human DNA
17	158.2	9.9	162820	5	AL138765 Human DNA
18	156.8	9.8	133615	5	AC092326 Homo sapi

19	156.8	9.8	170572	12	AC140894 Homo sapi
20	156.8	9.8	173271	12	AC141623 Homo sapi
21	156.8	9.8	173912	12	AC141075 Homo sapi
22	156.8	9.8	174428	12	AC136441 Homo sapi
23	156.8	9.8	180654	12	AC140896 Homo sapi
24	156.8	9.8	189646	12	AC140909 Homo sapi
25	156.8	9.8	195740	12	AC141269 Homo sapi
26	156.4	9.8	13009	5	AC130468 Homo sapi
27	156.4	9.8	198521	12	AC145723 Homo sapi
28	155.8	9.7	190144	5	AL590080 Human DNA
29	153.2	9.6	185511	5	AC093414 Homo sapi
30	152.4	9.5	145414	5	HS78P24 Human DNA
31	152.4	9.5	217292	5	AF288742 Homo sapi
32	152.2	9.5	98569	5	HS209B9 Human DNA
33	152	9.5	135005	5	HS860F19 Human DNA
34	152	9.5	162701	12	AC073317 Homo sapi
35	152	9.5	178650	5	AC010373 Homo sapi
36	151.8	9.5	96559	5	AC079347 Homo sapi
37	151.6	9.5	177688	5	AL136440 Human chr
38	151.6	9.5	202521	12	AC146953 Homo sapi
39	151	9.4	171183	5	AL358876 Human DNA
40	151	9.4	178820	5	AC020552 Homo sapi
41	150.8	9.4	56912	5	AL160176 Human DNA
42	150.6	9.4	184041	5	AC093496 Homo sapi
43	150.6	9.4	187159	5	AC090941 Homo sapi
44	150.4	9.4	23579	2	AX647373 Sequence
45	150.4	9.4	115231	5	HS785G19 Human DNA

ALIGNMENTS

RESULT 1	ES4511	3505 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	ES4511				
DEFINITION	UCP-2 promoter and use thereof.				
ACCESSION	ES4511.1	GI:18629692			
VERSION	JP 2000236886-A/1.				
KEYWORDS	JP 2000236886-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 3505)
AUTHORS	Toyota, Y., Kobayashi, M. and Igaki, S.
TITLE	UCP-2 promoter and use thereof
JOURNAL	Patent: JP 2000236886-A 1 05-SEP-2000;
COMMENT	TAKEDA CHEM IND LTD
OS	Homo sapiens (human)
PN	JP 2000236886-A/1
PD	05-SEP-2000
PF	22-DEC-1999 JP 1999364724
PR	

PI	YUKIO TOYOTA, MAKOTO KOBAYASHI, SHIGERU IGAKI
PC	C12N15/09, A61K45/00, A61P3/04, A61P3/06, A61P3/10, A61P9/12, PC
PC	A61P9/00, C12N1/21,
PC	C12N5/10, C1201/02, G01N33/15, G01N33/50//A61K31/711, A61K38/00,
PC	A61K48/00,
PC	(C12N15/09, C12R1:19), (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),
PC	(C12N5/10, C12R1:91), (C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
PC	C12R1:19),
PC	(C12N15/00, C12R1:91), (C12N5/00, C12R1:91)
CC	

FT	Key	Location/Qualifiers
FT	source	1..3505
FT		/organism='Homo sapiens (human)'

FEATURES	source	Location/Qualifiers
		1..3505
		/mol_type='genomic DNA'
		/db_xref='taxon:9606'

ORIGIN

Query Match 100.0%; Score 1603; DB 2; Length 3505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACCTGTAATTCAGTCTGTGAGAGTCCAGGTCAGAGAGCTGTGAGCCGAGGATTC 60
255 ACCTGTAATTCAGTCTGTGAGAGTCCAGGTCAGAGAGCTGTGAGCCGAGGATTC 314
61 AAGAGAGCCTGAGCAACACAGAGGAGCTGTGACTCAAAAGATTAATTAATTAGCCAG 120
315 AAGAGAGCCTGAGCAACACAGAGGAGCTGTGACTCAAAAGATTAATTAATTAGCCAG 374
121 GCTTGTGCTCATCCCTGTGTGCTCCAGTACTAGAGAGGAGAGATGAGATGCTTTGTC 180
375 GCTTGTGCTCATCCCTGTGTGCTCCAGTACTAGAGAGGAGAGATGAGATGCTTTGTC 434
181 CCAGAGAGTCAAGACGTGAGTGAAGCCAGGACCTGTGATTCAGCCGAGGCAAC 240
435 CCAGAGAGTCAAGACGTGAGTGAAGCCAGGACCTGTGATTCAGCCGAGGCAAC 494
241 AAAAAAGAGCCCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATTAATTAATTAAC 300
495 AAAAAAGAGCCCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATTAATTAATTAAC 554
301 CCTAAACACATCTCTTTTCAAAAGAGACTTTTAAGAGCTTCAATGCTGCTGTTG 360
555 CCTAAACACATCTCTTTTCAAAAGAGACTTTTAAGAGCTTCAATGCTGCTGTTG 614
361 ATCTCACTTCCCTTTTCAAGGCTCCACACTTTTAACAGTCTTTTTCAGAGATTAAT 420
615 ATCTCACTTCCCTTTTCAAGGCTCCACACTTTTAAAGCTTTTTCAGAGATTAAT 674
421 AGTATTAAGTTTGTGAATCCAGATCTTCCCTGTTTGAAGAGCCAGGAGGCAATTTT 480
675 AGTATTAAGTTTGTGAATCCAGATCTTCCCTGTTTGAAGAGCCAGGAGGCAATTTT 734
481 GGTCTGACAGGCTTTTGCATCTGTGCTGTTGCTGAGCAATCTCAAGCAAAATTTGCG 540
735 GGTCTGACAGGCTTTTGCATCTGTGCTGTTGCTGAGCAATCTCAAGCAAAATTTGCG 794
541 AGCTCTCCGGAAATGACAGCCAGACAGAGCTCAAGGCAAAACTGAGAACTCTGCGGA 600
795 AGCTCTCCGGAAATGACAGCCAGACAGAGCTCAAGGCAAAACTGAGAACTCTGCGGA 854
601 GGGAGACTCAGAGTGCACAAAAAACTTATCTTTTCTTTTCTTTTCTTTTCTTTCT 660
855 GGGAGACTCAGAGTGCACAAAAAACTTATCTTTTCTTTTCTTTTCTTTTCTTTCT 914
661 TTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 720
915 TTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 974
721 TTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 780
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REFERENCE
1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (2001)
2 (bases 1 to 199384)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (18-APR-2001) Masahiro Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:htp://hgp.gsc.riken.go.jp/,
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VERSION AF306570.1 GI:11037742  
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AUTHORS Schneitler, C., Oberkofler, H., Besterbauer, H. and Patsch, W.  
TITLE UCP2 promoter region and exon 1  
JOURNAL Unpublished  
2 (bases 1 to 3270)  
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AUTHORS Schneitler, C., Oberkofler, H., Besterbauer, H. and Patsch, W.  
TITLE Direct Submision  
JOURNAL Submitted (18-SEP-2000) Laboratory Medicine, LandesKliniken  
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VERSION DQ087219.1
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TITLE To cite this work please use: NIEHS-SNP, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA

(URL: <http://egp.gs.washington.edu>).

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DB	413 ATCTCACATTCCTTTTTCAGAGTCCACACTTTAACAGTCTTTTGCACAGATTAATA	472	
OY	421 AGTATATAGTTTCTGGAATCCAGATTCTCCCTGTTTGGACAGCCAGGGGCAATTTTT	480	
DB	473 AGTATATAGTTTCTGGAATCCAGATTCTCCCTGTTTGGACAGCCAGGGGCAATTTTT	532	
OY	481 GGCTGCAGGCTTTTGCAATCTGTTGCTGTGCTGACGAATCTCACAGCAAAATTTGCCG	540	
DB	533 GGCTGCAGGCTTTTGCAATCTGTTGCTGTGCTGACGAATCTCACAGCAAAATTTGCCG	592	

QY	541	AGCCTCTCCGAAATGACAGCCAGACAGAGCTCAGCCGCAAAAGCTTAGAGAACTGTGGCGGA	600
Db	593	AGCCTCTCCGAAATGACAGCCAGACAGAGCTCAGCCGCAAAAGCTTAGAGAACTGTGGCGGA	652
QY	601	GGAGAACTCACAGTGGCCAAATAAACTTATCTTTTCTTTTCTTTTCTTTTCTTTCTCT	660
Db	653	GGAGAACTCACAGTGGCCAAATAAACTTATCTTTTCTTTTCTTTTCTTTTCTTTTCTCT	712
QY	661	TTCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTCT	720
Db	713	TTCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTCT	772
QY	721	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	780
Db	773	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	832
QY	781	TCGTGTTTCCAGCTGTCTCTGTCAGAGACATAGCCTCGCGCTGTGTTTCTTTCCGATATA	840
Db	833	TCGTGTTTCCAGCTGTCTCTGTCAGAGACATAGCCTCGCGCTGTGTTTCTTTCCGATATA	892
QY	841	ATTATCCAGGCCCATCCAGCTCTGTGTCCCTCAGCTGTTTCCCTGGCAGTCCCTTCTGCT	900
Db	893	ATTATCCAGGCCCATCCAGCTCTGTGTCCCTCAGCTGTTTCCCTGGCAGTCCCTTCTGCT	952
QY	901	GGTGAAAAACATATATGAGCGCGCGCTGACAGAGGATATGATGTGATATCAGAAAGAT	960
Db	953	GGTGAAAAACATATATGAGCGCGCGCTGACAGAGGATATGATGTGATATCAGAAAGAT	1012
QY	961	GACTGAACGTCCTTTGGAGCTCCGTTTCTCTCATTTGTAAATGAGGTTATATCCAGCCTTC	1020
Db	1013	GACTGAACGTCCTTTGGAGCTCCGTTTCTCTCATTTGTAAATGAGGTTATATCCAGCCTTC	1072
QY	1021	TTCTATCTCCCAAAACGCAAGTGTGTTGTCGCGGACAGAGGCGCCAAATTGTTGAGCTGTAC	1080
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QY	1081	GCATCAGTTACCCCCACAGAGACGAGGTACGCCAATTTAAAGCGAACCAGGCCCGGTTCATC	1140
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QY	1141	TCCTGAGGCCCTTTTCTCATCCCAAGGCTGTGACAGGAGCTGTGGCCCGGCTGTGCC	1200
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QY	1201	TTGTCACTGTGGGGGGCGGCGCCGTTTGTCTGTGTGTGTATGAGAGCGTGAAGTCAAGCT	1260
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QY	1261	GGGTGCTCCCGCCCGCCGCGGAGCTTTATGTCTCTGTGCTCTTAAAGCCACAGGCCGCTCC	1320
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Db	1613	ACTTAAACAACGAGCCCGCTGAGAGCTTGTTTAGAAACCTGCTCT 1654	

RESULT 5
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LOCUS AP003717 156370 bp DNA linear PRI 27-APR-2002
DEFINITION Homo sapiens genomic DNA, chromosome 11q clone: RP11-167N4, complete
sequences.
ACCESSION AP003717 GI:20334343
VERSION AP003717.3
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 156370)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9111. Fax: 81-45-503-9170
URL: http://hgp.gsfc.riken.go.jp/
On Apr 26, 2002 this sequence version replaced gi:16904692.
COMMENT
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
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DB 44813 AAGAGCAGCCTGGACCAACAGGAGAGCCTGTCACTACAAAGATTAATAATTAGCCAG 44754
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DB 44513 ATCTCACTTCCCTTTTTCAGGCTCCACACTTTTAAAGTCTCTTTTGGCCAGGATATA 44454
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DB 44393 GGCTGAGAGCCTTGGATCTGTCTGTCTGTGTGTCAGCAATCTCACAGCAATTTGGCG 44334
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DB 44033 ATTATCCAGGCCCCATCCAGCTGTGTCCTTCACTGTTTCCCTGGAGAGTCCCTTCTGCT 43974
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DB 43973 GGTAAAAACATATGAGCGCGCGCTGACCAAGGCTGTATGTTGTGAATATCAGGAAGAT 43914
QY 961 GACTGAACGCTTTTGGAGCTCCGTTTCTTCAATTTTAAGAGAGTTAAATCCAGCCTTC 1020
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QY 1021 TTCTACTCCCAACAGCAGCTGTTTGTCCGCGCAGAGGCGCCAAATTTGGCTGTTTCTAC 1080
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DB 43613 GGGTGTCTCCGCGCGCGCGGCTTGT 43555
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DB 43554 ACCGGGGAGAGAGCGGCAACCCAGCGGAGCCCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 43495
QY 1381 CTTGT 1440
DB 43494 CTTGT 43435
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QY 1501 CGCAGAGAGGTGGTATTTTGTCCAGAGTATGAGGAGGCTGGGCTCCATTAAGAGAGATGTC 1560
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QY 1561 ACTTAGACACGCGCCGCTGAGCGCTTTAGAAACCGTCCT 1603
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RESULT 6
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LOCUS Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
DEFINITION AC024029
SEQUENCE 15 unordered pieces.
AC024029
AC024029.3 GI:7230916
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 155668)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 155668)
Waterston,R.H.
Direct Submission
Submitted (20-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7109555.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0167N04
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 16800; agarose-fp
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; sum-of-contigs
Quality coverage: 4.38 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
* 11378 14368: contig of 2991 bp in length
* 14369 14468: gap of unknown length
* 14469 20130: contig of 5662 bp in length
* 20131 20230: gap of unknown length
* 20231 25513: contig of 5283 bp in length
* 25514 25613: gap of unknown length

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ORIGIN

Query Match 97.6%; Score 1563.8; DB 12; Length 155668;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1598; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

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DB 70159 ACCGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAAGCCAGAGTTC 70100
QY 61 AAGAGAGCCCTGAGCAACAGAGGAGACTGTCACTCAAAAGATTAATAATTAAGTACAG 120
DB 70099 AAGAGAGCCCTGAGCAACATAGGAGAGCTGTCACTCAAAAGATTAATAATTAAGTACAG 70040
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DB 70039 GCTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGAGAGAGTACAGTCTGTGC 69980
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RESULT 7
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LOCUS Homo sapiens chromosome 11 clone R011-535C12, WORKING DRAFT
DEFINITION
SEQUENCE 23 unordered pieces.
AC019121
AC019121.3 GI:8440022
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 197031)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 197031)
AUTHORS Waterston,R.H.
TITLE Direct Submission

JOURNAL
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 10, 2000 this sequence version replaced gi:7105573.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NH0535C12
Summary Statistics -----
Sequencing vector: M13, 55%
Sequencing vector: plasmid, 45%
Chemistry: Dye-terminator Big Dye, 45% of reads
Chemistry: Dye-terminator Big Dye, 45% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 182418 bases at least Q40
Consensus quality: 187565 bases at least Q30
Consensus quality: 190012 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 194831; sum-of-contigs
Quality coverage: 4.10 in Q20 bases; agarose-fp
Quality coverage: 4.05 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
2971: contig of 2971 bp in length
2972
3071: gap of unknown length
3072
3764: contig of 2693 bp in length
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5766
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8569
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8669
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12866
12965: gap of unknown length
12966
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18582
18681: gap of unknown length
18682
23851: contig of 5170 bp in length
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23952
28414: contig of 4463 bp in length
28415
28514: gap of unknown length
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33296
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38749
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44926
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51785
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58856
58955: gap of unknown length
58956
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68389: gap of unknown length
68390
77123: contig of 8734 bp in length
77124
77223: gap of unknown length
77224
87292: contig of 10066 bp in length
87293
87392: gap of unknown length
87393
96029: contig of 8637 bp in length
96030
96129: gap of unknown length
96130
104791: contig of 8662 bp in length
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104891: gap of unknown length
104892
116912: contig of 12021 bp in length
116913
117012: gap of unknown length
117013
131368: contig of 14356 bp in length
131369
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131469
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142994
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ORIGIN
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Best Local Similarity 99.1%; Pred. No. 0;
Matches 1588; Conservative 0; Mismatches 11; Indels 4; Gaps 3;
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QY      61  AAGAGCAGCTTGACCAACAGAGGAGAGCTGCTCAACAAGATAATTAATTAATTAAGCAG 120
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QY      241  AAAAAGAGACCCGTGTCAAAAAATAAGTTAAATAATTAATTAATTAATTAATTAATTAAC 300
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QY      361  ATCTCCACTTCCTCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTTCCCAAGGATATA 420
DB      163718  ATCTCCACTTCCTCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTTCCCAAGGATATA 163777
QY      421  AGTATATAGTTTTCGAATCAGATTTCTTCTGTTTGAACAGCAGGAGGAGCAATTTT 480
DB      163778  AGTATATAGTTTTCGAATCAGATTTCTTCTGTTTGAACAGCAGGAGGAGCAATTTT 163837
QY      481  GGTCTGAGGCTTTTGATCTGTTCTGCTGTGCTCAGCAATCTCAGAGCAAAATTTGCCG 540
DB      163838  GGTCTGAGGCTTTTGATCTGTTCTGCTGTGCTCAGCAATCTCAGAGCAAAATTTGCCG 163897
QY      541  AGCCTCTCCGAAATGACACAGCCAGAGAGACTGAGCCAAAGAGTAGAAGACTGGCGGA 600
DB      163898  AGCCTCTCCGAAATGACACAGCCAGAGAGACTGAGCCAAAGAGTAGAAGACTGGCGGA 163957
QY      601  GGAAGACTCAGAGTCCACAAAAAATTATCTTTTCTTTTCTTTTCTTTTCTTTTCT 660
DB      163958  GGAAGACTCAGAGTCCACAAAAAATTATCTTTTCTTTTCTTTTCTTTTCTTTTCT 164017
QY      661  TTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 720
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QY      721  TTCTCTTTCTTTTCTTACATGAGCAAGATCTCTCATGAGAGAAATATCTGCTTACT 780
DB      164078  TTCTCTTTCTTTTCTTACATGAGCAAGATCTCTCATGAGAGAAATATCTGCTTACT 164137
QY      781  TCTGTTTCCAGGCTGCTTCTGACAGACATGCGCTCGGCGTGTCTTTTCCGCTATA 840
DB      164138  TCTGTTTCCAGGCTGCTTCTGACAGACATGCGCTCGG- GTGTTTCTTTCCGCTATA 164196
QY      841  ATTATCCAGGCCCATCCAGACTCTGTGCTCCCTCAGCTGTTCCCTGGAGTCCCTTCTCT 900
DB      164197  ATTATCCAGGCCCATCCAGACTCTGTGCTCCCTCAGCTGTTCCCTGGAGTCCCTTCTCT 164256
QY      901  GGTGAAACACATATGAGCGCGGCGCTGACCAAGGAGTGAAGTGAATATCAGAAAGAT 960
DB      164257  GGTGAAACACATATGAGCGCGGCGCTGACCAAGGAGTGAAGTGAATATCAGAAAGAT 164316
QY      961  GACTGAACGCTCTTTGGAGACTCCGTTTCTCATTTGTAATATGAGGTTAATACAGCTTC 1020
DB      164317  GACTGAACGCTCTTTGGAGACTCCGTTTCTCATTTGTAATATGAGGTTAATACAGCTTC 164376
QY      1021  TTCTACTCCCAACAGCAGTGTGTTGTCCTGAGGAGGAGGCCCAATGTTGGCTGTTCAC 1080
DB      164377  TTCTACTCCCAACAGCAGTGTGTTGTCCTGAGGAGGAGGCCCAATGTTGGCTGTTCAC 164436
QY      1081  GCATCAGTTACCCCAACAGAGAGGAGTGAAGCAATTAAGGAGCAACAGGCCGGTCCATC 1140
DB      164437  GCATCAGTTACCCCAACAGAGAGGAGTGAAGCAATTAAGGAGCAACAGGCCGGTCCATC 164496
QY      1141  TCCTGACGCTTTTCTCATCCAGGAGTGAACAGGAGCTGAGCTGGGCTCGGCTGTCC 1200
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QY      1201  TTGTCACTGCGGAGGCGCGGCTGTTGCTGTTGCTGTGTGTAGAGAGGTCAAGCT 1260
DB      164557  TTGTCACTGCGGAGGCGCGGCTGTTGCTGTTGCTGTGTGTAGAGAGGTCAAGCT 164616
QY      1261  GGGTGTCCCGGCGCGGCGGCTTAAAGTCCCTGAGTCCCTAAACGCCAGGCGGCTCC 1320
DB      164617  GGGTGTCCCGGCGCGGCGGCTTAAAGTCCCTGAGTCCCTAAACGCCAGGCGGCTCC 164676
QY      1321  ACCGAGGAGAAAGGCGGCAACCCAGCGAGGCCCAACGAGCTGTGTCGTTGCGGGCCA 1380
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QY      1381  CTTGTGTGCACTTCTGATGTGTTCTTCTCCCGACCAACGCGCGGCTGTAAACAATCG 1440
DB      164737  CTTGTGTGCACTTCTGATGTGTTCTTCTCCCGACCAACGCGCGGCTGTAAACAATCG 164796
QY      1441  ACAGCAGAGCGGATGCGAGAGCCCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
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QY      1561  ACTTAAAGACAGGCGCGGCTGAGACGCTTGTTAAGAAACCGTCTCT 1603
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[illegible]

QY	239	CAAAAAGAGCCCTGCTCAAAAAATPAGTTAAATPAAATPAAATPAAATAGTTAA	298
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QY	299	ACCCTAACACATCTTCTTTTCAAAAGAGACTTTAAGACCTTCATGTCGCTCGT	358
Db	1618	ACCCTAACACATCTTCTTTTCAAAAGAGACTTTAAGACCTTCATGTCGCTCGT	1677
QY	359	TGATCTCCACTTCCCTTTTTCAGCGTCCACCTTTTAAACAGTCTCTTTTG	417
Db	1678	TGATCTCCACTTCCCTTTTTCAGCGTCCACCTTTTAAACAGTCTCTTTTGCCAAAGATA	1737
QY	418	ATAAGTAAATAGTTTTCGGAAATCCAGATCTT	476
Db	1738	ATAAGTAAATAGTTTTCGGAAATCCAGATCTTTCCTGTGTGGACAGCAGGGGACAT	1797
QY	477	TTTGTGTGAGAGCCCTTGTGATCTGATCTGTCTGTGCTCAGACATCTCACAGCAATTT	536
Db	1798	TTTGTGTGAGAGCCCTTGTGATCTGATCTGTGTCTGTGTGCTCAGACATCTCACAGCAATTT	1857
QY	537	GCCGAGCCTTCGGGAATGACAGCCAGACAGAGCTCAGCGCAAAAGCTAGAGAACTGG	596
Db	1858	GCCGAGCCTTCGGGAA	1916
QY	597	CGGAGGAGACTCACAGTCCACAAAAAAATTATCTTTCTTTTCTTTTCTTTTCT	656
Db	1917	CGGAGGAGACTCACAGTCCACAAAAAAATTATCTTTCTTTTCTTTTCTTTTCT	1976
QY	657	TTCTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTCTCTCTCTCTCTCTCTCTCTCT	716
Db	1977	TTCTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTCTCTCTCTCTCTCTCTCTCTCT	2036
QY	717	TTCTTTCTTTCTTTTCTTTTCTTACATGCGAGATCTCTCATGCAAAATATCTGCTT	776
Db	2037	TTCTTTCTTTCTTTTCTTTTCTTACATGCGAGATCTCTCATGCGAAATATCTGCTT	2096
QY	777	GACTTCGTTCACAGCGCTTCGCGACAGACATAGCGCTCGGGGTGTTTTCTTTCCGC	836
Db	2097	GACTTCGTTCACAGCGCTTCGCGACAGACATAGCGCTCGGGGTGTTTTCTTTCCGC	2156
QY	837	TATATATTCCAGAGCCCATCCACAGCTGAGTCCCTCAGCTGTTCCTCTGG	894
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QY	895	TCTGCT	952
Db	2217	TCTGCTGGGTGAAAAACATATAGCGCGGCTGAA	2276
QY	953	AGGAAGATGACTGAACGTCTTT	1011
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QY	1012	CCAGCCTCTTCTACTCCCCCAAGCAATGTGTTGTC	1070
Db	2337	CCAGCCTCTTCTATATCCCAAAAGCAATGTGTTGTC	2396
QY	1071	GAGCTGTCACGCATCAGTTAACCCCAACAGACGAGTCAACCAATTAAGCGAAACAGGC	1130
Db	2397	GAGCTGTCACGCATCAGTTAACCCCAACAGACGAGTCAACCAATTAAGCGAAACAGGC	2456
QY	1131	CCGGTCACTTCCTGACGCGCTTTTCTATCCCAAGGCTGACAGGACAGCTGGCTGGGC	1190
Db	2457	CCGGTCACTTCCTGACGCGCTTTTCTATCCCAAGGCTGACAGGACAGCTGGCTGGGC	2516
QY	1191	CGGCTCTGCTGTCAGTGGCGGGGGGCGGCGGTTGCTTGTCGTGTGTAGAGACGTG	1256
Db	2517	CGGCTCTGCTGTCAGTGGCGGGGGGCGGCGGTTGCTTGTCGTGTGTAGAGACGTG	2576
QY	1251	AGGTCAACCTGAGTCTCCGCGCCCGCGCGCGGAGCTTT	1309
Db	2577	AGGTCAACCTGAGTCTCCGCGCCCGCGCGCGGAGCTTTAAGTGTCCCTGTCCCTAAAGC	2636
QY	1310	CAGGCGCTCCACCGGGGAGAAAGCGCAACCCACGCGAGCCCAACGCGCTGTTCGG	1368

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QY 1370 TTGGCGGGGACACCTGTTGCTGACGTTCTGATTTGTTCTTCCCGGACGAGCGGCGGCT 1429
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QY 1430 GTAAACCAATGACAGGAGGCGGCTGCGAGGCGCCGAGTCCGCGCTGCGAGAGCGAGCC 1489
Db 2755 TTAACCAATTTGACAGGAG--GCCGCTGCGAGGCGCCGAGTCCGCGCTGCGAGAGCGAGCC 2813
QY 1490 GCG----CGCTGCTTCCGAGAGGCTGAGTTGTTGCCAGGCT--AGGCGGCGCTGGCG 1542
Db 2814 GCGCGGCTGCTGCGAGGAGGCTGTTAGTTTTCGCCAGCGTTAGGCGGCGCTGCGCGC 2873
QY 1543 CCATAAAGAGAGAGTGCATTAGACACGCGCCCGCTGAGCGCTTTAGAAACCGTCC 1602
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QY 1603 T 1603
Db 2934 T 2934

RESULT 9
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LOCUS Homo sapiens chromosome 16 clone RP11-148M17, complete sequence.
DEFINITION AC136431
AC136431.3 GI:27356680
VERSION
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Doe Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 168721)
REFERENCE
AUTHORS Doe Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 168721)
REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.2.

FEATURES

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1.168721
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Best Local Similarity 73.9%; Pred. No. 1e-34;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

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Db 18786 AGAGCAGCTTGAGCAACATAGAGAGCTCATCTTACAAAATTAATTAATAGCTAGG 18845
QY 122 CTTAGTGCTCAATCCCTGTGCTCCAGCTAATAGGAGCGAAGTAGA----CTGCTT 177
Db 18846 CGTGTGAGCAATGCTGTAGTCCAGCTACTAGGAGGCTGAGTGGGAGATGCGCTTG 18905
QY 178 GTTCCAGAGAGTCAACATGCTGAGTACAGCCAGCTCACTGATTCACCTGCGGC 237
Db 18906 AGCCCAAGAGGTGAGAGATGCAATGAGCCGAGATTGACCA--CTGCACTTCAAGCTGGGT 18964
QY 238 AACCAAAAGAGACCCCTGTCCAAAATTAATTAATTAATTAATTAATTAATTAATTA 297
Db 18965 GACAGAGCAAGACCTTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTA 19024
QY 298 AACCTTAAC 307
Db 19025 ATCCCTAGAC 19034

RESULT 10
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LOCUS Homo sapiens chromosome 16 clone RP11-906M12, WORKING DRAFT
DEFINITION AC138962
AC138962.1 GI:27805374
SEQUENCE, 3 unordered pieces.
ACCESSION AC138962.1 GI:27805374
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
TITLE DOE Joint Genome Institute.
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 173113)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.2.

Project Information
Center Project Name: 1642708
Center Clone Name: RPCT-11_906M12

Summary Statistics
Consensus quality: 171480 bases at least Q40
Consensus quality: 171615 bases at least Q30
Consensus quality: 171780 bases at least Q20
Estimated insert size: 180000; agarose-IP estimation
Estimated insert size: 172913; sum-of-coverage
Quality coverage: 15.53 in Q20 bases; agarose-IP estimation
Quality coverage: 16.17 in Q20 bases; sum-of-coverage
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

OY	2 CCTGTAATTCACGACTGTGGAGAGTCCGAGAGTCAAGAGACTGCTTGAGGCACAGAATTCA	61
Dd	131562 CCGTAGATCCAAACATTTTGAAGGCCAAGGACAGTGGATTGCTTGAAGCCCAAGAGTTTG	131503
OY	62 AGAGCAGCCTGGACAACACAGGGAGACTGTCACTCAAAAGATAATTAATTAATGACAG	121
Dd	131502 AGACCAGCCTGGGCAACATAGAGAGACTCATCTCTACAAAAATTAACAAAATTAAGCTAAG	131443
OY	122 CTTAGTGCTCATCCCTGTGTGTCACGACTAATGAGGAGCAGAAATGAGA---CTGCTT	177
Dd	131442 CGTGTGGACATGCTGTAATGCCAGTACTAGGAGGCTGATGGGAGATGAGCTTG	131383
OY	178 GTTCCAGAGGATCAAGACTGCAAGTAGCTGAGACCAAGCACCTGCATTTCCAGCTGGGC	237
Dd	131382 AGCCCAAGAGTTCAGAGATGCAAGTAGCCGAGATTGCACCA-CTGCATCTCCAGCCTGGGGT	131324
OY	238 AACAAAAAGAACCCCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATTAATTAAGTTTA	297
Dd	131323 GACAGGCAAGACCCCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAG	131266
OY	298 AACCTTAAC	307
Dd	131263 ATCCCTTAGAC	131254

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RESULT 12
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LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-482B16, WORKING DRAFT
ACCESSION AC138897
VERSION AC138897.1 GI:27805309
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 175785)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 175785)
DOE Joint Genome Institute.
Direct Submissions
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 591493
Center clone name: RPC1-11_482B16
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Summary Statistics
Consensus quality: 175156 bases at least Q40
Consensus quality: 175239 bases at least Q30
Consensus quality: 175390 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 175585; sum-of-contrigs estimation
Quality coverage: 16.07 in Q20 bases; agarose-fp estimation
Quality coverage: 16.47 in Q20 bases; sum-of-contrigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
47298: contig of 47298 bp in length

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FEATURES	SOURCE
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*	47398: gap of unknown length
*	47399
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*	106634: gap of unknown length
*	175785: contig of 69151 bp in length
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Query Match: 9.9%; Score 158.4; DB 12; Length 175785;
Best Local Similarity 73.9%; Pred. No. 1e-34;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2
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QY 2 CCTGTAATTCACGTAAGTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGSCAGAGAGTTCA 61

Db 108733 CCTGTAATCCCAACACTTGTAGAGGCCAAGGCAAGTGGATTGCTTGAGCCCAAGAGATTGG 108674

Db 108673 AGACCAAGCCTGAGGCAACATAGAGAGACTCATCTCTACAAAAAATACAAAAATTAGCTAGG 108614

QY	122	177
CGTGTGCGCTCATCCCTGTGTGTCCTCCAGCACTAAGGAGGCGAGAAATAGG	CTGCTT	177
108613	CGTGTGCGCATGCTCTGTAGTCCAGCACTAAGGAGGCTGACGTGGGAGAGATGCTTG	108554

QY 178 GTCCAGAGCTCAAGATCGAGGAGCGAGACCCAGCACCCTGCTTCAGCCCTGGGC 237

Ddb 108553 AGCCCAAGAGCTCGAGATCGAGTCCAGGCCAATTGACCA - CTGCACTCCAGCCTGGGT 1084955

QY	238	108494	108435
ACACAAAGAGACCCCTGTCACAAAATAAGTTAATAATATATATATGTTA			
GACGAGACAGACCCCTGTCACAAAATAAGTTAATAATATATATATGTTA			

QY	298	AACCTAAC	307
Db	108434	ATCCCTAGAC	108425

RESULT 13
AC136434

LOCUS	189911.DP	DNA	linear	RG-01-NOV-2002
DEFINITION	AC136434			
DESCRIPTION	Human sapiens chromosome 16 clone	RP11-261E14	WORKING DRAFT	
SEQUENCE	4 unordered pieces.			
ACCESSION	AC136434			

VERSION	AC136434.1 GI:24463324
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

1 (bases 1 to 189911)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 189911)

DOE Joint Genome Institute.
DOE Joint Genome Institute.
Submitted (01-NOV-2002) Microarray Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive Walnut Creek, CA 94598, USA

```
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Project Name: 506699
Center clone name: RPI-11_261B14
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Summary Statistics
Consensus quality: 187721 bases at least Q40
Consensus quality: 188330 bases at least Q30
Consensus quality: 188586 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 189611; sum-of-coverage estimation
Quality coverage: 9.23 in Q20 bases; agarose-fp estimation
Quality coverage: 7.79 in Q20 bases; sum-of-coverage estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1304: contig of 1304 bp in length
* 1305 1404: gap of unknown length
* 1405 3583: contig of 2179 bp in length
* 3584 3683: gap of unknown length
* 3684 51653: contig of 47970 bp in length
* 51654 51753: gap of unknown length
* 51754 189911: contig of 138158 bp in length.
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/chromosome="16"
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3584..3683
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51654..51753
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FEATURES
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1305..1404
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ORIGIN
Query Match 9.9%; Score 158.4; DB 12; Length 189911;
Best Local Similarity 73.9%; Pred. No. 1e-34;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGAGTCTTGAGGCCGAGAGTTCA 61
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DB 188408 AGAGCAGCCTGGACAACAGAGGAGAGCTGTCACTCAAAAGATTAATAATTAGCCAG 188467
QY 122 CTTAGTGGCTCATCCCTGTGGTCCAGCTACTAGGAGGAGGAGAGTGA---CTGCTT 177
DB 188468 CGTGTGGGACATGCGCTGTAGTCCAGCTACTAGGAGGAGGAGTGAAGTGGCTTG 188527
QY 178 GTCCCAAGAGGTCAAGACTGAGTGAAGTGAAGCCAGCACTGCATTCCAGCTGGGC 237
DB 188528 AGCCCAAGAGGTGAGAGATGAGTGAAGCCAGATGAGCA-CTGCATCTCAGCTGGGT 188586
QY 238 AACAAAAAGAGCCCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAAGTTTA 297
DB 188587 GACAGAGCAAGACCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAAGCAG 188646
QY 298 AACCTTAAC 307
DB 188647 ATCCCTAGAC 188656
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LOCUS Homo sapiens chromosome 16 clone RP11-1307B12, complete sequence.
DEFINITION AC126760
ACCESSION AC126760
VERSION AC126760.4 GI:25989066
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
1 (bases 1 to 211419)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Unpublished
2 (bases 1 to 211419)
DOE Joint Genome Institute.
Direct Submission
Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 211419)
DOE Joint Genome Institute.
Direct Submission
Submitted (31-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 211419)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Submitted (01-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 1, 2002 this sequence version replaced gi:24431616.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
finishing completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
Location/Qualifiers
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/mol_type="genomic DNA"
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FEATURES
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/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 73.9%; Pred. No. 1.1e-34;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGAGTCTTGAGGCCGAGAGTTCA 61
DB 81719 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGAGTCTTGAGGCCGAGAGTTG 81778
QY 62 AGAGCAGCCTGGACAACAGAGGAGAGCTGTCACTCAAAAGATTAATAATTAGCCAG 121
DB 81779 AGAGCAGCCTGGACAACAGAGGAGAGCTGTCACTCAAAAGATTAATAATTAGCCAG 81838
QY 178 GTCCCAAGAGGTCAAGACTGAGTGAAGTGAAGCCAGCACTGCATTCCAGCTGGGC 237
DB 81839 CGTGTGGGACATGCGCTGTAGTCCAGCTACTAGGAGGAGGAGTGAAGTGGGAGGATGCTTG 81898
QY 122 CTTAGTGGCTCATCCCTGTGGTCCAGCTACTAGGAGGAGGAGAGTGA---CTGCTT 177
DB 81899 AGCCCAAGAGGTGAGAGATGAGTGAAGCCAGATGAGCA-CTGCATCTCAGCTGGGT 81957
QY 178 GTCCCAAGAGGTCAAGACTGAGTGAAGTGAAGCCAGCACTGCATTCCAGCTGGGC 237
DB 81957 AGCCCAAGAGGTGAGAGATGAGTGAAGCCAGATGAGCA-CTGCATCTCAGCTGGGT 81957
QY 238 AACAAAAAGAGCCCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAAGTTTA 297
DB 81958 GACAGAGCAAGACCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAAGCAG 82017
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Qy 298 AACCTTAAC 307
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Db 82018 ATCCTTAGAC 82027

RESULT 15

AC140522/c 235330 bp DNA linear HTG 25-FEB-2003
LOCUS Homo sapiens chromosome 16 clone RP11-826F21, WORKING DRAFT
DEFINITION

SEQUENCE, 5 unordered pieces.

AC140522

AC140522.1 GI:28557856

HTG; HTGS PHASE1; HTGS_DRAFT.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1611829

Center clone name: RP11-826F21

Summary Statistics

Consensus quality: 233805 bases at least Q40

Consensus quality: 234198 bases at least Q30

Consensus quality: 234471 bases at least Q20

Estimated insert size: 175000; agarose-fp estimation

Estimated insert size: 234930; sum-of-contigs estimation

Quality coverage: 13.22 in Q20 bases; agarose-fp estimation

NOTE: This is a 'working draft' sequence. It currently

consists of 5 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 20830: contig of 20830 bp in length

* 20831 20930: gap of unknown length

* 42778 42877: gap of unknown length

* 42878 78821: contig of 35944 bp in length

* 78822 78921: gap of unknown length

* 78922 131770: contig of 52849 bp in length

* 131771 131870: gap of unknown length

* 131871 235330: contig of 103460 bp in length.

Location/Qualifiers

1. 235330

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="16"

/clone="RP11-826F21"

/clone_lib="RP11 human BAC library 11"

20831..20930

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78822..78921 /estimated_length=unknown
gap 131771..131870 /estimated_length=unknown
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Best Local Similarity 73.9%; Pred. No. 1.1e-34;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
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| | | | |
Db 2105 CTTGTAATTCAGTCTGTGAGAGTCCGAGGTGAGAGGAGTCTGTTGAGCCAGAGTTTG 2046
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Qy 62 AGAGCAGGCTGAGCAACAGAGGAGGAGTCTGCTACAAAGAAATTAATTAATTGAGCAG 121
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Qy 122 CTTAGTGTCTATCCCTGTGTGAGTCCAGCTACTAGAGGAGGAGGAGTCTGCTT 177
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Db 1985 CTTAGTGTCTATCCCTGTGTGAGTCCAGCTACTAGAGGAGGAGGAGTCTGCTT 177
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Qy 178 GTCCAGAGGTGAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 237
| | | | |
Db 1925 AGCCAAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1867
| | | | |
Qy 238 AACAAAAAGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 297
| | | | |
Db 1866 GACAGAGCAAGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1807
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Qy 298 AACCTTAAC 307
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Db 1806 ATCCTTAGAC 1797

Search completed: June 5, 2006, 22:27:25
Job time : 10860.7 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 1394.65 Seconds
(without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_1857

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: geneseqn1980s:*
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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	433.8	27.1	9314	12	ADG65405
3	152	9.5	135005	12	ADQ19501
4	150.4	9.4	23579	10	ADCB7112
5	149.4	9.3	186510	10	ADB24797
6	148.8	9.3	151909	14	ABE96535
7	147.4	9.2	81099	11	ACN45018
8	147.2	9.2	110000	14	AE61124
9	147	9.2	110000	10	ADG70447
10	147	9.2	110000	10	ABZ79565
11	146.8	9.2	7739	4	AA136824
12	146.8	9.2	7739	8	ABX59812
13	146.8	9.2	7739	12	ADJ30562
14	146.8	9.2	226475	9	AAE58279
15	146.4	9.1	41150	10	ADL13819
16	146.4	9.1	41150	14	AE18343
17	146.4	9.1	44348	12	ADN48556
18	145.4	9.1	31749	4	AAK72959

C	19	145.4	9.1	78925	3	AAC99888
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C	22	145.4	9.1	143947	15	AER35247
C	23	145.4	9.1	143947	15	AER64068
C	24	145.4	9.1	143947	15	AER63985
C	25	144.8	9.0	53122	11	ACN43998
C	26	144.8	9.0	110000	11	ACN43998_5
C	27	144.6	9.0	2096	8	ACCT72436
C	28	144.6	9.0	93500	13	ADT77142
C	29	144.4	9.0	32169	5	ABA14358
C	30	144	9.0	109906	6	ABK94411
C	31	144	9.0	109906	12	AD108112
C	32	144	9.0	158417	13	ADS36461
C	33	143.8	9.0	11006	14	AE61101
C	34	143.6	9.0	58822	9	ADA02540
C	35	143.6	9.0	58822	10	ADA72278
C	36	143.6	9.0	58822	10	ADB95788
C	37	143.6	9.0	110000	12	ADN06353_0
C	38	143.6	9.0	110000	13	ADN94372_0
C	39	143.6	9.0	145616	14	ABD17971
C	40	143.6	9.0	174472	14	ADZ13139
C	41	143.6	9.0	174703	11	ACN44738
C	42	143.6	9.0	276276	11	ACN44350
C	43	143.4	8.9	2005	5	AAF93841
C	44	143.4	8.9	2005	14	ADY63190
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ALIGNMENTS

RESULT 1	AAA62932	standard, DNA, 3505 BP.
ID	AAA62932	
AC	AAA62932;	
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DT	02-NOV-2000	(first entry)
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DE	DNA containing human uncoupling protein-2 (UCP-2) promoter region.	
XX		
KM	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;	
KM	hypotension; hyperlipidaemia; anti-pyretic; de.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200039315-A1.	
XX		
PD	06-JUL-2000.	
XX		
PF	22-DEC-1999;	99NO-JP007198.
XX		
PR	24-DEC-1998;	98JP-00366719.
XX		
PA	(TAKE) TAKEDA CHEM IND LTD.	
XX		
PI	Toyoda Y, Kobayashi M, Igaki S;	
XX		
DR	WPI; 2000-452407/39.	
XX		
PT	DNA with promoter region containing regulator sequence of uncoupling protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,	
PT	hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in	
PT	therapy.	
XX		
PS	Claim 4; Fig 1-6; 43pp; Japanese.	
XX		
CC	This invention relates to DNA comprising a promoter region containing the	
CC	regulatory sequences of human uncoupling protein-2 (UCP-2). Included in	
CC	the invention are a recombinant vector containing the DNA sequence, cells	
CC	transformed by the vector, and a method for screening for compounds or	
CC	salts that can promote or inhibit the UCP-2 promoter activity using the	

CC transformants. The DNA and cells transformed using it can be used to
CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic
CC and anti-pyretic drugs. The present sequence represents DNA containing
CC the UCP-2 promoter sequences

Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 1603; DB 3; Length 3505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 255 ACCTGTAATTCAGTACTGTGAGAGTCCAGGTCAAGAGCTGCTTGAGGCCAGAGTTC 314
QY 61 AAGAGAGCCTGGAACAACAGGAGAGCCTGTCACTAACAAGATTAATTAATTAAGCAG 120
DB 315 AAGAGAGCCTGGAACAACAGGAGAGCCTGTCACTAACAAGATTAATTAATTAAGCAG 374
QY 121 GCTTAGTGTGCTCATCCCTGTGTGTCCAGCTACTAGGAGGAGAGAGTGTGTGTC 180
DB 375 GCTTAGTGTGCTCATCCCTGTGTGTCCAGCTACTAGGAGGAGAGAGTGTGTGTC 434
QY 181 CCGAGAGGTGAACAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 240
DB 435 CCGAGAGGTGAACAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 494
QY 241 AAAAAGAGAGCCGTGTCAAAAAATATAATTAATTAATTAATTAATTAATTAATTAAT 300
DB 495 AAAAAGAGAGCCGTGTCAAAAAATATAATTAATTAATTAATTAATTAATTAATTAAT 554
QY 301 CCTAAACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
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QY 361 ATCTCCATCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 615 ATCTCCATCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 674
QY 421 AGTATATAGTTTTCGGAATCAGATTTCTTCCGTTTGAAGAGAGGAGGAGCAATTTT 480
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DB 855 GGGAGAGCTCAGAGGCGACAAAAAACTTATATCTTTTCTTTTCTTTTCTTTTCTTTCT 914
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DB 1515 GGGTGTCCCGGCGCGGCGCGGCGCTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1574
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DB 1695 ACAGCAGAGGCGGCTGCGAGAGCCCAAGTCCGCGCTGAGAGAGCAGCCGAGCTGCT 1754
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DB 1815 ACTTAAGACACGGGCGCGCTGTGAGCGCTGTGTGAAGAACCTGTCT 1857
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DB 1155 GGTGAAAAACATATGGCGCGGCTTGAACAGAGGTGAAGTGTGTAATTCAGGAAGAT 1214
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DB 1215 GACTGAACGCTTTTGGAGTCCGTTTCTCATTTGTAATAATGAGGTAAATACAGGCTTC 1274
QY 1021 TTCTACTCCCAACAGCAGTGTGTGTCCGAGCAGAGGAGCCCAATTTGTGTGTTCAC 1080
DB 1275 TTCTACTCCCAACAGCAGTGTGTGTCCGAGCAGAGGAGCCCAATTTGTGTGTTCAC 1334
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DB 1335 GCATCAGTTTACCCCAAGAGAGGAGTGAATTAAGGAGCAACAGAGCCGAGTCATC 1394
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DB 1395 TCTCAGAGCCTTTTCTCATCCAGAGCTGGAACAGAGCTGAGCTGAGCTCCGCTCTGCC 1454
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DB 1515 GGGTGTCCCGGCGCGGCGCGGCGCTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1574
QY 1321 ACCGAGGAGAGAGGAGCGGAGCCCAAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1380
DB 1575 ACCGAGGAGAGAGGAGCGGAGCCCAAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1634
QY 1381 CTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
DB 1635 CTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1694
QY 1441 ACAGCAGAGGCGGCTGCGAGAGCCCAAGTCCGCGCTGAGAGAGCAGCCGAGCTGCT 1500
DB 1695 ACAGCAGAGGCGGCTGCGAGAGCCCAAGTCCGCGCTGAGAGAGCAGCCGAGCTGCT 1754
QY 1501 CGCAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
DB 1755 CGCAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1814
QY 1561 ACTTAAGACACGGGCGCGCTGTGAGCGCTGTGTGAAGAACCTGTCT 1603
DB 1815 ACTTAAGACACGGGCGCGCTGTGAGCGCTGTGTGAAGAACCTGTCT 1857

RESULT 2
ADG65405
ID ADG65405 standard; DNA; 9314 BP.
XX
DB ADG65405;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human uncoupling protein 2 (UCP2) gene.
XX
KW anorectic; antidiabetic; immunomodulator; gene therapy; haplocloning;
KW uncoupling protein 2; mitochondrial; proton carrier; UCP2;
KW polymorphic site; haplotype; haploclon pair; obesity; diabetes;
KW immunological disorder; body mass defect; thermoregulation defect; human;
KW gene; de; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key
FH Location/Qualifiers
FT 1283
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
FT 1714
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT 2051
FT variation
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FT      XX
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FT      XX
FT      16-JUL-2002; 2002US-00197019.
FT      XX
FT      25-JAN-2001; 2001WO-US002485.
FT      XX
FT      (CHEW/) CHEW A.
FT      (DENT/) DENTON R R.
FT      (GILS/) GILSON C R.
FT      (NAND/) NANDABALAN K.
FT      (PARK/) PARKS K E.
FT      XX
FT      Chew A, Denton RR, Gilson CR, Nandabalan K, Parks KE;
FT      WI; 2004-051505/05.
FT      DR
FT      P-PSDB; ADG65407.
FT      XX
FT      Haployping Uncoupling Protein 2 gene of an individual comprises
FT      identifying the phased sequence of nucleotides at polymorphic sites of
FT      the gene and assigning a haplotype or haplotype pair consistent with the
FT      phased sequence.
FT      PS
FT      Claim 1; SEQ ID NO 1; 64pp; English.
FT      XX
FT      The invention describes haployping the uncoupling protein 2
FT      (mtochondrial, proton carrier) (UCP2) gene of an individual comprising
FT      identifying the phased sequence of nucleotides at polymorphic sites (PS)1
FT      -23 for at least one copy of the individual's UCP2 gene and assigning to
FT      the individual a UCP2 haplotype or haplotype pair that is consistent with
FT      the phased sequence. The composition and methods are useful in
FT      haployping and/or genotyping the UCP2 gene in an individual to e.g.
FT      screen for drugs targeting the UCP2 protein to treat a condition or
FT      disease predicted to be associated with UCP2 activity. The disease or
FT      condition may include obesity, diabetes, immunological disorders and
FT      other diseases associated with defects in body mass and thermoregulation.
FT      This sequence represents the human uncoupling protein 2 (UCP2) gene.
FT      CC
FT      Sequence 9314 BP; 1904 A; 2619 C; 2371 G; 2397 T; 0 U; 23 Other;
FT      XX
FT      Query Match      27.1%; Score 433.8; DB 12; Length 9314;
FT      Best Local Similarity 97.9%; Pred. No. 5.9e-83;
FT      Matches 461; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

```


CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in AOC8548-ADc87616 encode GPCR's of the
CC invention.

SQ Sequence 23579 BP; 6524 A; 5062 C; 5419 G; 6574 T; 0 U; 0 Other;

Query Match 9.4%; Score 150.4; DB 10; Length 23579;

Best Local Similarity 72.4%; Pred. No. 5.6e-22;

Matches 223; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY 2 CCTGTAATTCAGACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTCA 61

Db 14855 CCTATTAAGCCGACACTTTGGAGAGCTGAGGTGGTGATCATCTTGAGGCCAGAGTTTG 14914

QY 62 AGAGCAGCTTGACACACAGGAGAGCTGTCTACTACAAAGATTAATTAATTAGCAGG 121

Db 14915 AGACGACATGGCCACATGCTGAACCCGCTCTACTAATAAATACAAAATTAGCCAGG 14974

QY 122 CTTAGTGGCTCATCTCTGTGCTCCAGCTACTAGGAGGC--AGAACTAGACTGCTTG 178

Db 14975 CTTGTGTGTGATCCTATATATCCAGTACTTGGAGGCTGAGAGCAAGAAATCGCTTG 15034

QY 179 TCCAGAGGTGACAGTGCAGTGAAGCTGAGACCCAGCCACTTGCCAGCCTGGGCA 238

Db 15035 AACCGGAGGCGGAGGTTCGAGTGAAGCTGAGATTGTGCCA-TTCACCTCGGCTGGGCA 15093

QY 239 ACAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 298

Db 15094 ACGGAGCAAGACTGTCTCTTAATAAATAAATAAATAAATAAATAAATAAATAAAT 15153

QY 299 ACCCTAAA 306

Db 15154 AAATATA 15161

RESULT 5

ADE24797/c

ID ADE24797 standard; DNA; 186510 BP.

XX AC ADE24797;

XX DT 29-JAN-2004 (first entry)

XX DE Human endothelin-1, EDN1, gene.

XX KM ds: gene; human; vascular disease; endothelin-1; EDN1;

XX KM coronary artery disease; myocardial infarction.

XX OS Homo sapiens.

XX FH Key location/Qualifiers

XX FT variation replace(157790,C)

XX FT /*tag= a /standard_name= "Single nucleotide polymorphism"

XX FT /*tag= b /standard_name= "Single nucleotide polymorphism"

XX FT /*tag= b /standard_name= "Single nucleotide polymorphism"

XX PN US2003143544-A1.

XX PD 31-JUL-2003.

XX PF 09-JAN-2002; 2002US-00043715.

XX PR 09-JAN-2002; 2002US-00043715.

XX PA (VITI-) VITIVITY INC.

XX PI Mccarthy J;

XX WPI; 2003-874790/81.

DR P-PSDB; ADE24798, ADE24801.

XX

PT Identifying a subject as a candidate for a particular therapy to treat a

PT vascular disease or disorder, particularly coronary artery disease or

PT myocardial infarction, comprises detecting polymorphisms of the

PT endothelin-1 gene.

XX

XX

PS

Claim 58; SEQ ID NO 1; 177bp; English.

SQ Sequence 186510 BP; 56192 A; 36427 C; 37117 G; 56774 T; 0 U; 0 Other;

Query Match 9.3%; Score 149.4; DB 10; Length 186510;

Best Local Similarity 74.1%; Pred. No. 1.7e-21; Indels 5; Gaps 2;

Matches 217; Conservative 0; Mismatches 71; Indels 5; Gaps 2;

QY 1 ACCGTAAATTCAGACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTTC 60

Db 175801 ACCTGTAATCCGACACTTTGGAGATCGAGGAGAAAGATTATTAGGCCAGAGTTT 175742

QY 61 AAGACAGCTTGACACACAGGAGAGCTGTCTACTACAAAGATTAATTAATTAGCCAG 120

Db 175741 GAGACAGCCTGGGTAACAAGTAGAGCGATCTCTCAAAAAATTAATAATTAGCTGG 175682

QY 121 GCTTAGTGGCTCATCTCTGTGCTCCAGCTACTAGGAGGAGAGTAGA---CTGCT 176

Db 175681 GCATGTGTGTGACCTGTGATGCCAGCTACTCAGAGAGGCTGAGGTGGAGATCGCTT 175622

QY 177 TGTCCAGAGGTGACAGTGCAGTGAAGCTGAGACCCAGCCACTTGCCAGCCTGGG 236

Db 175621 GAGCCCAAGAGGTGAGACCTGTGATGAGCTGTGTTCAATGCCA-CTGCAGTCCAGCTGG 175563

QY 237 CAACAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTA 289

Db 175562 CAACAGAGAGAGACCTGTCTCAAAACAAACAAACAAACAAACAAACAAACAA 175510

RESULT 6

AEB96535/c

ID AEB96535 standard; DNA; 151909 BP.

XX AC AEB96535;

XX DT 06-OCT-2005 (first entry)

XX DE Human CABIN1 gene, SEQ ID 19.

XX KM hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;

XX KM liver cirrhosis; fibrosis; hepatoma; SNP detection; CABIN1; ds.

XX OS Homo sapiens.

XX FH Key location/Qualifiers

XX FT variation 7588 /*tag= a /standard_name= "Single nucleotide polymorphism"

XX FT /*tag= b /standard_name= "Single nucleotide polymorphism"

XX FT /*tag= c /standard_name= "Single nucleotide polymorphism"

XX FT /*tag= d /standard_name= "Single nucleotide polymorphism"

XX FT variation 15316 /*tag= d

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Query Match
Best Local Similarity 9.3%; Score 148.8; DB 14; Length 151909;
Matches 220; Conservative 0; Mismatches 77; Indels 5; Gaps 2;
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DB      60437 AAGCAGCCTGGACAACACAGGAGAGAC-CTGTCACTCAAGAAATTAATTAATTAGCCAG 60378
QY      121 GCTTAGTGCTCATCCCTGTGTGTCCTCACTACTAGGAGGAGAGAGAGAGAGAGAGAGAG 179
DB      60377 GATATGATGTCACACCTGTGTGTCCTCACTACTAGGAGGAGAGAGAGAGAGAGAGAG 60318
QY      180 ---CCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCAGCTGATTCAGAGCTGGG 236
DB      60317 GAGCCAGAGAGTCAAGAGTGAAGTGAAGCCAGCCAGCTGATTCAGAGCTGATGGG 60258
QY      237 CAACAAAAAGAGACCTGTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 296
DB      60257 CAACAGAGTGAAGCCTGTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAAT 60198
QY      297 AA 298
DB      60197 AA 60196

RESULT 7
ACN45018/c
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XX
AC ACN45018;
XX
DT 18-NCV-2004 (first entry)
XX
DE Human genomic sequence hCG17395.
XX
KM Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
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PN      WO2003073826-A2.
XX
XX      12-SEP-2003.
XX
XX      28-FEB-2003; 2003WO-US006235.
XX
XX      01-MAR-2002; 2002US-00087192.
XX
XX      (SAGR-) SAGRES DISCOVERY.
XX
XX      Morris DW;
XX
XX      WPI; 2003-328604/31.
XX
XX      Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX      PT comprises a nucleotide sequence.
XX
XX      Claim 1; SEQ ID NO 1756; Opp; English.
XX
XX      The present invention relates to novel DNA and protein sequences which
XX      CC are associated with carcinomas. The sequences are useful for: (i) for
XX      CC screening drug candidates; (ii) for screening of bioactive agent capable
XX      CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
XX      CC a bioactive agent capable of modulating the activity of CAP; (iv) for
XX      CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
XX      CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
XX      CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
XX      CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
XX      CC determining Carcinoma Associated (CA) gene copy number. In addition, the
XX      CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
XX      CC carcinoma including lymphoma. The present sequence is one such CA coding
XX      CC sequence. Note: This patent is an equivalent to basic patent
XX      US2002182586A1, for which no sequence data was published
```

Sequence 81099 BP; 20015 A; 18716 C; 19786 G; 22439 T; 0 U; 143 Other;

Query Match
Best Local Similarity 9.2%; Score 147.4; DB 11; Length 81099;
Matches 218; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

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QY      62 AGAGCAGCCTGGACAACACAGGAGAGACCTGTCACTCAAGAAATTAATTAATTAGCCAG 121
DB      18751 AGACAGCCTGGACAACATGAAAGACTATCTCTCAAAAAATTAATTAATTAGCCAG 18692
QY      122 CTTAGTGCTCATCCCTGTGTGTCCTCACTACTAGGAGGAGAGAGAGAGAGAGAGAGAG 179
DB      18691 CTTGTGTCTCAGCCTGTGTGTGTCCTCACTACTAGGAGGAGAGAGAGAGAGAGAGAG 18632
QY      180 ---CCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCAGCTGATTCAGAGCTGGGC 237
DB      18631 AGCCTGGAGTTCAGAGCTCAAGTGAAGCCTGTGTGAGCCA-CTGCACTCAGAGCTGGGT 18573
QY      238 AAGAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 296
DB      18572 GACAGAGAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 18514
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WP Fragment Name Begin End
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WP AEA61124_1 100001 210000
WP AEA61124_2 200001 310000
WP AEA61124_3 300001 383432
ID AEA61124 standard; DNA; 383432 BP.
XX
AC AEA61124;
XX
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25-AUG-2005 (first entry)

Human SLC4A4 gene genomic sequence SEQ ID NO:34.

DNA methylation; biomarker; cancer; gene; ds; SLC4A4.

Homo sapiens.

US2005130172-A1.

16-JUN-2005.

27-JAN-2004; 2004US-00765790.

16-DEC-2003; 2003US-00737082.

(FARB) BAYER CORP.

Beard C, Burgess C, Gannon A, Harvey J, Lechner JF, Li Z; WPI; 2005-456991/46.

GENBANK; AF011390, NM_003759.

Identifying nucleic acid sequences as biomarker for disease, by identifying nucleic acid sequences comprising methylated CpG site and down-regulated in diseased cells and comparing its expression level with demethylated nucleic acid.

Claim 11; SEQ ID NO 34; 27pp; English.

The invention relates to a method (M1) for identifying one or more nucleic acid sequences useful as a biomarker for a disease to be detected. (M1) involves identifying nucleic acid sequences comprising methylated CpG site in promoter-first exon region and that are down-regulated in diseased cells, comparing expression level of nucleic acid sequences with that of demethylated nucleic acid sequences and identifying nucleic acid sequences exhibiting increase in expression after demethylation. Also described: (1) detecting (M2) the presence or stage of a disease in a subject, which involves determining the degree of methylation of one or more CpG sites on nucleic acid sequences in a biological sample obtained from the subject, and determining the presence of, predisposition to, or stage of the disease in the subject based on the degree of methylation; (2) monitoring the onset, progression, or regression of a disease in a subject; (3) determining the efficacy of a test compound for inhibiting a disease in a subject; and (4) a kit (I) useful for diagnosis, prognosis, staging, monitoring, and therapeutic treatment of a disease. (M1) is useful for identifying one or more nucleic acid sequences useful as a biomarker for a disease to be detected, where the nucleic acid sequences are useful for detecting, the presence or stage of a disease such as cancer e.g. colorectal cancer in a subject. The present sequence represents a specifically claimed human genomic sequence for use in the method of the invention. Note - The sequence data for this patent is not represented in the printed specification but was obtained in electronic format from the USPTO web site.

Sequence 383432 BP; 113010 A; 69169 C; 74959 G; 126294 T; 0 U; 0 Other;

Query Match 9.2%; Score 147.2; DB 14; Length 110000;

Best Local Similarity 74.0%; Pred. No. 4.3e-21;

Matches 213; Conservative 0; Mismatches 73; Indels 2; Gaps 2;

2 CCTGTAATTCACGACTGTGTAGAGTCCGAGGTCCAGAGACTGTGTAGGCCAGAGATTCA 61

90502 CTTGTACTCCGACGACTTTGAGAGGTGAGGTAGTGAATCCCTTGAGCCGACGAGATTG 90551

62 AGAGCAGCCTCGACCAACACAGGAGAGCC-TGTCACTCAAAAGATTAATTAATGACG 120

90562 AGACGAGCCTGGGCAATATGGCAAAACCTGTCTCTCAAAAAAGACAAGATAAGCCAG 90621

121 GCTTATGTGCTCATCTCCTGTGTGTCCGACTACTAGAGGAGGACGAAGTAGACTGCTTGTTC 180

90622 GTGTGTGTGTGACCACTGTGTGTGTCCGACTTCTGTGGAGGGCTGTAGGTGTGACACTTGA 90681

Oy		181	CCAGGAGCTCAACAATCGACGTGAAGTGCAGAACCACGACTCCTCATTTCCAGCCTGGGCCAAC	240
D6		90682	CCAAGAGCTGAACTGTGTGTGTGTGTCGCAAAGATTGTGTGCA-CTGCACTCCAGCCTTGSTTAAC	90740
Oy		241	AAAAAGAGACCTCTGCTCAAAAATAAATTAAATTAAATTAAATAATAA	288
D6		90741	AGATAGTAGACCTCTGCTCAAAACAAAAACAAAAACAAAAACAAAAACA	90788
	RESULT 9			
	ADG70447_0/c			
WP	Sequence split info	5 fragments	LOCUS ADG70447 Accession Adg70447	
MP	Fragment Name	Begin End		
WP	ADG70447_0	1 110000		
WP	ADG70447_1	100001 210000		
WP	ADG70447_2	200001 310000		
WP	ADG70447_3	300001 410000		
WP	ADG70447_4	400001 410846		
ID	ADG70447 standard; DNA;	410846 BP.		
XX AC	ADG70447;			
XX DT	11-MAR-2004 (first entry)			
DE	Human ANGE-CLD8-CLLD7 hybrid gene.			
KM XX	ANGE; CLD8; CLLD7; ANGE-CLD8; ANGE-CLLD7; CLLD7-CLD8;			
KW KM	ANGE-CLD8-CLLD7; anti-allergic; antiasthmatic; dermatological;			
RN RN	antipyretic; anti-inflammatory; gene therapy; Ige-mediated disease;			
KM KW	ANGE 1; single nucleotide polymorphism; ds.			
XX OS	Chimeric.			
OS OS	Homo sapiens.			
FH FH	Key Location/Qualifiers			
FT FT	variation replace(186655..G) /*tag= a /standard_name= "Single nucleotide polymorphism"			
FT FT	variation replace(338770..G) /*tag= b /standard_name= "Single nucleotide polymorphism"			
FT FT	variation replace(360186..G) /*tag= c /standard_name= "Single nucleotide polymorphism"			
FN FN	Moz2003000727-A2.			
PX PX	03-JAN-2003.			
PF PF	21-JUN-2002; 2002MO-GH002859.			
PR PR	21-JUN-2001; 2001GB-00015211.			
PPR PPR	21-JUN-2001; 2001GB-00015212.			
PA PA	(ISIS-) ISIS INNOVATIONS LTD.			
PI PI	Zhang Y, Mofatt M, Cookson W, Tinsley J;			
DR DR	WPI; 2003-201405/19.			
XX CC	New nucleic acid sequence comprising an ANGE, CLD8 or CLLD7 mRNA, or their hybrid, useful for screening agents for treating Igs-mediated diseases, e.g. asthma, atopy, hay fever, eczema, atopie dermatitis, or allergic rhinitis.			
PS PS	Claim 12; Fig 5; 429pp; English.			
XX CC	The invention relates to a novel isolated or recombinant nucleic acid sequence comprising an ANGE, CLD8 or CLLD7 mRNA, or ANGE-CLD8, ANGE-CLLD7, CLLD7-CLD8, or ANGE-CLD8-CLLD7 hybrid mRNA sequence, its complement, homologue or fragment. The novel nucleic acid sequences have			

KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;	PR	21-SEP-2000; 2000US-0234274P.
KW	neurological disease; infection; human; secreted protein;	PR	25-SEP-2000; 2000US-0234997P.
KW	musculoskeletal system; ds.	PR	25-SEP-2000; 2000US-0234998P.
XX		PR	26-SEP-2000; 2000US-0235484P.
OS	Homo sapiens.	PR	27-SEP-2000; 2000US-0235834P.
XX		PR	27-SEP-2000; 2000US-0235836P.
PN	WO200155367-A1.	PR	29-SEP-2000; 2000US-0236327P.
XX		PR	29-SEP-2000; 2000US-0236327P.
PD	02-AUG-2001.	PR	29-SEP-2000; 2000US-0236369P.
XX		PR	29-SEP-2000; 2000US-0236369P.
PF	17-JAN-2001, 2001WO-US001338.	PR	29-SEP-2000; 2000US-0236370P.
XX		PR	02-OCT-2000; 2000US-0236802P.
XX		PR	02-OCT-2000; 2000US-0237037P.
XX		PR	02-OCT-2000; 2000US-0237038P.
PR	31-JUN-2000; 2000US-0179065P.	PR	02-OCT-2000; 2000US-0237039P.
PR	04-FEB-2000; 2000US-0180628P.	PR	02-OCT-2000; 2000US-0237040P.
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PR	16-MAR-2000; 2000US-0189874P.	PR	20-OCT-2000; 2000US-0240360P.
PR	17-MAR-2000; 2000US-0190076P.	PR	20-OCT-2000; 2000US-0241212P.
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PR	11-JUL-2000; 2000US-0217487P.	PR	08-NOV-2000; 2000US-0246475P.
PR	11-JUL-2000; 2000US-0217496P.	PR	08-NOV-2000; 2000US-0246475P.
PR	14-JUL-2000; 2000US-0218290P.	PR	08-NOV-2000; 2000US-0246477P.
PR	26-JUL-2000; 2000US-0220963P.	PR	08-NOV-2000; 2000US-0246477P.
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PR	14-AUG-2000; 2000US-0225270P.	PR	08-NOV-2000; 2000US-0246532P.
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PR	14-AUG-2000; 2000US-0225758P.	PR	08-NOV-2000; 2000US-0246611P.
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PR	22-AUG-2000; 2000US-0226688P.	PR	17-NOV-2000; 2000US-0249209P.
PR	23-AUG-2000; 2000US-0227009P.	PR	17-NOV-2000; 2000US-0249210P.
PR	30-AUG-2000; 2000US-0228924P.	PR	17-NOV-2000; 2000US-0249211P.
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PR	01-SEP-2000; 2000US-0229343P.	PR	17-NOV-2000; 2000US-0249213P.
PR	01-SEP-2000; 2000US-0229344P.	PR	17-NOV-2000; 2000US-0249214P.
PR	01-SEP-2000; 2000US-0229345P.	PR	17-NOV-2000; 2000US-0249215P.
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PR	05-SEP-2000; 2000US-0229513P.	PR	17-NOV-2000; 2000US-0249217P.
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PR	06-SEP-2000; 2000US-0230438P.	PR	17-NOV-2000; 2000US-0249244P.
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PR	08-SEP-2000; 2000US-0232081P.	PR	01-DEC-2000; 2000US-0250160P.
PR	12-SEP-2000; 2000US-0231968P.	PR	01-DEC-2000; 2000US-0250391P.
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PR	14-SEP-2000; 2000US-0232399P.	PR	05-DEC-2000; 2000US-0256719P.
PR	14-SEP-2000; 2000US-0232400P.	PR	06-DEC-2000; 2000US-0251479P.
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PR	14-SEP-2000; 2000US-0233063P.	PR	08-DEC-2000; 2000US-0251869P.
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PR	21-SEP-2000; 2000US-0234223P.		

PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Baraesh SC, Ruben SM;
XX
XX WPI; 2001-451937/48.
DR
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including musculoskeletal
PT cancers and also for testing and detection e.g. diagnosis.
XX
XX
PS Example 2; SEQ ID NO 3189; 781pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AAL3666-AAL3766) and proteins
CC (AAB03087-AAB04109) associated with the musculoskeletal system useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. The genes are isolated from a range of human tissues
CC disclosed in the specification. The nucleic acids, proteins, antibodies
CC and (ant)agonists are useful in the diagnosis, treatment and prevention
CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.
CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
CC bacterial, fungal and parasitic infections. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
Query Match 9.2%; Score 146.8; DB 4; Length 7739;
Best Local Similarity 77.5%; Pred. No. 2.4e-21;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;
QY 2 CCTGTAAATTCAGTCTGTGAGAGTCCGAGGTCAGAGAGTCTGTGAGCCAGAGTTCA 61
DB 5631 CCTATATATCCCAACACTTGTGGAGGCCGAGGTGGAGAGATGGCTTGAGTCAGATGTTCA 5512
QY 62 AGAGCAGCCTTGAGCAACACAGGAGGA-CCTGTCACTCAAAAGATAATTAATTAGCCAG 120
DB 5571 AGACCACTCTGGGCAACATAGGAGACCTGACTCTCAATATATTTAAAAATTCGCTGG 5512
QY 121 GCTTAGTGGTCACTCCTGTGTGTCCTCAGACTACTAGGAGGAGAGAGTATCCCTT 176
DB 5511 GTGTAGTGGACATACCTGTGTGTCCTCAGCTAGTGTGGAGGCCAGAGAGATCCCTT 5452
QY 177 TGTCCAGAGAGTCAAGACTGCACTGAGCTGAGACCCAGCCACTGCAATTCAGCCCTGG 236
DB 5451 GAGCCCAAGAGGTCAAGGCTGCAATGAGCTGCAATCTTGGCA-CTGCATCTCAGACCTGG 5393
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAATAAGTTAATA 276
DB 5392 CAACAGACTGAGACCTGTCTCAAAAAACAAAAA 5353
RESULT 12
ABX59812/C
ID ABX59812 standard; cDNA: 7739 BP.
XX
XX ABX59812;
AC
XX
XX 26-FEB-2003 (first entry)
DT
XX
XX cDNA encoding novel human musculoskeletal system antigen #2156.
DE
XX
XX Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KM re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KM

KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height; weight;
KW hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
XX Homo sapiens.
OS
XX
XX US2002147140-A1.
PN
XX
XX 10-OCT-2002.
PD
XX
XX 17-JAN-2001; 2001US-00764877.
PF
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
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PR 11-JUL-2000; 2000US-0217496P.
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PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
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PR 14-AUG-2000; 2000US-0225757P.
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PR 22-AUG-2000; 2000US-0226888P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.
PA (RUBEN/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-128199/12.
DR
XX
XX Isolated nucleic acid molecules encoding musculoskeletal system
PT associated polypeptides, useful for detecting disorders, e.g. cancer.
XX
XX Disclosure; SEQ ID NO 3189; 321pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals or
CC humans. The nucleic acid: stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-
CC related complex; stimulates chondrocyte growth, thus they can be used to
CC enhance bone and periodontal regeneration and aid in tissue transports or
CC bone grafts; prevents skin aging due to sunburn by stimulating
CC keratinocyte growth; prevents hair loss, since FGF family members
CC activate hair-forming cells and promotes melanocyte growth; stimulates
CC growth and differentiation of hematopoietic cells and bone marrow cells
CC when used in combination with other cytokines; maintains organs before
CC transplantation or for supporting cell culture of primary tissues;
CC induces tissue of mesodermal origin to differentiate in early embryos;
CC increases or decreases the differentiation or proliferation of embryonic
CC stem cells, besides, haematopoietic lineage; modulates mammalian
CC characteristics, such as, body height, weight, hair colour, eye colour,
CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
CC cosmetic surgery); modulates mammalian metabolism; changes mammal's metal
CC state or physical state by influencing biorhythm, circadian rhythms,
CC depression, tendency for violence, tolerance for pain, reproductive
CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or
CC stress; increases or decreases storage capabilities, fat content, lipid,
CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components. This sequence encodes a novel human musculoskeletal system
CC antigen. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspso.gov/sequence.html?DocID=20020147140
XX
XX
SQ Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
Query Match 9.24; Score 146.8; DB 8; Length 7739;
Best Local Similarity 77.54; Pred. No. 2.4e-21;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;
QY 2 CCTGTATTCCAGTACTGTGAGAGTCCGAGGTACGAGAGCTGTTGAGCCAGAGTTCA 61
DB 5631 CCTATATCCCAACACTTTGGAGGCCGAGGTGGAGAGATGCGCTTGAGTCCAGATGTCA 5572
QY 62 AGAGCAGCTTGACACACACAGGGAGA CCTGTCACTCAAAAGAAATTAATTAATAGCAG 120
DB 5571 AGACACGCTGGGCAACATGAGGAGACCTGACCTCAATATTAATTTAAAAATTCGCTGG 5512
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DB 5511 GTGTAGTGACATACCTGTGTGTCGAGCTAGTTGGAGAGCCAGGACGAGATCGCTT 5452
QY 177 TGTCCAGAGAGTCAAGACTGCACTGAGTGAAGCCAGCAGCTGATTCAGCCCTGG 236
DB 5451 GAGCCAGAGAGTCAAGAGCTGCAATGAGTCAATCTTGCA-CTGACATCCAGCCTGG 5393
QY 237 CAACAAAAGAGACCTGTCTCAAAAATAATTAATAA 276

DB 5392 CAACAGACTGAGACCTGTCTCAAAAACAAAACAAA 5353
RESULT 13
ADJ30562/C
ID ADJ30562 standard; DNA; 7739 BP.
XX
XX ADJ30562;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human musculoskeletal system-associated genomic DNA - SEQ ID 3189.
XX
XX musculoskeletal system; cytosolic; osteopathic; cancer; osteoporosis;
KW gene therapy; vaccine; human; ds.
XX
XX Homo sapiens.
XX
XX US2004009488-A1.
XX
XX 15-JAN-2004.
XX
XX 13-SEP-2002; 2002US-00242515.
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XX 31-JAN-2000; 2000US-0179065P.
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XX 04-FEB-2000; 2000US-0180628P.
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XX 24-FEB-2000; 2000US-0184664P.
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XX 02-MAR-2000; 2000US-0186350P.
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XX 16-MAR-2000; 2000US-0189874P.
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XX 19-MAY-2000; 2000US-0205515P.
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XX 01-SEP-2000; 2000US-0229345P.
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XX 05-SEP-2000; 2000US-0229509P.
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XX 05-SEP-2000; 2000US-0229513P.
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XX 06-SEP-2000; 2000US-0230437P.
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XX 06-SEP-2000; 2000US-0230438P.
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XX 08-SEP-2000; 2000US-0231243P.
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XX 08-SEP-2000; 2000US-0231244P.
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XX 08-SEP-2000; 2000US-0231413P.
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XX 08-SEP-2000; 2000US-0231414P.

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PR 08-SEP-2000; 2000US-0232080P.
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PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234224P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
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PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
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PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246533P.
PR 08-NOV-2000; 2000US-0246534P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.

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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI
XX WPI; 2004-090458/09.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX
XX Disclosure; SEQ ID NO 3189; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytoskeletal and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated genomic DNA of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC http://seqdata.uspto.gov/sequence.html?DocID=20040009488.
XX
XX Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
SQ

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Query Match 9.2%; Score 146.8; DB 12; Length 7739;
Best Local Similarity 77.5%; Pred. No. 2.4e-21;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;

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QY 2 CCTGTATTTCCAGTACTGTGAGAGTCCAGAGTCTGTTAGCGCAGAGTTCA 61
DB 5631 CCTATATCCCAACACTTTGGAGGCCGAGGTGGAGATGCTTGTCAGTAGTTCA 5572
QY 62 AGAGCAGCCTGAGCAACACAGGAGGA-CCTGTCACTCAAGAATAATAATTAGCCAG 120
DB 5571 AGACCAAGCTGGGCAATATGGAGAGACCTGACTTCAATTAATTTAAAAATTCGCTGG 5512
QY 121 GCTTAGTGCTCACTCCCTGTGTGCCAGTACTAGGAGGCAAGTAGGA---CTGCT 176
DB 5511 GTGATGTGGCAATACCTGTGTGCCAGTACTAGGAGGCAAGGAGATGCTT 5452
QY 177 TGTCCAGAGGTCAGACCTGCACTGAGTGAACACCAAGCACTGATTCAGCCCTGG 236
DB 5451 GAGCCAGAGGTCAGAGGCTGCAATGATGCAATCTTGCA-CTGCATTCAGCCCTGG 5393
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAAATAATTAATAA 276
DB 5392 CAACAGACTGAGACCTGTCTCAAAAAAACAACAAAA 5353

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RESULT 14
AAD58279
ID AAD58279 standard; DNA; 226475 BP.
XX AAD58279;
AC
XX 20-NOV-2003 (first entry)
DT

XX	Human tumour suppressor gene, lmt reverse complement DNA.
XX	Tumour suppressor gene, lmt; cancer; therapy; cyrostatic; human; ds.
XX	Homo sapiens.
XX	MO200306869-A1.
XX	14-AUG-2003.
XX	07-FEB-2003; 2003WO-AU000126.
XX	07-FEB-2002; 2002AU-00000371.
XX	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX	Cook WD, Mccaw BJ;
XX	WPI; 2003-646311/61.
XX	New nucleic acid molecule, useful for screening a subject for the presence of an aberration in a gene encoding an lmt.
XX	Claim 10; Page 233-299; 373pp; English.
XX	The invention relates to novel tumour suppressor gene, referred to as lmt. The invention also relates to the field of cancer therapy and cancer diagnostics. The nucleic acid molecule is useful for screening a subject for the presence of an aberration in a gene encoding an lmt. The present sequence is human lmt reverse complement DNA
XX	Sequence 226475 BP; 61024 A; 41761 C; 40916 G; 57494 T; 0 U; 25280 Other;
XX	Query Match 9.2%; Score 146.8; DB 9; Length 226475;
XX	Best Local Similarity 74.1%; Pred. No. 6.4e-21;
XX	Matches 212; Conservative 0; Mismatches 72; Indels 2; Gaps 2;
QY	2 CCTGTAAATTCAGTACTGTGAAGTCCGAGGTCAGAGGACTGCTTGAGGCCAGAGTTCA 61
DB	41614 CCTGTAATCCAGACATTTGGAGGCCGAGGCCGTGTGATCACTTGAGGTCAAGAGTTG 41673
QY	62 AGAGAGGCTGGAACAACAAGGAGGAGCTGTGACTTAAGAAATTAATAATTAAGGCAG 121
DB	41674 AGACGAGCTGGCCGACATGGCAACACGTTTACTTAATAATTAATAATTAATGACAG 41733
QY	122 CTTATGAGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGGAGAGTAGAGACTGCTTG-TC 180
DB	41734 CACAGTGTGACACACTGTATATCCAGCTATTTAGGAGGCTGAGGAGCAACTGCTTGAAC 41793
QY	181 CCAGAGGTCAGACCTGAGCTGAGCTGAGACCCAGCACCCTGATTCACGCTGGGCAC 240
DB	41794 CTGGAGAGCGGAGGTTGACATGAGACTGATCATGACA-CTGCACCTCCAGCCTGGGTGAC 41852
QY	241 AAAAAGAGACCTGTCTCAAAAATTAAGTTAAATTAATAATAATA 286
DB	41853 AGAGCAAGACTGTGCTCAAAAAAATTAATAAAAAAAGAAATTA 41898
XX	RESULT 15
XX	ADL13819
XX	ID ADL13819 standard; DNA; 41150 BP.
XX	XX ADL13819;
XX	DT 06-MAY-2004 (first entry)
XX	DE Osteoarthritis-associated polymorphic nucleotide #351.
XX	ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
XX	joint space narrowing; osteophyte development; joint pain;
XX	osteoarthritis; SNP; single nucleotide polymorphism.

[illegible]

Tue Jun 6 12:04:07 2006

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 ; Search time 11100.1 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_1857

Perfect score: 1603

Sequence: 1 acctgaattccagctactgtc.....cgctgtctagaacgcgtcct 1603

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593.2	37.0	941	2	BG720951 602692616
2	303	18.9	314	1	AA903751 0K64C05.8
3	150.8	9.4	836	13	CZ458737 MCF746k19
4	146.4	9.2	1033	3	BM556801 AGENCOURT
5	146.4	9.1	315	1	A1961957 wt40904.x
6	146.4	9.1	592	4	BX486310 DKFZP686B
7	145.2	9.1	554	11	AO784105 HS 3250.A
8	143.8	9.0	675	11	AO313572 RRC11-10
9	143.6	9.0	444	11	AQ088791 HS 3002.A
10	143.6	9.0	721	8	CR773238 DKFZP470D
11	143.4	8.9	417	11	AQ215619 HS 3217.B
12	143.4	8.9	454	9	DB322788 DB322788
13	143.4	8.9	551	4	BX487140 DKFZP686G
14	142.8	8.9	2821	6	BC029972 Homo sapi
15	142.6	8.9	746	14	AG014790 Homo sapi
16	142	8.9	916	8	CR980253 CR980253
17	141.8	8.8	444	7	BE349022 ht48a11.x
18	141.8	8.8	641	3	BM555373 AGENCOURT
19	141.8	8.8	809	12	BZ603262 WHAARF45TF

C 20	141.8	8.8	1792	6	CR602256	CR602256 full-length
C 21	141.8	8.8	1941	6	CR616604	CR616604 full-length
C 22	141.4	8.8	751	12	BZ606730	BZ606730 WHAARF11TR
C 23	141.2	8.8	483	10	W45205	W45205 zc24f10.r1
C 24	141.2	8.8	558	11	AQ480483	AQ480483 RBC1-11-2
C 25	141	8.8	408	7	BE138484	BE138484 xr75h02.x
C 26	141	8.8	749	14	AG014791	AG014791 Homo sapi
C 27	141	8.8	1295	2	BG432839	BG432839 602496047
C 28	140.8	8.8	374	4	BX954311	BX954311 DKFZP781A
C 29	140.8	8.8	561	9	DB358919	DB358919 DB358919
C 30	140.8	8.8	4833	6	CR936701	CR936701 Homo sapi
C 31	140.6	8.8	400	11	AQ007744	AQ007744 CTT-HSP-2
C 32	140.2	8.7	589	9	DB382632	DB382632 DB382632
C 33	140.2	8.7	647	7	BB883545	BB883545 BB883545
C 34	140.2	8.7	750	14	AG015272	AG015272 Homo sapi
C 35	140.2	8.7	2149	6	CR936757	CR936757 Homo sapi
C 36	139.8	8.7	470	4	CD102612	CD102612 AGENCOURT
C 37	139.8	8.7	606	13	CZ465897	CZ465897 MCF75111
C 38	139.8	8.7	705	14	AG013775	AG013775 Homo sapi
C 39	139.8	8.7	723	14	DX360777	DX360777 MGOQ.CH25
C 40	139.6	8.7	547	9	DA315473	DA315473 MGOQ.CH25
C 41	139.6	8.7	821	13	CZ449889	CZ449889 MCF730923
C 42	139.4	8.7	721	9	DA571947	DA571947 DA571947
C 43	139.2	8.7	500	1	AL712995	AL712995 DKFZP686K
C 44	139.2	8.7	510	7	AW949355	AW949355 EST361425
C 45	139.2	8.7	556	3	BU664577	BU664577 cl11b11.

ALIGNMENTS

RESULT 1
BG720951/c
LOCUS
DEFINITION
602692616P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825178 5', mRNA sequence.
ACCESSION
BG720951
VERSION
BG720951.1 GI:14000138
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 941)
NIH-MGC <http://mgc.nci.nih.gov/>, National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: L1AM10737 row: 0 column: 03
High quality sequence stop: 666.
location/Qualifiers
1. 941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4825178"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+), Site_1: BamHI, Site_2: SalI-xhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTAAVN-3', size-selected for average insert size 2.2 kb and normalized to ROP 5. This is a

ORIGIN

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 37.0%; Score 593.2; DB 2; Length 941;
Best Local Similarity 95.3%; Pred. No. 1.5e-94;
Matches 667; Conservative 0; Mismatches 23; Indels 10; Gaps 5;

509 TGTTCCTCAGCATCTCAGACAAATTTGCCAGGCTCTCCGAAATGACAGGACAG 568
702 TGTTCCTCAGCATCTCAGACAAATTTGCCAGGCTCTCCGAAATGACAGGACAG 644
569 AGCTCAGGCGAAAGTAGAGAACTGGCGAGGAGAGACTCAGAGTCCCAAAAAAAT 628
643 AGCTCAGGCGCGAAAGTAGAGAACTGGCGAGGAGAGACTCAGAGTCCCAAAAAAAT 584
629 TATATC---TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 684
583 TATATCAGTTCGAGTGGTGTGTTCTGTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 524
685 TCTTTCT 740
523 TCTTTCT 464
741 TGGCAAGATCTCTCATGAGCAAAATATATGCTGCTTGAATCTTCTTCCAGGCTCT 800
463 TGGCAAGATCTCTCATGAGCAAAATATATGCTGCTTGAATCTTCTTCCAGGCTCT 404
801 GCCAGAGACCATGCGCTCGCGGTCTTTCTTTCCGCTATAA--TTATCAGAGCCATCC 859
403 GCCAGAGACCATGCGCTCGCGGTCTTTCTTTCCGCTATAA--TTATCAGAGCCATCC 344
860 GCTCTGATCCCTCAGCTGTTCCCTGCAATCCCTTCTGCTGCTGCTGCTGCTGCTG 919
343 GCTCTGATCCCTCAGCTGTTCCCTGCAATCCCTTCTGCTGCTGCTGCTGCTGCTG 284
920 CCGGCGGACCAAGGCTGTAAGTGTGTAATATCAGGAATGACTGAAGCTTTTGGGAC 979
283 CCGGCGGACCAAGGCTGTAAGTGTGTAATATCAGGAATGACTGAAGCTTTTGGGAC 224
980 TCGGTTCTCTATGTAATGAGGTTAATACAGGCTTCTTCTACTCCCAAGCGAC 1039
223 TCGGTTCTCTATGTAATGAGGTTAATACAGGCTTCTTCTACTCCCAAGCGAC 164
1040 GTGTTTGTCCCGGCGAGGCGCCCAATGTTGCTGTTCAAGCATCAGTTAACCCACAG 1099
163 GTGTTTGTCCCGGCGAGGCGCCCAATGTTGCTGTTCAAGCATCAGTTAACCCACAG 104
1100 GACGGGTCAGCAATTAAGAGCGAACAGGCGCGGTCATCTCTGACGCTTTTTCAT 1159
103 GACGGGTCAGCAATTAAGAGCGAACAGGCGCGGTCATCTCTGACGCTTTTTCAT 44
1160 CCCAGGCTGAGACAGGAGCTGGGCTGGGCGCGCTCTGC 1199
43 CCCAGGCTGAGACAGGAGCTGGGCTGGGCGCGCTCTGC 4

RESULT 2
AA903751 314 bp mRNA linear EST 09-JUN-1998
LOCUS 064605.81 NCI CGAP GC4 Homo sapiens cDNA IMAGE:1518728 3'
DEFINITION similar to gb:K17360_rnal HOMEOBOX PROTEIN HOX-D4 (HUMAN);, mRNA
sequence.
ACCESSION AA903751 GI:3038874
VERSION AA903751.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Bukariyote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
1 (bases 1 to 314)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNT at:
www.bio.11nl.gov/bdrp/image/image.html
Insert length: 521 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amerisham
High quality sequence stop: 297.
Location/Qualifiers
1. 314
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1518728"
/feature_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: pTZ19-3-Pac1; 1st strand cDNA was prepared
from 3 pooled germ cell tumors, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTZ19 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES

source

ORIGIN

Query Match 18.9%; Score 303; DB 1; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.1e-43;
Matches 314; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

653 TTCTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 712
1 TTCTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
713 TTCTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 772
61 TTCTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
773 CTTGACTTCTGTTTCCAGCTGCTTCTGCGAGGACCATGCGTGGCGTGTCTTTCTTT 832
121 CTTGACTTCTGTTTCCAGCTGCTTCTGCGAGGACCATGCGTGGCGTGTCTTTCTTT 180
833 CCGCTATATTAATTCAGGCGCCATCCAGCTGCTGCTCCCTCACTGTTCCCTGGCAGTCC 892
181 CCGCTATATTAATTCAGGCGCCATCCAGCTGCTGCTCCCTCACTGTTCCCTGGCAGTCC 240
893 CTTCTGCTGGTGAACAACATATAGCGCGCGCTGACAGAGGTGAAGTGTGAATATC 952
241 CTTCTGCTGGTGAACAACATATAGCGCGCG CTGACAGAGGTGAAGTGTGAATATC 299

953 AGGAAGATGACTGAA 967
300 AGGAAGATGACTGAA 314

RESULT 3
CZ458737 836 bp DNA linear GSS 20-OCT-2005
LOCUS MCF746K19TF Human MCF7 breast cancer cell line library (MCF7.1)
DEFINITION Homo sapiens genomic clone MCF7_46K19, genomic survey sequence.
ACCESSION CZ458737 GI:77936089

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 836)
Volk,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brehner,J.H., Bajarewicz,K., Paris,P., Tao,Q., Kowal,D., Lapuk,A.V., Kuo,W.-L., Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Yan,F.-C., de Jong,P., Peyzner,P. and Collins,C.
Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project
Unpublished (2005)
CONTACT: Volk SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Classes: BAC ends.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/note="Vector: pECRAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN

Query Match 9.4%; Score 150.8; DB 13; Length 836;
Best Local Similarity 73.7%; Pred. No. 2e-16;
Matches 233; Conservative 0; Mismatches 77; Indels 6; Gaps 3;

QY 1 ACCGTGAATTCAGTCTGAGAGCCGAGTCAAGAGCACTGTTGAGGCGAGAGTTC 60
DB 158 ACTGTAAATCCAGCACTTTGGAGGCTGAGGAGAGATCCCTTGAATCCAGAGATT 217
QY 61 AAGAGAGCCTGAGCAACAAGAGAGA-CCTGTCACTACAAAGATTAATTAATTAAGCA 119
DB 218 GAGACAGCCTGGTCAACATAGGAGACCTGTCTCTACAGTAATTTAAATTTAGCTG 277
QY 120 GGTTAAGTGGCTATCCCTGTGTGTCCAGTACTAGGAGAGGAGAAAGTAGGA----CTGC 175
DB 278 GGGCTGTGTGTGACACCTGTGTGTCCAGTACTTGGAGGCTGAAGCAGAGAAATCAT 337
QY 176 TTGTCCAGAGAGGTCAAGACTGAGTGAAGCCAGCCAGCTGCATTTCCAGGCTGG 235
DB 338 TGAACCCAGAGAGTTAAGGCTGAGTGAAGCCGAGATTTGCCCA-CTACACTCCAGGCTGG 396
QY 236 GCAACAAAAAGAGACCTGTCTCAAAAAAATTAAGTTAATTAATTAATTAATTAAGTT 295
DB 397 GTGACAGAGTGAAGAACCTGTCTCAAAAAAAGAAAAAGTAATTAATTAATTAAGTT 456
QY 296 TAAACCTTAACCAT 311
DB 457 CAATCTCTTAATTCAT 472

RESULT 4
BMS56801/c 1033 bp mRNA linear EST 20-FEB-2002
LOCUS BMS56801/c
DEFINITION AGENCOURT_6540722 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737964

ACCESSION 5', mRNA sequence.
VERSION BMS56801 GI:18798321
KEYWORDS BMS56801.1
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1033)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: L1AM12748 row: 0 column: 21
High quality sequence stop: 606.

FEATURES
source
Location/Qualifiers
1..1033
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737964"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

ORIGIN

Query Match 9.2%; Score 146.8; DB 3; Length 1033;
Best Local Similarity 77.5%; Pred. No. 9.7e-16;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;

QY 2 CCTGTAAATCCAGTACTGTGAGAGTCCGAGTCAAGAGCACTGTTGAGGCGAGAGTTCA 61
DB 316 CTTATATATCCCAACACTTTGGAGGCTGAGGTGGAGAGATGCTTGAATCAAGTAGTTCA 257
QY 62 AGAGCAGCCTGAGCAACAAGAGAGA-CCTGTCACTACAAAGATTAATTAATTAAGCAG 120
DB 256 AGACAGCCTGGGCAACATAGGAGACCTGACTTAACAATTAATTTAAATTTAGCTGG 197
QY 121 GCTTAAGTGGCTATCCCTGTGTGTCCAGTACTAGGAGGAGCAAGTAGGA----CTGCT 176
DB 196 GTGTAGTGCACATTAACCTGTGTGTCCAGTACTAGTGGAGGCCAGAGCAGAGATCGCTT 137
QY 177 TTGTCCAGAGAGGTCAAGACTGAGTGAAGCCAGCCAGCTGCATTTCCAGGCTGG 236
DB 136 GAGCCAGAGAGTCAAGGCTGCAATGAGCTGCAATTTGCA-CTGCACTCCAGCTGGG 78
QY 237 CACAAAAAGAGACCTGTCTCAAAAAAATTAAGTTAATTA 276
DB 77 CAACAGACCGAGACCTGTCTCAAAAAACAAAAACAAAA 38

RESULT 5
A1961957/c 315 bp mRNA linear EST 09-MAR-2000
LOCUS A1961957
DEFINITION wt40904.x1 NCI CGAP Paul Homo sapiens cDNA clone IMAGE:2509974 3'
similar to contains Alu repetitive element, mRNA sequence.
ACCESSION A1961957
VERSION A1961957.1 GI:5754659
KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE AUTHORS	1 (bases 1 to 315) NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
COMMENT	Life Technologies catalog #: 11548-013 DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW at: www-bio.lnl.gov/bbrp/image/image.html Insert length: 1397 Std Error: 0.00 Seq primer: -40up from Glocbo High quality sequence stop: 314. Location/Qualifiers 1..315
FEATURES	

Query Match	146.4;	DB 1,	length 315;
Best Local Similarity	74.6%;		
Matches 212; Conservative	0;	Mismatches 66;	Indels 6; Gaps 2;

QY	2	CCTGTAATTCAGACTCTGTGAGAGTCCAGAGTCAGAGCTTGAAGCCAGAGATTCA	61
Db	284	CCTGTAATTCAGACTCTTGGAGGCCAGAGCAGAAAGATTGCTTGAATCCAGAGATTG	225
QY	62	AGAGCAGCCTTGACAACACAGGAGACC---TGTCACTACAAAGATTAAATTATGACC	118
Db	224	AGACTAGCCTGTGGCAACATAGTAGAACCTCATCTCTACAAAAAAATGAAACAAATTATGCC	165
QY	119	AGGCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGGAGGCAAGT---AGGACTGC	175
Db	164	GCGCGTGTGTGTCATGCTCTGTATGTTCCAGCTACTGGGGAGACTGAGGTGGAGGATTTGC	105
QY	176	TTGTCCACGAGAGTCAAGCTGCACTGAGCTGAGACCCAGCCACTTGATTTCAAGCTGG	235
Db	104	TGACCTCGGTGTGTAAGGCTGCACTGAGCTAGATTCATGCCAATGCACTTCACGCTTAA	45
QY	236	GGAACAAAAAGAGACCTGTCTCAAAAAAATAAGTTAAATTAATA	279
Db	44	GGAACAGCAAGACCCCTGTCTCAAAAAAATAAAAAAAA	1

RESULT 6	592 bp	linear	EST 04-SEP-2001
LOCUS	BX486310		
DEFINITION	DKEPDB68B08251_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone		
ACCESSION	DKEPDB68B08251 5', mRNA sequence.		
VERSION	BX486310		
KEYWORDS	BX486310.1 GI:31949871		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		

REFERENCE	1 (bases 1 to 592)
AUTHORS	Anorge, W., Krieger, S., Regier, T., Rittmüller, C., Schwager, B., Memes, H.W., Well, B., Amlid, C., Osanger, A., Fobo, G., Han, M. and Wieman, S.
TITLE	EST (Anorge, W., Krieger, S., Regier, T., Rittmüller, C., et al.)
JOURNAL	Unpublished (2003)
COMMENT	Contact: MIPS

FEATURES

SOURCE

```

/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="DKFZp686B0825.1"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="686 (synonym: hicc)"
/vector="pTriplex2; site_1: SfilA, site_2: SfilB
cdna_collection"

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ORIGIN

Query Match	9.1%	Score 146.4	DB 4	Length 592
Best Local Similarity	74.3%	Pred. No. 1.2e-15		
Matches 211	Conservative 0	Mismatches 71	Indels 2	Gaps 2

QY	1	ACCTGTAATTCACAGTACGTGAGAGTCCGAGAGTCAGAGGACTGCTGAGGGCAGAGAGTTC	60
Db	287	ACCTGTAATTCACAGACTTTTGAGAGGCTGAGGACAGTGGATCACTTGAGTCCAGAGATTC	228
QY	61	AAGAGCAGCCTTGACAAACACAGGGAGACTT-GTCACTACAAAGATAATTAATTAGCCA	119
Db	227	GAGACACAGCCTGGGCAACATAGTAGCACCTCATCTCTCAAAAAATATACAAAAATTAGCCA	168
QY	120	GGCTTAGAGGTACTCCCTGTGGTCCGACGTACTAGAGGAGGACAGAAAGTAGAGACTGTCTGT	179
Db	167	GCTGTGGTGGGACAGCCTGTGATGTTCTTAGCTACTCGGAGACTCAGGTGGATCACTTGAG	108
QY	180	CCAGAGAGTCAAGACTGTGACAGTGAAGCTGAGCCAGCCACTGCATTCCAGCTTGGGCAA	239
Db	107	CCCGGAGAGAGAGGTTACAGTGAAGCTAGATCGTACCA-CTGCACCTCAGCCTGGGCAA	49
QY	240	CAAAAGAGACCTGTCTCAAAAAAATAAGTTAAATTAATTAATA	283
Db	48	CAGAGTAGACCTGTCTCAAGAGAAAAAATTAATTAATA	5

RESULT 7	
AQ784105	
LOCUS	AQ784105 554 bp DNA linear GSS 03-AUG-1999
DEFINITION	HS_3250_A2_H10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3250 Col=20 Row=O, genomic survey sequence.
ACCESSION	AQ784105
VERSION	AQ784105.1 GI:5691729
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Chordata; Craniota; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Euarcharia; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 554)
AUTHORS	Mahaitas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

TITLE Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
COMMENT Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
CONTACT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 3250 row: 0 column: 20
Seq primer: T7
Class: BAC ends
High quality sequence stop: 554.

FEATURES
source

Location/Qualifiers
1. .554
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=3250 Col=20 Row=0"
/sex="male"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC clones in E-Coli DH10B"

ORIGIN

Query Match 9.1%; Score 145.2; DB 11; Length 554;
Best Local Similarity 74.3%; Pred. No. 2.1e-15;
Matches 211; Conservative 0; Mismatches 68; Indels 5; Gaps 2;
QY 2 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGTGAGGCCAGAGTTCA 61
140 CTTATATTTAGACACTTTGGAGGCGGAGGTGGCGAGTACTTGAAGTCAGAGTTCA 199
QY 62 AGAGCAGCTTGACACACAGGAGGAGCTGTCTACTACAAAGATTAATTAATTTAGCCAG 121
200 AGACGAGCTTGACACACAGGAGGAGCTGTCTACTACAAAGATTAATTAATTTAGCCAG 259
QY 122 CTGATGAGCTCATCCCTGTGCTCCAGCTACTAGGAGGAGGAGGAGGAGGAGGAGGAGG 179
260 TGTGTGTGCACTGCTGTATTCCTCACTCTCACTGAGGAGGAGGAGGAGGAGGAGGAGG 319
QY 180 --CCAGAGAGTCAAGCTGCAAGTGAAGTGAAGCCAGCACTGCACTTCAGGCTGGC 237
320 AACCCAGAGTGGAGGCTGCAATGAGCTGAGATTTGGCA-CTGCACTCCAGCTGGGT 378
QY 238 AACAAAAGAGACCTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 281
379 GATTAAGCGAGACCTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 422
DB

RESULT 8 AQ13572/c 675 bp DNA linear GSS 04-MAY-1999
LOCUS RPC11-101F17.TV RPC1-11 Homo sapiens genomic clone RPC1-11-101F17,
DEFINITION genomic survey sequence.
ACCESSION AQ13572
VERSION AQ13572.1 GI:4045035
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 675)
REFERENCE Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K.,
AUTHORS Berry, K., Granger, D., Suh, E., White, C., de Jong, P. and Venter, J.C.
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building

JOURNAL Unpublished (1998)
COMMENT Other GSSs: RPC11-101F17.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@igr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.igr.org/tcd/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1. .675
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7538536"
/db_xref="taxon:9606"
/clone="RPC1-11-101F17"
/sex="male"
/cell_type="Lymphocytes"
/clone_1lb="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC library"

ORIGIN

Query Match 9.0%; Score 143.8; DB 11; Length 675;
Best Local Similarity 69.8%; Pred. No. 3.5e-15;
Matches 238; Conservative 0; Mismatches 97; Indels 6; Gaps 3;
QY 1 ACCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGTGAGGCCAGAGTTTC 60
444 ACCTGTATTCAGTACTGTGAGAGGCGGAGGTCAGAGTGTGATCACTGAGTCAGAGATTTC 385
QY 61 AAGAGCAGCTTGACACACAGGAGGAG-CTGTCTACTACAAAGATTAATTAATTAATTAATTA 119
384 AAGATCAGCTTGACACACAGGAGGAG-CTGTCTACTACAAAGATTAATTAATTAATTAATTA 325
QY 120 GGTATGAGCTCATCCCTGTGCTCCAGCTACTAGGAGGAGGAGGAGGAGGAGGAGGAGG 175
324 GGCATGTGTGCACTGCTGTATTCCTCACTCTCACTGAGGAGGAGGAGGAGGAGGAGGAGG 265
QY 176 TTGTCCAGAGGTCAGAGTGAAGTGAAGCCAGCACTGCACTTCAGGCTGG 235
264 TGAATCCAGAGGCGGAGGTTGCAGTGAGCCAGAGTGTGCA-CTGCACTCCAGCTGG 206
QY 236 GCAACAAAAGAGACCTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 295
205 GTGACAAAAGTGAATTTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 146
QY 296 TAAACCTTAACACATCTCTTTTCAAGAGAGCTCTTA 336
145 CTATACCTTCTTCTCATCTTACTTGAGATGATCAATTA 105
DB

RESULT 9 AQ088791/c 444 bp DNA linear GSS 26-AUG-1998
LOCUS HS_3002_A1_F05_MF CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey
sequence.
ACCESSION AQ088791
VERSION AQ088791.1 GI:3457702
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 444)
AUTHORS Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GQ, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3002 row: K column: 9
Class: BAC ends
High quality sequence stop: 444.
Location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3002 Col=9 Row=K"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 9.0%; Score 143.6; DB 11; Length 444;
Best Local Similarity 70.3%; Pred. No. 4.1e-15;
Matches 222; Conservative 0; Mismatches 89; Indels 5; Gaps 2;
QY 3 CTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGTTGAGCCAGAGATTCAA 62
DB 335 CTGTAAATTCAGAGACTTTGGAGGCTGAGCGGGTGGATCTCTGAGCTCAGAGATTCAA 276
QY 63 GAGACAGCTGGAGACAACAGGAGAGACCTGTCACTACAAAGATTAAATTAGCCAGC 122
DB 275 GACTAGCTGGCTTAACATGGTGAACCTGTCTACTAAATAACAAATTAAGCCAGGC 216
QY 123 TTAGTGGCTCATCTCTGTGTGCTCCAGCTACTAGGAGGAGAGAGTGA-----CTGCTTG 178
DB 215 GTGTGGACATATCTCTATATCCAGCTCTTTGGAGGCTGAGGAGAGATGCTTGA 156
QY 179 TCCAGAGAGTCAAGACTGAGTGAAGTGAACCCAGCCACTGCACTTCAGGCTTGAGCA 238
DB 155 GCTTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 97
QY 239 ACGAAAAAGAGACCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAATAAGTTAA 258
DB 96 ACGAGCGCAGACATGTTCAAAAAATAATAATAATAATAATAATAATAATAATAATAATA 37
QY 299 ACCCTAAACACATCTT 314
DB 36 GGCTGAGAAAAGTCTGT 21

RESULT 10
LOCUS CR773238 721 bp mRNA linear EST 23-SRP-2004
DEFINITION DKFZp470D2113_r1_470 (synonym: pliv1) Pongo pygmaeus cDNA clone
ACCESSION CR773238
VERSION CR773238.1 GI:52616511
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 721)
AUTHORS Ottenwelder,B., Obermaier,B., Deutschenbauer,S., Schallp,A., Mewes,H.W., Weill,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE Pongo pygmaeus mRNA (Ottenwelder,B., Obermaier,B., Deutschenbauer,S., et al.)
JOURNAL Unpublished (2004)
PUBMED
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp470D2113) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneId=DKFZp470D2113
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

ORIGIN
Query Match 9.0%; Score 143.6; DB 8; Length 721;
Best Local Similarity 71.9%; Pred. No. 3.8e-15;
Matches 230; Conservative 0; Mismatches 84; Indels 6; Gaps 3;
QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGTTGAGCCAGAGTTCA 61
DB 95 CTGTACTCTCCAGACATTTGGAGGCGCAAGGCAAGTGATCACTGAGGTCAAGAGTTCA 154
QY 62 AGAGCAGCTGGAGACAACAGGAGAG--CTGTACTCAAAAGATTAAATTAGCCAG 120
DB 155 AGAGTACCTGGGCAACATGTGAGACCTGTCTCAAAATAATCAAAATAATTAGCCAG 214
QY 121 GCTTAGTGGCTATCTCCCTGTGTCCAGCTACTAGGAGGAGAGAGTGA-----CTGCT 176
DB 215 GCATGTGGGTGACCTGTAGTCCAGCTACTTTGGAGGCTGAGGAGAGATCACTT 274
QY 177 TGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGCACTTCAGGCTTGG 236
DB 275 AAACCGGGGGGGCGAGGTGGCAATGAGCTGAGACTCCGCA--CTGCACTGAGGCTGAG 333
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAATAAGTTT 256
DB 334 CAACAGAGTGAAGTCAAGTCTCAAAAAATAATAATAATAATAATAATAATAATAATAATA 393
QY 297 AAACCTAAACACATCTCT 316
DB 394 AAGATATTAAATTTT 413

RESULT 11
LOCUS AQ215619/c 417 bp DNA linear GSS 19-SRP-1998
DEFINITION HS_3217_B2_A01.MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=2 Row=B, genomic survey
ACCESSION AQ215619
VERSION AQ215619
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 417)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3217 row: B column: 2
Class: BAC ends
High quality sequence stop: 417.
Location/Qualifiers
1. 417
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3217 Col=2 Row=B"
/sex="male"
/clone_1ib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 8.9%; Score 143.4; DB 11; Length 417;
Best Local Similarity 74.0%; Pred. No. 4.5e-15;
Matches 208; Conservative 0; Mismatches 71; Indels 2; Gaps 2;
QY 2 CCTGTATTCACGACTGTGAGAGTCCGAGTGCAGAGACTGCTTGAGGCCAGAGTTCA 61
DB 413 CCTATATCCAGACTTTATAGTGTGAGCGGGGTGATCCTCTGAGGTGAGAGTTGC 354
QY 62 AGAGCAGCCTGACCAACACAGGAGAGCT-GTCACTCAAAAGATAATTAATTAGCCAG 120
DB 353 AGACCACTGACGACATGATGTGAACCTCTCTCTAATAATTCAAACTTACACAG 294
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGACAGAGTAGAGCTGTCTC 180
DB 293 GTGTGGTGGACATGTCTGTAGTCCAGCTGCTTGGAGAGTGAAGCAATAGCTTGA 234
QY 181 CCAAGAGGTCAAGACTGAGTGAAGTGAACCCAGCACTGCTTCAAGCTTGGCAAC 240
DB 233 CCGGGGGGCAAAAGGCTGCTGAGTGAAGTGTGCCA-CTGCACCTCAAGCTGGGGGAC 175
QY 241 AAAAAGAGACCTGTCTCAAAAATAAGTTAATAATTAATAA 281
DB 174 AGAAAGAGACTGTCTCAAAAAAAAAAAAAAAAAAAAAA 134

RESULT 12
DB322788/c 454 bp mRNA linear EST 04-DEC-2005
LOCUS DB322788 NT2NE2 Homo sapiens cDNA clone NT2NE2000864 3', mRNA
DEFINITION sequence.
ACCESSION DB322788
VERSION DB322788.1 GI:83261293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 454)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsutitani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Matsushima,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
1. 454
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2NE2000864"
/cell_type="leukocarcinoma"
/cell_line="NT2"
/clone_1ib="NT2NE2"
/note="Vector: pME18SFU3; mRNA from NT2 neuron after the
differentiation of NT2 neuronal precursor cells"

ORIGIN
Query Match 8.9%; Score 143.4; DB 9; Length 454;
Best Local Similarity 73.4%; Pred. No. 4.4e-15;
Matches 212; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
QY 2 CCTGTATTCACGACTGTGAGAGTCCGAGTGCAGAGACTGCTTGAGGCCAGAGTTCA 61
DB 293 CCTGTAGTCCACAGACTTTGGAGGCCGAGGTGGCGGATGCTTGAGTCAAGAGTTGC 234
QY 62 AGAGCAGCCTGACCAACACAGGAGAG-CTGTCTCAAAAGATAATTAATTAGCCAG 120
DB 233 AGAGCAGCCTGGCCCAACATGTGAACCTGTCTCTAATAATAATTAATTAGCCG 174
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGACAGAGTAGAG-CTGC 175
DB 173 GCATGTGGGGACAGCGCTGTGTGTTTCACTCTCGGAGGCTGAGGAGAAATTGCT 114
QY 176 TTGTCCCAAGAGGTCAAGACTGAGTGAAGTGAACCCAGCACTTCATTCAGCTTGC 235
DB 113 TGAGCTGTGGAGGTGAGAGTGTGAGTGGCCAGAGATGTATCCACTTCACCTGCTG 54
QY 236 GCAACAAAAGAGACCTGTCTCAAAAATAAGTTAATAATTAATAA 284
DB 53 GCAACAGAGCAAGACTGTCTCAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 13
BX487140/c 551 bp mRNA linear EST 04-SEP-2003
LOCUS BX487140 DKEP686G22255.r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKFZP686G22255 5', mRNA sequence.
ACCESSION BX487140
VERSION BX487140.1 GI:31951470
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Oy	62	AGAGAGGCTGAGACACACAGGGAGA	-CCTGTCACTACAAAGAAATTAATTAATTAAGCAG	120
Db	1746	AGACCAAGCTGGGCAACACACAGATTCCCTCTTA	CAAAAAATACAAAAATCAGTCAG	1805
Oy	121	GCTTAGTGGCTCATCTCTGTGGTCCAGCTACTAGGAGGACAGAGT	--AGACCTGCTT	177
Db	1806	GTGTGTGTGGCACACACTTGTAGTCCCACTATTACGAGAGGCTGAGGTGGAGGATTGCCCT		1865
Oy	178	GTCCAGAGAGTCAAGACTGACAGTAGTGTAGACCCACACCACTCGACATTCCAGGCTGGGG	237	
Db	1866	GAGCCTTAAGTGAAGCTGCAGTAGAGCTGTGATATACGCA	-CTGCATCTTCAGCCTGGGT	1924
Oy	238	AACAAAAAGAGACCTGTCTCAAAAAAATTAAGTTAAATTAATTAATTAATTAATTAAGTTTA	297	
Db	1925	GACAGAGTGAAGACTGTGTCTCTTAATAAATATATATATATAAATAAATAAATAAGTTA	1984	
Oy	298	AACCTTAACACATTTCTTTT	319	
Db	1985	AAAAATCAATTAATAACTTAATTT	2006	

RESULT 15	
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LOCUS	746 bp DNA linear GSS 16-FEB-2005
DEFINITION	Homo sapiens genomic DNA, 21q region, clone: 762015N19, genomic survey sequence.
ACCESSION	AG014790 AG006505
VERSION	AG014790.1 GI:3650008
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in Database (1998)
2 (bases 1 to 746)
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Direct Submission
Submitted (22-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences

COMMENT On Feb 6, 1999 this sequence version replaced gi:2992383.
AG006505: Submitted (27-Mar-1998).

FEATURES	Location/Qualifiers
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/db_xref="taxon:9606"
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/map="21q"
/clone="762015N19"
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						Gaps	3

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Db 44 CCTGTAAATTCAGCACCTTTGGAGGCTCAGAGGAGCAAAATGCTTGAGGCCAGGAGTTCG 103

QY 62 AGAGCAGCCTGGACAAACA CAGGAGAA - CCTGTCACTACAAAGTAATTAATTAATGACCG 120

Db 104 AGACCAAGCCTGGAAAACA TGGCAAAACCCACCTTACAAAATAATACAAAAATTATGCGAG 163

QY 121 GCTTAGTGGCATATCCCTGTGGTCCAGCTACTAGGAGGAGAGAGTAGTAGCTGCTGT - 179

Db 164 GCATATAGGCACATCCCTGTAGTCTCAGAGTACTAGGAGGAGCTGAGAGTGGAGGCGCTTCTTT 223

QY 180 ---CCAGAGAGTCAAGACTCAGAGACTGAGACCCGACCACTGCAATTCAGCCTGGG 236

Db 224 GAGCCGAGGAGGCGAAGGCTGAGTGAAGTGAATCAGGCCA-CTGTATCTCCAGCCTGGG 282

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Db 283 TGACGAGACCCGAGACCTGTCTCTCAAAAAAAGAAAAAGTAAATTAATTAAGCATACAGT 340

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:58:22 ; Search time 410.645 Seconds
(without alignments)
7304.087 Million cell updates/sec

Title: US-09-869-098A-1_COPY_255_1857

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1587.8	99.1	39754	3	US-09-949-016-14689
3	153.4	9.6	601	3	US-09-949-016-16596
4	152.2	9.5	61461	3	US-09-949-016-16419
5	149.6	9.3	126237	3	US-09-949-016-16674
6	149.6	9.3	126237	3	US-09-949-016-16675
7	149.4	9.3	13023	3	US-09-949-016-16282
8	149.4	9.3	63783	3	US-09-949-016-13576
9	149	9.3	601	3	US-09-949-016-13538
10	148.4	9.3	29171	3	US-09-949-016-12283
11	148.4	9.3	29171	3	US-09-949-016-12509
12	147.2	9.2	601	3	US-09-949-016-28523
13	147.2	9.2	601	3	US-09-949-016-60956
14	147.2	9.2	99370	3	US-09-949-016-12816
15	147.2	9.2	99370	3	US-09-949-016-17540
16	146.8	9.2	601	3	US-09-949-016-17651
17	146.8	9.2	35423	3	US-09-949-016-16780
18	146.8	9.1	24221	3	US-09-949-016-14964
19	146	9.1	119981	3	US-09-949-016-11884
20	146	9.1	119981	3	US-09-949-016-13606
21	144.6	9.0	93778	3	US-09-949-016-15086
22	144.6	9.0	131254	3	US-09-949-016-13734
23	144.4	9.0	601	3	US-09-949-016-56159

24	144.2	9.0	16230	3	US-09-949-016-14788	Sequence 14788, A
25	144.2	9.0	17607	3	US-09-949-016-15968	Sequence 15968, A
26	143.8	9.0	601	3	US-09-949-016-150302	Sequence 150302, A
27	143.8	9.0	39601	3	US-09-949-016-16045	Sequence 16045, A
28	143.6	9.0	18508	3	US-09-949-016-13843	Sequence 13843, A
29	143.6	9.0	157032	3	US-09-949-016-16502	Sequence 16502, A
30	143.2	8.9	601	3	US-09-949-016-11235	Sequence 71235, A
31	143.2	8.9	601	3	US-09-949-016-71236	Sequence 71236, A
32	143.2	8.9	40641	3	US-09-949-016-13376	Sequence 13376, A
33	143.2	8.9	55130	3	US-09-949-016-11850	Sequence 11850, A
34	143	8.9	30820	3	US-09-949-016-17145	Sequence 17145, A
35	143	8.9	58821	3	US-09-949-016-15897	Sequence 15897, A
36	143	8.9	58824	3	US-09-949-016-12615	Sequence 12615, A
37	142.8	8.9	8133	3	US-09-659-791A-10	Sequence 10, Appl
38	142.8	8.9	17348	3	US-09-949-016-17403	Sequence 17403, A
39	142.4	8.9	601	3	US-09-949-016-162454	Sequence 162454, A
40	142.4	8.9	57605	3	US-09-949-016-13259	Sequence 13259, A
41	142.4	8.9	68702	3	US-09-949-016-16328	Sequence 16328, A
42	142.2	8.9	93894	3	US-09-949-016-13629	Sequence 13629, A
43	141.8	8.8	15222	3	US-09-949-016-11916	Sequence 11916, A
44	141.8	8.8	15223	3	US-09-949-016-16912	Sequence 16912, A
45	141.8	8.8	44971	3	US-09-949-016-17049	Sequence 17049, A

ALIGNMENTS

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RESULT 1
US-09-949-016-15281
; Sequence 15281, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTUR, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15281
; LENGTH: 11808
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15281

Query Match 99.1%; Score 1587.8; DB 3; Length 11808;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1600; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 23 ACCTGTAATTCAGTCTGAGAGTCCGAGGCTGAGGAGCTGTTGAGGCCAGGAGTTC 82
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QY 61 AAGAGCAGCTGAGCAACAGAGGAGCCTGTACTCAAGATTAATTAATTAAGCCAG 120
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DB 83 AAGAGCAGCTGAGCAACAGAGGAGCCTGTACTCAAGATTAATTAATTAAGCCAG 142
|||||

QY 121 GCTTAGTGCTCATCCCTGTGTCCTCACTACTAGGAGGAGGAGGAGGAGGAGGAGG 180
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DB 143 GCTTAGTGCTCATCCCTGTGTCCTCACTACTAGGAGGAGGAGGAGGAGGAGGAGGAGG 202
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QY 181 CCAAGAGGTCAACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 240
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DB 203 CCAAGAGGTCAACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 262
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QY 241 AAAAAGAGACCCTGTCTCAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAAC 300
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Oy	361	ATCTGCATCTCCCTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAAGATATA	420
Db	383	ATCTGCATCTCCCTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAAGATATA	442
Oy	421	AGTATATAGTTTTCGGAATCCAGATCTTCCCTGTTTGACAAGCAGAGGGAGCAATTTT	480
Db	443	AGTATATAGTTTTCGGAATCCAGATCTTCCCTGTTTGACAAGCAGAGGGAGCAATTTT	502
Oy	481	GGTCTGACAGGCTTTGCACTGTCTGTCTGTGTGCTCAGCAATCTCACAGCAATTTGCCG	540
Db	503	GGTCTGACAGGCTTTGCACTGTCTGTCTGTGTGCTCAGCAATCTCACAGCAATTTGCCG	562
Oy	541	AGCCTCTCCGGAATGACACAGCCACAGAGCTCAGCCGAAAAGCTAGAGAACTTGCGGGA	600
Db	563	AGCCTCTCCGGAATGACACAGCCACAGAGCTCAGCCGAAAAGCTAGAGAACTTGCGGGA	622
Oy	601	GGGAGACTCACAGTGGCCCAAAAAAATTAACTTTCTTTTCTTTTCTTTCTTTCT	660
Db	623	GGGAGACTCACAGTGGCCCAAAAAAATTAACTTTCTTTTCTTTTCTTTCTTTCT	682
Oy	661	TTCCTTTCTTCTTCTTCTTCTTCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTC	720
Db	683	TTCCTTTCTTCTTCTTCTTCTTCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTC	742
Oy	721	TTTCTTTCTTTTCTTTTCTTAATGACAAATCTCTCATGACAGAAATAATCTGCCTTAGT	780
Db	743	TTTCTTTCTTTTCTTTTCTTAATGACAAATCTCTCATGACAGAAATAATCTGCCTTAGT	802
Oy	781	TCTGTTTCCAGCGTGGCTTCTGACAGAGACAAATGCGTGGCGGTCTTTCTTCCGCTATA	840
Db	803	TCTGTTTCCAGCGTGGCTTCTGACAGAGACAAATGCGTGGCGGTCTTTCTTCCGCTATA	862
Oy	841	ATTATTCACAGGCCATCCCAGACTCTGGTCCCCCTCAGCTTTCCCTGACAGTCCCTTGCCT	900
Db	863	ATTATTCACAGGCCATCCCAGACTCTGGTCCCCCTCAGCTTTCCCTGACAGTCCCTTGCCT	922
Oy	901	GGTGAAAAACAATATGCGCGCGGCTGACACAGGCTGTAAAGTGTGAAATATCAGAAAGAT	960
Db	923	GGTGAAAAACAATATGCGCGCGGCTGACACAGGCTGTAAAGTGTGAAATATCAGAAAGAT	982
Oy	961	GACTGAAAGTCTTTTGGAGCTCGGTTTCTCATTTGTAAAAATGSAAGTTAATCCAGCCTTC	1020
Db	983	GACTGAAAGTCTTTTGGAGCTCGGTTTCTCATTTGTAAAAATGSAAGTTAATCCAGCCTTC	1042
Oy	1021	TTCTACTCCCCCAAAGCAAGTGTGTGTCGCCGGCCAGAGGGCCCAATGTTGAGCTGTTCAC	1080
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Oy	1081	GCATCAGTTACCCCAACAGAGACGGGTCAGCAATTAAAGGGAACAGAGCCCGGTCATC	1140
Db	1103	GCATCAGTTACCCCAACAGAGAGGGTCAGCAATTAAAGGGAACAGAGCCCGGTCATC	1162
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Oy	1201	TTGTACAGTGGGGGGGGGGCCGGTTTCTGTCTGTGTGTAAAGAGCGTGAAGTCAAGCT	1260
Db	1223	TTGTACAGTGGGGGGGGGGCCGGTTTCTGTCTGTGTGTAAAGAGCGTGAAGTCAAGCT	1282
Oy	1261	GGGTGCTCCCGCCCGCCGCGGGGCTTTAATGTCTCCCTGTCTCTAAACGCCAGGCGCTCC	1320
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Db      1463  ACAGGAGGCGCGGTGCGAGAGGCCCAAGTCCCGCCTGACGAGAGCCAGCCGCGCTGAGCT 1522
Qy      1501  CGCAGAGGCTGAGTAGTTTGGCCACGCTAGGGGGGCTGGGCCCATAAAGAGAAAGTGC 1560
Db      1523  CGCAGAGGCTGAGTAGTTTGGCCACGCTAGGGGGGCTGGGCCCATAAAGAGAAAGTGC 1582
Qy      1561  ACTTAAGACACGGCCCCGCTGAGCGCTTGTAGAAAACGCTCT 1603
Db      1583  ACTTAAGACACGGCCCCGCTGAGCGC-TGTTAGAAAACGCTCT 1624

RESULT 2
US-09-949-016-14689
; Sequence 14689, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ For Windows Version 4.0
; SEQ ID NO 14689
; LENGTH: 39754
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(39754)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689

Query Match      99.1%; Score 1587.8; DB 3; Length 39754;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1600; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      61  AAGACAGCCTGGACAACAACAGGAGACCTGTCACTACAAAGAAATTAATTAATCCAG 120
Db      27998  AAGACAGCCTGGACAACAATAGGAGACCTGTCACTACAAAGAAATTAATTAATCCAG 28057
Qy      121  GCTTAGTGCTATCCCTGTGTGCTCCAGCTTACTTAGGAGGACAGAAATAGAGCTGTTGTC 180
Db      28058  GCTTAGTGCTATCCCTGTGTGCTCCAGCTTACTTAGGAGGACAGAAATAGAGCTGTTGTC 28117
Qy      181  CCAGAGGTCAAAGACTGACGTAGCTGAGACCCAGCCACTGTGATTCAGAGCTGGGCAAC 240
Db      28118  CCAGAGGTCAAAGACTGACGTAGCTGAGACCCAGCCACTGTGATTCAGAGCTGGGCAAC 28177
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Db	29378 ACACGCGAGCGCGGTTCGCGAGAGGCCCAAGTCCCGCTTCGAGAGACGACGCGCGCTCGCT	29437
QY	1501 CGCAGGAGGGGTGGGTGTTGGCCACAGTAAAGGGGGGCTGGGGCCATTAANAAGAGAAAGTGC	1560
Db	29438 CGCAGGAGGGGTGGGTGTTGGCCACAGTAAAGGGGGGCTGGGGCCATTAANAAGAGAAAGTGC	29497
QY	1561 ACTTAAGACACGCGCCCGCTGACGCGTTGTTAGAAACCGTCTCT	1603
Db	29498 ACTTAAGACACGCGCCCGCTGACGCG-TGTTAGAAACCGTCTCT	29539

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RESULT 3
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; Sequence 165996, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165996
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-165996

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[illegible]

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? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CLO01307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FASTSEQ for Windows Version 4.0
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? LENGTH: 61461
? TYPE: DNA
? ORGANISM: Human
? US-09-949-016-16419

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[illegible]

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1      RESULT 5
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4      : Patent No. 6812339
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: VENTER, J. Craig et al.
9      : TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
10     : WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
11     : FILE REFERENCE: CL001307
12     :
13     : CURRENT APPLICATION NUMBER: US/09/949,016
14     :
15     : CURRENT FILING DATE: 2000-04-14
16     :
17     : PRIOR APPLICATION NUMBER: 60/241,755
18     :
19     : PRIOR FILING DATE: 2000-10-20
20     :
21     : PRIOR APPLICATION NUMBER: 60/237,768
22     :
23     : PRIOR FILING DATE: 2000-10-03
24     :
25     : PRIOR APPLICATION NUMBER: 60/231,498
26     :
27     : PRIOR FILING DATE: 2000-09-08
28     :
29     : NUMBER OF SEQ ID NOS: 207012
30     :
31     : SOFTWARE: FastSeq for Windows Version 4.0
32     :
33     : SEQ ID NO 16674
34     :
35     : LENGTH: 126237
36     :
37     : TYPE: DNA
38     :
39     : ORGANISM: Human

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US-09-949-016-16674

Query Match	9.34	Score 149.6	DB 3	Length 126337
Best Local Similarity	75.04	Pred. No. 3.7e-26		
Matches 213; Conservative	0	Mismatches 69	Indels 2	Gaps 2

OY	1	ACCTGTAAATCCAGACTGCTGGAGAAGTCCAGAGTCAGAGAGCATGCTTGAGGCCAGAGTTTC	60
Dd	21590	ACCTGTAAATCCAGCACTTTGGGAAGGCCAAGGAGAGAGATCATCATGAGCCCCGGAGTTT	215311
OY	61	AAGAGCAGCCTGGACAACACAGGGAAA-CCTGTCACTACCAAAGATAAATAATTAGCCA	119
Dd	21530	GAGACCAGTCTGGGCAACACAGGGAAGCCCACTCTTAACAAACAAAAAATTAGCTG	214711
OY	120	GGCTTAGTGGCATCCCTGTGTGTGCCAGCTACTAGGAGAGCGAAGTAGTAGACTGCTTGT	179
Dd	21470	GGCATATGATGCATGCTGTGTGTGCCAGCTATGTGGGAGCTGAGGCGACGACTGCTTGA	214111
OY	180	CCCAGAGGTCAAGACTGCAGTAGAGCTTGAGCCCAAGCCACTTGACATTTCCAGCTTGGCAA	239
Dd	21410	GCCCGGAGGTCAAGACTGCTGTGAGCTGTGACTGTGCCA-CTGCACCTACAGCCTGGGTGA	213521
OY	240	CAAAAAGAGACCCGTGCTCAAAAATAATAGTTAAATAATAATAA	283
Dd	21351	CAGAGTAGAGACCTGTCTTGGAAAAAACAACAAAAAACCCAAACA	21308

RESULT 6
US-09-949-016-16675/c

```

; Sequence 16675, Application US/03949016
; Patent No. 6812339
;
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 16675
; LENGTH: 126237
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16675

```

Query Match	Score	149.6	DB 3	Length	126237
Best Local Similarity	75.0%	Prd.	3.7e-26		
Matches	213	Conservative	0	Mismatches	69
				Indels	2
				Gaps	2
Qy	1	ACCTGTAATTCAGACTCTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC	60		
Db	21590	ACCTGTATCCAGACATCTTGGAGGCGAAGCGAGAGATCAATCAAGACCCGGAGT	21531		
Qy	61	AAGAGCAGCCTGGACAACAGGAGAG-CCTGTCACTACAAAGATTAATTAATTAGCA	119		
Db	21550	GAGACCACTGTGGGCAACACAGGAGACCCCATCTTCAACAAACAAAAATTAGCTG	21471		
Qy	120	GGCTTAGTGCTATCCCTGTGCTCCAGTCTTACGAGAGGCAGAAAGTAGACTGTTGT	179		
Db	21470	GGCATATGATGCACTGTCTGTGTCCACGTTAGTGAGGAGCTGAGAGCACTGTTGA	21411		
Qy	180	CCGAGAGAGTCAAGACTGCACTGAGCTGAGACCCACCACTGTCATTCAGAGCTGGCAA	239		
Db	21410	GCCCGAGAGTCAAGACTGCTGTGAGCTGTGACCTGTGCCA-CTGCATCTACAGCCTGGTGA	21355		
Qy	240	CAAAAGAGACCTGTCTCAAAAATTAAGTTAAATTAATTAATA	283		


```
Db 319 GCATGCTACGAGCAGCTTTAGTCTAGCTACTCGAGAGCTGAGAGAGATACCTG 260
Qy 177 TGTCCAGAGAGGTCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 236
Db 259 GAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 201
Qy 237 CAACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 296
Db 200 CAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 141
Qy 297 AAACCTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345
Db 140 TAACAAAAATATCTTATTATTACTTATATAGTATTTAAAGATTACTACA 92
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RESULT 10
US-09-949-016-12283
Sequence 12283, Application US/09949016

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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12283
LENGTH: 29171
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(29171)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12283
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Query Match 9.3%; Score 148.4; DB 3; Length 29171;
Best Local Similarity 75.9%; Pred. No. 3.9e-26;
Matches 223; Conservative 0; Mismatches 66; Indels 5; Gaps 3;

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Qy 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGAGTCCGAGAGTCCGAGAGTCCGAGAGTTC 60
Db 5933 ACCTGTAATTCAGTACTGTGAGAGTCCGAGAGTCCGAGAGTCCGAGAGTTC 5992
Qy 61 AAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119
Db 5993 AAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6052
Qy 120 GGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 176
Db 6053 GGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6112
Qy 177 TGTCCAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 236
Db 6113 TGAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6171
Qy 237 CAACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290
Db 6172 CAATAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6225
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RESULT 11
US-09-949-016-13509
Sequence 13509, Application US/09949016

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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13509
LENGTH: 29171
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(29171)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13509
```

Query Match 9.3%; Score 148.4; DB 3; Length 29171;
Best Local Similarity 75.9%; Pred. No. 3.9e-26;
Matches 223; Conservative 0; Mismatches 66; Indels 5; Gaps 3;

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Qy 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGAGTCCGAGAGTCCGAGAGTCCGAGAGTTC 60
Db 5933 ACCTGTAATTCAGTACTGTGAGAGTCCGAGAGTCCGAGAGTCCGAGAGTTC 5992
Qy 61 AAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119
Db 5993 AAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6052
Qy 120 GGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 176
Db 6053 GGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6112
Qy 177 TGTCCAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 236
Db 6113 TGAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6171
Qy 237 CAACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290
Db 6172 CAATAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6225
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RESULT 12
US-09-949-016-28523/C
Sequence 28523, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28523
LENGTH: 601
TYPE: DNA

OY	771	TGCGTGAAGCTCTGTTTCCAGAGCGCTCTGACAGAACCAATGAGCTCGGCGCTGTTTCT	830
Db	121	TGCTTAACTCTGTTTCCAGCGCTCTTCTGCAAGAACATGCGCTGG-GTGTTTTTCT	179
OY	831	TTCCGCTAATTAATTCAGGCCCATCCAGCTCTGTTCCCTCAAGCTGTTCCCTGGAGT	890
Db	180	TTCCGCTAATTAATTCAGGCCCATCCAGCTCTGTTCCCTCAAGCTGTTCCCTGGAGT	239
OY	891	CCCTTCTGCTGTTGAACAACATATGAGCGCGGCGCTGACAGAGGTGAATGATGTGATA	950
Db	240	CCCTTCTGCTGTTGAACAACATATGAGCGCGGCGCTGACAGAGGTGAATGATGTGATA	299
OY	951	TCAGGAAGATGACTGAACGTCCTTTGGGACTCCGTTTCTCATTTGTAATGAGATTAT	1010
Db	300	TCAGGAAGATGACTGAACGTCCTTTGGGACTCCGTTTCTCATTTGTAATGAGATTAT	359
OY	1011	ACCAAGCTTTCTTACTCTCCCAAGGCAAGCTGTTTGTCTCCGGCCAGAGGGCCCAATTGTT	1070
Db	360	ACCAAGCTTTCTTACTCTCCCAAGGCAAGCTGTTTGTCTCCGGCCAGAGGGCCCAATTGTT	419
OY	1071	GAGCTGTTCAGCATGATTAAACCCCAACAGAGCGGTCAGCAATTAAAGGCGAACAGGC	1130
Db	420	GAGCTGTTCAGCATGATTAAACCCCAACAGAGCGGTCAGCAATTAAAGGCGAACAGGC	479
OY	1131	CCGAGTCATCTCTGAGCGGCTTTTCTCATCCAGGACTGGAACAGGCAGCTGGCTGGGCC	1190
Db	480	CCGAGTCATCTCTGAGCGGCTTTTCTCATCCAGGACTGGAACAGGCAGCTGGGCCGGCC	539
OY	1191	CGGCTCTGCTTTGACGTCGGG	1213
Db	540	CGGCTCTGCTTTGACGTCGGG	562

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RESULT 2
US-09-925-065A--566754
; Sequence 566754, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 566754
; LENGTH: 5662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-566754

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Query Match	34.3%	Score 550.6;	DB 5;	Length 562;
Best Local Similarity	99.6%;	Pred. No. 7,11e-129;		
Matches	561;	Conservative	1;	Mismatches 0; Indels 1; Gaps 1;
Qy	651	TTTTCTTCTTTCTTTCTTTCTGTCGTTCGTCTTCTCTCTCTCTCTCTCTT		710
Dd	1	TTTTCTTCTTTCTTTCTTTCTTGCTTTCTGTCTTCCCTCTCTCTCTCTTT		60
Qy	711	CTTTCCTCTTTCTTTCTTTTCTTCTACATGGCAAGATCTCTATGGGAATAATC		770

Db	61	CTTTCCTCTCTCTTCTTTCTTTTTCCTAATGGAAGATCTCTCATGCGAAGATAATC	120
QY	771	TGCTTGAATCTCTGTTTCCAGAGCTGCTTTGCGCAGAGCAATGCGCTGGCGTGTCTTCT	830
Db	121	TGCCTTGAATCTCTGTTTCCAGAGCTGCTTTGCGCAGAGCAATGCGCTGGCG-GTGTTTCT	179
QY	831	TTCCGCTATAATATTCAGAGCCCATCCAGCTCTGATCCCTCTCAGCTGTTCCCTGACAGT	890
Db	180	TTCCGCTATAATATTCAGAGCCCATCCAGCTCTGATCCCTCTCAGCTGTTCCCTGACAGT	239
QY	891	CCCTTCTGCTGTGTGAAAACACATATGCGGCCGCGCTTGACAGGGGTGTAAGTGTGATA	950
Db	240	CCCTTCTGCTGTGTGAAAACACATATGCGGCCGCGCTTGACAGGGGTGTAAGTGTGATA	299
QY	951	TCAGAGAATGACTGAAAGCTTTGGGAGCTCGTTTTCTCATTTGTAAAATGAGAGTTAAT	1010
Db	300	TCAGAGAATGACTGAAAGCTTTGGGAGCTCGTTTTCTCATTTGTAAAATGAGAGTTAAT	359
QY	1011	ACAGAGCTTCTTACTCTCCCAAACGCAAGTGTGTGTCGCGGCAGAGGGCCCAATTGTT	1070
Db	360	ACAGAGCTTCTTACTCTCCCAAACGCAAGTGTGTGTCGCGGCAGAGGGCCCAATTGTT	419
QY	1071	GGCTGTTCACGCATCACTTACCCCAAGAGAGGGTCAAGCAATTTAAAGGGAACCAAGGC	1130
Db	420	GGCTGTTCACGCATCACTTACCCCAAGAGAGGGTCAAGCAATTTAAAGGGAACCAAGGC	479
QY	1131	CGGCTGCATCTCTGAGCGGCTTTTCTCATCCAGAGGCTGGAACAGGCAAGCTGAGCTGGGC	1190
Db	480	CGGCTGCATCTCTGAGCGGCTTTTCTCATCCAGAGGCTGGAACAGGCAAGCTGAGCTGGGC	539
QY	1191	CGGCTGTGAGCTTGTCAAGTGGG	1213
Db	540	CGGCTGTGAGCTTGTCAAGTGGG	562

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RESULT 3
US-10-301-480-268288/C
; Sequence 268288, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268288
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-268288

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	Query Match	Similarity	Score	538-6;	DB	Length	561;
	Beet Local	Similarity	99.5%;	Pred.	No. 7.9e-126;		
	Matches	Conservative	1;	Mismatches	0;	Indels	2; Gaps 2;
Oy	877	TGTTCCCTGGCAGTCCCTTCGTGCTGTGTAACATATGCGCGCCTTGACCAGGGTG					936
Dd	561	TGTTCCCTGGCAGTCCCTTCGTGCTGTGTAACATATGCGCGCCTTGACCAGGGTG					502
Oy	937	TAAGTGTGAATATCAGAAGATGACTGAACGCTTTTGGGACCTCCGTTTCTCATTTGTA					996
Dd	501	TAAGTGTGAATATCAGAAGATGACTGAACGCTTTTGGGACCTCCGTTTCTCATTTGTA					442
Oy	997	AAATGGAGATTAAATACACGCCTTCCTTCACTCCCCCAAACGACGCTGTGTGCCGAGCAG					1056
Dd	441	AAATGGAGATTAAATACACGCCTTCCTTCACTCCCCCAAACGACGCTGTGTGCCGAGCAG					382

QY	1057	AGGGCCCAATTGTTGGCTGTTCACGCATCAGTTACCCCCACAGACGGGTGAGCCAATTA	1118
Db	351	AGGG-CCAATTGTTGGCTGTTCACGCATCAGTTACCCCCACAGACGGGTGAGCCAATTA	323
QY	1117	AAGGGAACCAAGGCCGGTCCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGACAGGC	1176
Db	322	AAGGGAACCAAGGCCGGTCCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGACAGGC	263
QY	1177	AGCTGGCCTGGGACCCGGCTCTGCTCTTGTTCACGTGGGGGGGCCGGGCCGTTTGTCTGTG	1238
Db	262	AGCTGGCCTGGG-CCGGCTCTGCTCTTGTTCACGTGGGGGGGCCGGGCCGTTTGTCTGTG	204
QY	1237	TGTGTAGAGAGCGTGAAGTCAACGCTGGAGTCTCCCGCCCCCGAGGGGCTTTTAGTGTCCCT	1298
Db	203	TGTGTAGAGAGCGTGAAGTCAACGCTGGAGTCTCCCGCCCCCGAGGGCTTTTAGTGTCCCT	144
QY	1297	GGTCCCTTAAACGCCCAAGGCGCTCCACCGAGGGAGAAAGGCGGAACTCCAGCGAGCCCA	1356
Db	143	GGTCCCTTAAACGCCCAAGGCGGCTCCACCGAGGGAGAAAGGCGGAACTCCAGCGAGCCCA	84
QY	1337	CGGCTGTTGTGCGTTGGCGGGGCAACTGTGTGTCGAGTTTGATTGGTTCTTCCCCCGA	1416
Db	83	CGGCTGTTGTGCGTTGGCGGGGCAACTGTGTGTCGAGTTTGATTGGTTCTTCCCCCGA	24
QY	1417	CAACGCGGCGGCTGAACCAATC	1439
Db	23	CAACGCGGCGGCTGAACCAATC	1

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RESULT 4
US-10-301-480-881697/C
; Sequence 881697, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 881697
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-881697

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Query Match	33.6%;	Score 538.6;	DB 12;	Length 561;
Best Local Similarity	99.5%;	Pred. No. 7.9e-126;		
Matches 560;	Conservative 1;	Mismatches 0;	Indels 2;	Gaps 2;

QY	877	TGTTCCCTGGCAGTCCCTTCTGCTGGTAAAAACATATGGGCGCGCTACACAGGGTG	936
Db	561	TGTTCCCTGGCAGTCCCTTCTGCTGGTAAAAACATATGGGCGCGCTACACAGGGTG	502
QY	937	TAAGTGTGAAATATCAGAGAAGATGACGAAGCTTTGGGACTTCGGTTCCCTCATTTGTA	996
Db	501	TAAGTGTGAAATATCAGAGAAGATGACGAAGCTTTGGGACTTCGGTTCCCTCATTTGTA	442
QY	997	AAATGGAGGTTAATACCAAGCCTTCTTCTACTCCCAAAACGACAGTGTTTGTCGCCGCCAG	1056
Db	441	AAATGGAGGTTAATACCAAGCCTTCTTCTACTCCCAAAACGACAGTGTTTGTCGCCGCCAG	382
QY	1057	AGGGGCCAATTGTTGGCTGTTACAGCAGTCAGTTACCCCAACGAGACGGGTGAGCCAATTA	1116
Db	381	AGGGGCCAATTGTTGGCTGTTACAGCAGTCAGTTACCCCAACGAGACGGGTGAGCCAATTA	323

QY	1117	AAGCGAAACCAAGGCGCCGGTCCATCTCCTGACGCGCTTTTCTCATCCCAAGGCTGGACAAGGC	1176
Db	322	AAGCGAAACCAAGGCGCCGGTCCATCTCCTGACGCGCTTTTCTCATCCCAAGGCTGGACAAGGC	263
QY	1177	AGCTGAGCTGGGGCCCGGCTCTGCTCTTGTCAAGTGCGGGAGGCGGACCGGTTTCTGTGCTG	1236
Db	262	AGCTGAGCTGGGG - CGGGCTTGCTTGTCAAGTGCGGGAGGCGGACCGGTTTGTGTGCTG	204
QY	1237	TGTGTAGAGAGCTGAGGTCAACGCTGGGTGCTCCCGCCCGCGGGGCGCTTTAGTGTCCCT	1296
Db	203	TGTGTAGAGAGCTGAGGTCAACGCTGGGTGCTCCCGCCCGCGGGGCGCTTTAGTGTCCCT	144
QY	1297	GGTCCCTTAAAGCCAGAGCCGCTCCACCGGGGGANAAGGCGCGAACCACGCGAGGCCCAA	1356
Db	143	GGTCCCTTAAAGCCAGAGCCGCTCCACCGGGGGANAAGGCGCGAACCACGCGAGGCCCAA	84
QY	1357	CGGCGTTTGTGGTGTGCGGGGCAACGTGTGCTCAGTTGATTTGGTTCCTTCCCCGA	1416
Db	83	CGGCGTTTGTGGTGTGCGGGGCAACGTGTGCTCAGTTGATTTGGTTCCTTCCCCGA	24
QY	1417	CACGCGGCGGCTGTAAACCAATC	1439
Db	23	CACGCGGCGGCTGTAAACCAATC	1

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RESULT 5
US-09-925-065A-177131/c
; Sequence 177131, Application US/09925065A
; Publication No. US204018104B1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ. ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177131
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-177131

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Query Match	33.2%	Score 531.6;	DB 4;	length 554;
Best Local Similarity	99.5%;	Pred. NO. 4.7e-124;		
Matches 553; Conservative	1;	Mismatches 0;	Indels 2;	Gaps 2;

QY	877	TGTTCCCTGGCAGTCCCTTCTGCTGGTGAACACATATGGCGCGGCTATCCAGGGTG	936
Db	554	TGTTCCCTGGCAGTCCCTTCTGCTGGTGAACACATATGGCGCGGCTATCCAGGGTG	495
QY	937	TAACTGTGTGAATATCAGGAAGATGACTGAACGTCCTTGGGACTCCGTTTCCATATTGA	996
Db	494	TAACTGTGTGAATATCAGGAAGATGACTGAACGTCCTTGGGACTCCGTTTCCATATTGA	435
QY	997	AAATGGAGGTTAATATCCAGCCTTCTTCTATCTCCCAACGCAAGTGTTTGTCCCGGCACG	1055
Db	434	AAATGGAGGTTAATATCCAGCCTTCTTCTATCTCCCAACGCAAGTGTTTGTCCCGGCACG	375
QY	1057	AGGGCCCAATGTGTGGCTGTACAGCATCAGTTACCCCAAGGACGGGTGACGCCAATTATTA	1118
Db	374	AGGG-CCAAATGTGTGGCTGTACAGCATCAGTTACCCCAAGGACGGGTGACGCCAATTATTA	316

QY 1117 AAGGCAACCAAGGCCGCTGCATCTCTGAAGCCTTTTCTCATCCAGAGGCTGACAGGC 1176
DB 315 AAGGCAACCAAGGCCGCTGCATCTCTGAAGCCTTTTCTCATCCAGAGGCTGACAGGC 256
QY 1177 AGCTGGCCTGGAGCCCGGCTCTGCTTGTCACTGTCGGGGGGCCGGCCCGTTTGTCTGTC 1236
DB 255 AGCTGGCCTGGAG-CCGGCTCTGCTTGTCACTGTCGGGGGGCCGGCCCGTTTGTCTGTC 197
QY 1237 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGCGCCCGCGAGGCTTTAGTGTCTCT 1296
DB 196 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGCGCCCGCGAGGCTTTAGTGTCTCT 137
QY 1297 GGTCTCTTAAAGCCGAGGCGCTCTCAAGCGGGGAGAAAGCGCGAACCCGACGCGACCA 1356
DB 136 GGTCTCTTAAAGCCGAGGCGCTCTCAAGCGGGGAGAAAGCGCGAACCCGACGCGACCA 77
QY 1357 CGGCTGTGTGGTTCGGTTCGGGGGCAAGCTGTGCTGAGTTCGATTTGGTTCCTTCCCCGA 1416
DB 76 CGGCTGTGTGGTTCGGTTCGGGGGCAAGCTGTGCTGAGTTCGATTTGGTTCCTTCCCCGA 17
QY 1417 CAACGCGGCGGCTGTA 1432
DB 16 CAACGCGGCGGCTGTA 1

RESULT 6

US-09-925-065A-177131/c
Sequence 177131, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827, 135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 177131
LENGTH: 554
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-177131

Query Match 33.2%; Score 531.6; DB 5; Length 554;
Best Local Similarity 99.5%; Pred. No. 4,7e-124;
Matches 553; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 877 TGTTCCTGGAGTCTCTTCTGCTGTGTAACACATATAGCGCGGCTGACAGGCTG 936
DB 554 TGTTCCTGGAGTCTCTTCTGCTGTGTAACACATATAGCGCGGCTGACAGGCTG 495
QY 937 TAAGTGTGAATATCAGAAATGACTGAACGCTTTGGAGCTCCGTTTCTCATTTGA 996
DB 494 TAAGTGTGAATATCAGAAATGACTGAACGCTTTGGAGCTCCGTTTCTCATTTGA 435
QY 997 AAATGAGGTTAATACAGGCTCTTCTACTCTCCCAAACGACGTTGTTTCTCCGAGCAG 1056
DB 434 AAATGAGGTTAATACAGGCTCTTCTACTCTCCCAAACGACGTTGTTTCTCCGAGCAG 375
QY 1057 AGGCGCAATTGTTGCTGTTTCAAGCATCATTAACCCCAAGAGAGGCTGACGCAATTA 1116

DB 374 AGGG-CCAAATTGTGGCTTTACAGCTCAGTTATCCCAAGAGAGCGGTCAAGCAATTA 316
QY 1117 AAGGCAACCAAGGCCGCTGCATCTCTGAAGCCTTTTCTCATCCAGAGGCTGACAGGC 1176
DB 315 AAGGCAACCAAGGCCGCTGCATCTCTGAAGCCTTTTCTCATCCAGAGGCTGACAGGC 256
QY 1177 AGCTGGCCTGGAGCCCGGCTCTGCTTGTCACTGTCGGGGGGCCGGCCCGTTTGTCTGTC 1236
DB 255 AGCTGGCCTGGAG-CCGGCTCTGCTTGTCACTGTCGGGGGGCCGGCCCGTTTGTCTGTC 197
QY 1237 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGCGCCCGCGAGGCTTTAGTGTCTCT 1296
DB 196 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGCGCCCGCGAGGCTTTAGTGTCTCT 137
QY 1297 GGTCTCTTAAAGCCGAGGCGCTCTCAAGCGGGGAGAAAGCGCGAACCCGACGCGACCA 1356
DB 136 GGTCTCTTAAAGCCGAGGCGCTCTCAAGCGGGGAGAAAGCGCGAACCCGACGCGACCA 77
QY 1357 CGGCTGTGTGGTTCGGTTCGGGGGCAAGCTGTGCTGAGTTCGATTTGGTTCCTTCCCCGA 1416
DB 76 CGGCTGTGTGGTTCGGTTCGGGGGCAAGCTGTGCTGAGTTCGATTTGGTTCCTTCCCCGA 17
QY 1417 CAACGCGGCGGCTGTA 1432
DB 16 CAACGCGGCGGCTGTA 1

RESULT 7

US-10-197-019-1
Sequence 1, Application US/10197019
Publication No. US20030207284A1
GENERAL INFORMATION:
APPLICANT: Chew, Anne
APPLICANT: Denton, R. Rex
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Mandabalan, Krishnan
APPLICANT: Parks, Katie E.
TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
FILE REFERENCE: MMH-0042US
CURRENT APPLICATION NUMBER: US/10/197, 019
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02485
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 9314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1714)..(1714)
OTHER INFORMATION: PS2: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2051)..(2051)
OTHER INFORMATION: PS3: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (2124)..(2124)
OTHER INFORMATION: PS4: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2287)..(2287)
OTHER INFORMATION: PS5: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (2408)..(2408)
OTHER INFORMATION: PS6: polymorphic base adenine or guanine

1	FEATURE:	
2	NAME/KEY: allele	
3	LOCATION: (4768) .. (4768)	
4	OTHER INFORMATION: PS7:	polymorphic base adenine or guanine
5	FEATURE:	
6	NAME/KEY: allele	
7	LOCATION: (4785) .. (4785)	
8	OTHER INFORMATION: PS8:	polymorphic base guanine or adenine
9	FEATURE:	
10	NAME/KEY: allele	
11	LOCATION: (4813) .. (4813)	
12	OTHER INFORMATION: PS9:	polymorphic base thymine or cytosine
13	FEATURE:	
14	NAME/KEY: allele	
15	LOCATION: (4882) .. (4882)	
16	OTHER INFORMATION: PS10:	polymorphic base adenine or cytosine
17	FEATURE:	
18	NAME/KEY: allele	
19	LOCATION: (4976) .. (4976)	
20	OTHER INFORMATION: PS11:	polymorphic base thymine or adenine
21	FEATURE:	
22	NAME/KEY: allele	
23	LOCATION: (5600) .. (5600)	
24	OTHER INFORMATION: PS12:	polymorphic base cytosine or thymine
25	FEATURE:	
26	NAME/KEY: allele	
27	LOCATION: (5820) .. (5820)	
28	OTHER INFORMATION: PS13:	polymorphic base thymine or guanine
29	FEATURE:	
30	NAME/KEY: allele	
31	LOCATION: (6536) .. (6536)	
32	OTHER INFORMATION: PS14:	polymorphic base thymine or adenine
33	FEATURE:	
34	NAME/KEY: allele	
35	LOCATION: (6607) .. (6607)	
36	OTHER INFORMATION: PS15:	polymorphic base guanine or adenine
37	FEATURE:	
38	NAME/KEY: allele	
39	LOCATION: (6617) .. (6617)	
40	OTHER INFORMATION: PS16:	polymorphic base cytosine or thymine
41	FEATURE:	
42	NAME/KEY: allele	
43	LOCATION: (6872) .. (6872)	
44	OTHER INFORMATION: PS17:	polymorphic base cytosine or guanine
45	FEATURE:	
46	NAME/KEY: allele	
47	LOCATION: (6966) .. (6966)	
48	OTHER INFORMATION: PS18:	polymorphic base guanine or adenine
49	FEATURE:	
50	NAME/KEY: allele	
51	LOCATION: (7036) .. (7036)	
52	OTHER INFORMATION: PS19:	polymorphic base cytosine or thymine
53	FEATURE:	
54	NAME/KEY: allele	
55	LOCATION: (7086) .. (7086)	
56	OTHER INFORMATION: PS20:	polymorphic base adenine or guanine
57	FEATURE:	
58	NAME/KEY: allele	
59	LOCATION: (8100) .. (8100)	
60	OTHER INFORMATION: PS21:	polymorphic base cytosine or thymine
61	FEATURE:	
62	NAME/KEY: allele	
63	LOCATION: (8221) .. (8221)	
64	OTHER INFORMATION: PS22:	polymorphic base guanine or adenine
65	FEATURE:	
66	NAME/KEY: allele	
67	LOCATION: (8677) .. (8677)	
68	OTHER INFORMATION: PS23:	polymorphic base thymine or adenine
69	PS-10-157-019-1	

Query Match	27.1%	Score 433.8	DB 7	Length 9314
Best Local Similarity	97.9%	Pred No. 1.1e-98		
Matches 461, Conservative	0	Mismatches 7	Indels 3	Gaps 2

QY	1133	GGTCATCTCTGACGGCTTTTCTCATCCAGGGCTGAAGGACGCTGGCGTGGGCGC	1192
Db	1	GGTCATCTCTGACGGCTTTTCTCATCCAGGGCTGAAGGACGCTGGGCGTGGGCGC	60
QY	1193	GCTTCGCTTGTACAGTGCGGGGGGCGGCCGCTTGTCTGTGTGTAGAGAGCTGAG	1252
Db	61	GCTTCGCTTGTACAGTGCGGGGGGCGGCCGCTTGTCTGTGTGTAGAGAGCTGAG	120
QY	1253	GTCAAGCTGGGTGCTCCCGCGCCCGCGGGGGCTTTAGTGTCCCTGATCCCTAAACGGCAG	1312
Db	121	GTCAAGCTGGGTGCTCCCGCGCCCGCGGGGGCTTTAGTGTCCCTGATCCCTAAACGGCAG	180
QY	1313	GCCTCTCCACCGGGGGAGAAAGCGCGAACCACCGAGCCCAA	1372
Db	181	GCCTCTCCACCGGGGGAGAAAGCGCGAACCACCGAGCCCAA	240
QY	1373	CCGGGGCAACCTGTGTGTGACAGTTCTGTATGTGTCTTCCCGCAGCAACGGGGCGGCTGT	1432
Db	241	CCGGGGCAACCTGTGTGTGACAGTTCTGTATGTGTGTCTTCCCGCAGCAACGGGGCGGCTGT	300
QY	1433	ACCAATCGACAGCGAGGCGCGGTGCGCGAGGGCCCAAGTCCCGCCTGTGACGAGACGACCGCG	1492
Db	301	ACCAATCGACAGCGAGGCGCGGTGCGCGAGGGCCCAAGTCCCGCCTGTGACGAGACGACCGCG	360
QY	1493	CGCTTCGCTCGCAGAGGGGTGGGTATGTTTCCCGACGTAAGGGGGGCTGGGCCATAAAGA	1552
Db	361	CGCTTCGCTCGCAGAGGGGTGGGTATGTTTCCCGACGTA--GGGGGCTGGGCCATAAAGA	419
QY	1553	GGAAGTCACTTAAGACAGCGCCCGCGCTGACGCTTGTGAAGAACGCTCTT	1603
Db	420	GGAAGTCACTTAAGACAGCGCCCG--TGAAGCTTGTGAAGAACGCTCTT	468

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RESULT 8
US-10-719-993-6827/C
; Sequence 6827, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001496
; CURRENT APPLICATION NUMBER: US/10/719, 993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6827
; LENGTH: 160556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) _ (160556)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-719-993-6827

```

	Query Match	9.84;	Score 157.8;	DB 9;	Length 160556;
	Best Local Similarity	68.34;	Pred. No. 4.5e-28;		
	Matches 233;	Conservative 1;	Mismatches 103;	Indels 4;	Gaps 1;
QY	2	CCTGTATATTCAGTACTGTGTAGAGAGTCCGAGTACAGAGACTGCTTGAGGCGCAGAGTCA	61		
Db	30072	CCTGTATCCTACGACTTTTGGAGGCGCAAGGCAGGTGAGTATACGTGAGGTCAAGAGTTGC	30011		
QY	62	AGAGCAGCCTTGACAAACACAGGGAGACTGTCACTTCCAAAGATAAATAATTAGCCAGG	121		
Db	30012	AGACAGCAGCCTTGACAAACATGTGTACACTGTCTCTATAAAATACAAAATAATTAGCCAGG	29953		
QY	122	CTTAGTAGGCTCATCCCTGTGTGTCGCCAGTACTCTAGGGAGGCGAGAGTAGGA-----CTGCTT	177		
Db	29952	YGTGAGTTTGCGGCGCCTGTATGTCCCAAGCTACTTGGAGGCTGAGGCGAGAGAAATCACTTG	29893		

Qy	178	GTCCAGAGGCTCAAGACTGAGGACGTAGACCCAGCACTGGATTCAGCCGGGC	237
Db	29892	AAACCAGAGGTGAGGTTACAGTGACCTTAGATTGGCACTCGCACTCGACCTCGGGT	29833
Qy	238	AACAAAAAGAGACCTGTCTCAAAAAATTAAGTTAAATTAATATATATAATTAAGTTTA	297
Db	29832	GACAGAGTGAACCTCTGTCTCAAAAAAAATTTAAATCAATTGGAAAAAAATTTAAATTAAT	29773
Qy	298	AACCTAAACACATCTCTTTTCAAGAGGACCTCTTAAG	338
Db	29772	ATAGCTAGAAACAACCTTGATGACAAAAATGTGTACTTAAG	29732

```

RESULT 9
US-10-723-860-2320/c
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

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Query Match	9.5%	Score 152;	DB 9;	Length 135005;
Best Local Similarity	80.04;	Pred. No. 1.2e-26;		
Matches 216;	Conservative	0;	Mismatches 50;	Indels 4; Gaps 3;
QY	1	ACCTGTAATTCACACTACTGTGAGAGTCCGAGGTCAGAGAGCTCTTGAGGCCAGAGTTC	60	
Db	84870	ATCTGTAACTCTCAGACACTTTGGGGGCGAGAGTATGAGAGATTCTTGAGGCCAGAGTTC	84761	
QY	61	AAGAGCACCCTGACAAACACAGGAGA--CCTGTCACTACAAAGAAATTAATTAATAGCC	118	
Db	84760	AAGACTACTCTGGGGCAACATAGTGAGACCCTGTCTCTTAACAAAAATAGAAAAATTAATGTC	84701	
QY	119	AGCTTATGTGCTCATCCCTGTGCTCCAGCTACTTAGGGAGCGAAGTAGACTGCTTG	178	
Db	84700	GGGTATGTGTGCACATGCTGTAGTCTCCAGCTACTCAGAGGCTGAGGTATGAGATTCTTG	84641	
QY	179	-TCCAGAGAGTCGAAGACTGAGATGAGACTGAGACCCAGCACTCGAATTCAGGCTGGGC	237	
Db	84640	AGCTCAGAGAGTTCAGAGGCGGACAGACTGAGACGTGCCA-CTGTACTCCAACTGGGC	84582	
QY	238	AAACAAAAAGAGACCCTGTCTCAAAAAATTA	267	
Db	84581	AAACAGAACAGACCTGTCTCAAAAAATTA	84552	

```

RESULT 10
US-10-756-149-1719/C
/ Sequence 1719, Application US/10756149
/ Publication No. US20050181375A1
/ GENERAL INFORMATION:
/ APPLICANT: Azi2, Natasha
/ APPLICANT: Zlotnik, Albert
/ TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
/ TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
/ FILE REFERENCE: file
/ CURRENT APPLICATION NUMBER: US/10/756,149
/ CURRENT FILING DATE: 2004-01-12

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```

; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version
; SEQ ID NO 1719
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-1719

```

```

Query Match      9.5%; Score 152; DB 10; Length 135005;
Best Local Similarity - 80.0%; Pred. No. 1.2e-26;
Matches 216; Conservative 0; Mismatches 50; Indels 4; Gaps 3;

```

QY	1	ACCTGTAATTC	CAAGTACTGTGAGAGAGTCCAGAGGCTCAGAGACTGCTTGAGAGCCAGAGAGTTC	60
QY <td>84820</td> <td>ATCTGTATATCT</td> <td>CAAGCACTTTGGAGGCGAGAGGTAGAGGATTCCTTGAGAGGCGAGAGTTC</td> <td>84761</td>	84820	ATCTGTATATCT	CAAGCACTTTGGAGGCGAGAGGTAGAGGATTCCTTGAGAGGCGAGAGTTC	84761
Db <td>61</td> <td>AAGAGCAGCCTTGACAA</td> <td>CACAGGAGAG - CTGTCTCACTACAAAGATTAATAATTAGCC</td> <td>118</td>	61	AAGAGCAGCCTTGACAA	CACAGGAGAG - CTGTCTCACTACAAAGATTAATAATTAGCC	118
QY <td>84760</td> <td>AAGACTATCTCTGGGCAACATAGTAGAGCCCTCTCTCTCAAAAAATATAGAAAAATTAGTC</td> <td></td> <td>84701</td>	84760	AAGACTATCTCTGGGCAACATAGTAGAGCCCTCTCTCTCAAAAAATATAGAAAAATTAGTC		84701
Db <td>119</td> <td>AGGCTTATGTCCTCATCCCTGTGTGTCCAGCTACTATAGGGAGCGAGAGTAGAGCTGCTTG</td> <td></td> <td>178</td>	119	AGGCTTATGTCCTCATCCCTGTGTGTCCAGCTACTATAGGGAGCGAGAGTAGAGCTGCTTG		178
QY <td>84700</td> <td>GGGTATGTGTGCATGTCCCTGTATGTCCCACTACTCAGAGAGCTGTAGGTAGGATTCCTTG</td> <td></td> <td>84641</td>	84700	GGGTATGTGTGCATGTCCCTGTATGTCCCACTACTCAGAGAGCTGTAGGTAGGATTCCTTG		84641
Db <td>179</td> <td>-TCCAGAGAGTCAAGACTGCACTGAGTACTGAGACCCAGCCACTGTGATTTCCAGCCTTGAGC</td> <td></td> <td>237</td>	179	-TCCAGAGAGTCAAGACTGCACTGAGTACTGAGACCCAGCCACTGTGATTTCCAGCCTTGAGC		237
QY <td>84640</td> <td>AGCTTCAGAGAGTGAAGCGGCGAGCTGAGCTGAGCACTGATGCCA - CTGTATCTCCAACTGTGGC</td> <td></td> <td>84582</td>	84640	AGCTTCAGAGAGTGAAGCGGCGAGCTGAGCTGAGCACTGATGCCA - CTGTATCTCCAACTGTGGC		84582
Db <td>238</td> <td>AACAAAAAGAGACCCCTGTCTCAAAAAATA</td> <td>267</td> <td></td>	238	AACAAAAAGAGACCCCTGTCTCAAAAAATA	267	
QY <td>84581</td> <td>AACAGAAACAGACCTGTCTCAAAAAATA</td> <td>84552</td> <td></td>	84581	AACAGAAACAGACCTGTCTCAAAAAATA	84552	

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RESULT 11
US-09-925-065A-822292/C
; Sequence 822292, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 822292
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-822292

```

Query Match	Similarity	Score	DB	Length
Best Local	74.1%	150.6	1	558
Matches	217	Conservative	1	Mismatches 70; Indels 5; Gaps 2

QY	2	CCTGTAATCCAGTACTGTGAGAGTCCGAGTCCAGAGACTCTTGAGCCGAGATTCA	61
DB <td>345</td> <td>CCTGTAATCCAGCACTTTGGAGGCCAAGGAGAGTGAATTACTTGAGGTCAAGAGTTCA</td> <td>286</td>	345	CCTGTAATCCAGCACTTTGGAGGCCAAGGAGAGTGAATTACTTGAGGTCAAGAGTTCA	286
QY <td>62</td> <td>AGAGAGCCTGGACAACAACAGGAGACCTGTCACTTACAAGAATTAATTAATTAGCAGG</td> <td>121</td>	62	AGAGAGCCTGGACAACAACAGGAGACCTGTCACTTACAAGAATTAATTAATTAGCAGG	121
DB <td>285</td> <td>AAGCAGCCTGGCAACAACAGGTGAACCGGTCTTACTTAATAAATCAAAAATTAAGCAGG</td> <td>226</td>	285	AAGCAGCCTGGCAACAACAGGTGAACCGGTCTTACTTAATAAATCAAAAATTAAGCAGG	226


```

Oy      122  CTTATGGGCTATACCCCTGGATGCCAGGCTACGTGGAGGAGGAAGTAGAGACTGTTGT - - 179
Db      225  TGTGTGGTGGCAAGCCCTTAATGCCAGCTACCTTGGAGAGGCTGAGCAGGGGGGGTTGCTTG 166
Oy      180  --CCGAGGAGGTCAAGACTGCAGTAGAGTGAAGCCAGCCACTGCATTCAGACTGGGC 237
Db      165  AACCTGGGAGGTGGAGGTTGCAGTAGCCAGATCACGTGTA - CTGGCCCTCAGGCTGGGG 107
Oy      238  AACAAAAAGAGACCCCTGTCTCAAAAAAATNAGTTAAATTAATATAATATAAAAA 290
Db      106  AACTAAGTAGACTCTGTCTCAAAAAAATATAATATAATATAATATAATATAAAAA 54

```

```

RESULT 12
US-09-925-065A-839930
; Sequence 839930, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 839930
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-925-065A-839930

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[illegible]

RESULT 13
US-09-925-065A-822292/c
; Sequence 822292, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:

```

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 822292
LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-822292

Query Match          9.4%; Score 150.6; DB 5; Length 558;
Best Local Similarity 74.1%; Pred. NO. 2e-27;
Matches 211; Conservative 1; Mismatches 70; Indels 5; Gaps 2;
```

Qy	2	CCTGTAAATTCAGATCTGTGAGAGTCCAGGCTCAGAGACCTGTGAGGGCAGAGATTCA	61
Db	345	CCGTATATCCAGCACTTTGGGAGGCCAAGCAGGTGGATTACTTGAAGTCAGAGATTCA	286
Qy	62	AGAGCAGCCTGGAACAACACAGGAGACTGTCTACTACAAAGATTAATTAATTGCCAGG	121
Db	285	AGACCGCCTGGCCAAACAGGTGAACCCGTCTCTACTAAATAATCAAAAATTAGCCAGG	226
Qy	122	CTTAGAGGCTCAATCCCTGTGTGCCAGCTACATAGGAGGACGAGATGAGACTGGTGT--	179
Db	225	TGTGTGTGTGCATGCTGTGTATGTCCAGCTACTTGGAGGCTGAGAGCAGGGGGGTTGCTTG	166
Qy	180	--CCAGAGGTCAAAGCTGACGTGAGCTGAGCCCAAGCCACTGCATTCCAGCTGGGC	237
Db	165	AACCTGGAGGTGGAGGTTGCAGTGAAGCCAAATGACAGYCA-CTGCCCTCAGAGCTGGGG	107
Qy	238	AACAAATAAGAACCTCTCTCAAAAAATTAAGTTAAATTAATTAATTAATTAATTAATTA	290
Db	106	AACTAAGTAGACTGTCTCAAAAAAAAAAAAAAAAAAAGATTAAATAATTAATA 54	

```

RESULT 14
US-09-925-065A-839930
Sequence 839930, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Man-
title of invention: Nucleotide Polymorph
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 839930

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:44:48 ; Search time 46.7267 Seconds
(without alignments)
4040.340 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_1857
Perfect score: 1603
Sequence: 1 acctgttaaccagctactgt.....cgctgttagaaccgtcct 1603

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New.*
1: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US10_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US11_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US60_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/Pdata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	8.7	2312	US-11-293-697-880	Sequence 880, App
2	136.8	8.5	54550	US-11-318-813-42	Sequence 42, App1
3	134.6	8.4	2252	US-11-293-697-1292	Sequence 1292, App
4	132	8.2	2374	US-11-293-697-441	Sequence 441, App
5	130.2	8.1	3226	US-11-293-697-723	Sequence 723, App
6	129.8	8.1	4156	US-10-511-937-453	Sequence 453, App
7	129.6	8.1	4987	US-10-505-928-433	Sequence 433, App
8	129.6	8.1	4987	US-11-251-465-4	Sequence 4, App1
9	129.6	8.1	5014	US-11-251-465-5	Sequence 5, App1
10	129.4	8.1	2682	US-11-293-697-1324	Sequence 1324, App
11	128.4	8.0	54550	US-11-318-813-42	Sequence 42, App
12	128.2	8.0	3097	US-11-293-697-1206	Sequence 1206, App
13	127.8	8.0	2889	US-10-511-937-627	Sequence 627, App
14	127.8	8.0	2889	US-11-293-697-2187	Sequence 2187, App
15	127.8	7.9	2140	US-11-293-697-513	Sequence 513, App
16	126.8	7.9	2460	US-11-293-697-595	Sequence 595, App
17	126.8	7.9	2915	US-11-293-697-59	Sequence 59, App1
18	126.4	7.9	2849	US-11-293-697-404	Sequence 404, App
19	126.2	7.9	1801	US-11-293-697-1829	Sequence 1829, App
20	126.2	7.9	2393	US-11-293-697-2395	Sequence 2395, App
21	126	7.9	394191	US-10-506-549-3	Sequence 3, App1
22	125.6	7.8	1237	US-10-511-937-430	Sequence 430, App
23	125.6	7.8	138941	US-10-489-730-10	GENERAL INFORMATION
24	125.4	7.8	1853	US-11-293-697-2266	Sequence 2266, App
25	125.4	7.8	2105	US-11-293-697-122	Sequence 122, App

C	26	125.4	7.8	2949	7	US-11-293-697-426	Sequence 426, App
C	27	125	7.8	4086	7	US-11-301-554-1801	Sequence 1801, App
C	28	125	7.8	138941	6	US-10-489-730-10	GENERAL INFORMATION
C	29	124.6	7.8	2646	7	US-11-293-697-550	Sequence 550, App
C	30	124	7.7	1601	7	US-11-328-161-25	Sequence 25, App1
C	31	124	7.7	1645	7	US-11-328-161-12	Sequence 12, App1
C	32	124	7.7	2324	7	US-11-293-697-82	Sequence 82, App1
C	33	124	7.7	3766	7	US-11-293-697-647	Sequence 647, App1
C	34	124	7.7	5515	6	US-10-524-021-1	Sequence 1, App1
C	35	123.8	7.7	2330	7	US-11-293-697-1980	Sequence 1980, App
C	36	123.8	7.7	2168	7	US-11-293-697-1286	Sequence 1286, App
C	37	123.8	7.7	2648	7	US-11-293-697-807	Sequence 807, App
C	38	123.8	7.7	2308	7	US-11-293-697-1274	Sequence 1274, App
C	39	123.4	7.7	56580	6	US-10-553-298-1	Sequence 1, App1
C	40	123.4	7.7	1762	7	US-11-293-697-1638	Sequence 1638, App
C	41	123.2	7.7	1956	7	US-11-293-697-2159	Sequence 2159, App
C	42	123	7.7	2059	7	US-11-293-697-1623	Sequence 1623, App
C	43	123	7.6	1629	6	US-10-511-937-444	Sequence 444, App
C	44	122.4	7.6	2731	7	US-11-293-697-1412	Sequence 1412, App
C	45	122.4	7.6				

ALIGNMENTS

RESULT 1
US-11-293-697-880
; Sequence 880, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 880
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-880

Query Match 8.7%; Score 139; DB 7; Length 2312;
Best Local Similarity 76.2%; Pred. No. 2.4e-15;
Matches 211; Conservative 0; Mismatches 60; Indels 6; Gaps 3;

QY	1	ACCTGAATTCAGTACTGTGAGAGTCCGAGGCTGAGAGCACTGAGGCCAGAGTTC	60
DB	1142	ACCTGAATTCAGTACTGTGAGAGTCCGAGGCTGAGAGCACTGAGGCCAGAGTTC	1201
QY	61	AAGAGAGCCTGAGCAACACAGGAGAC-CTGTACTACAAAGATTAATTAAGCA	119
DB	1202	AAGAGAGCCTGAGCAACATAGTGAACCTTGTCTACAAATTAATTAATTAAGCTG	1261
QY	120	GGCTTGTGCTATTCCTGTGTCTCCAGTACTATAGGAGGCAAGTATGAG-CTGC	175
DB	1262	GGCTTGTGCTATTCCTGTGTCTCCAGTACTATAGGAGGCAAGTATGAG-CTGC	1321
QY	176	TTGTCCAGAGGTCAAGCTGAGTGTGAGCCAGCCAGCTGATTCAGGCTGG	235
DB	1322	TGAGCCAGAGGTCAAGCTGAGTGTGAGCCAGCCAGCTGATTCAGGCTGG	1380
QY	236	GCAACAAAAGAGACCTGTCTCAAAAATTAAGTTAA	272
DB	1381	GCAACAAAAGAGACCTGTCTCAAAAATTAAGTTAA	1417

RESULT 2
US-11-318-813-42
; Sequence 42, Application US/11318813

Publication No. US20060105381A1
GENERAL INFORMATION:
APPLICANT: Eilipais Bioherapeutics Corporation
APPLICANT: Peltekova, Vanya D
APPLICANT: Siminovitich, Katherine A
APPLICANT: St George-Hyslop, Peter H
APPLICANT: Rubin, Laurence A
APPLICANT: Peltekova, Vanya D
APPLICANT: Muntle, Richard F
TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIATED WITH INFLAMMATORY BOWEL DISORDERS
FILE REFERENCE: ELP-020
CURRENT APPLICATION NUMBER: US/11/318,813
CURRENT FILING DATE: 2005-12-27
PRIOR APPLICATION NUMBER: US/10/327,188
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/362,700
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/343,338
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/427,529
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/362,717
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 54550
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (4809)..(4809)
OTHER INFORMATION: n can be a or t or g or c

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3 LOCATION: (5164)..(5164)
4 OTHER_INFORMATION: n can be a or t or g or c
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6 NAME/KEY: misc_feature
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18 NAME/KEY: misc_feature
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52 OTHER_INFORMATION: n can be a or t or g or c
53 FEATURE:

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	Query Match	8.5%	Score 136.8	DB 7	Length 54550
	Best Local Similarity	69.5%	Pred. No. 6,2e-15		
	Matches 228	Conservative 0	Mismatches 94	Indels 6	Gaps 3
QY	2	CCTGTAAATTCAGTACTGTAGAGAGTCCGAGGTACAGAGACTGCTTANAGCCACAGATTCA	61		
Db	46202	CATGTAAATCCAGACACTTTGTGAGAGGCCAAGGTAGTGGATACCTGAGGCCAGAGATTCA	46261		
QY	62	AGACACACCTGGACCAACACAGGAGA--CCTGTACATCAAAAGAAATTAATTAACCAAG	120		
Db	46262	AGACACACCTGGACCATGGTAGAAACCTGTCTCTAATAAAATTAATAATTAACCAAG	46321		
QY	121	GCTTAGTGGCTCATCCCTGTGGTCCCACTACTAGGAGGACAGAAATGAGACTGCTTGT-	179		
Db	46322	GTTGTGCTGGCAGGAGCTCTTAATCCGGCTTACTCTGGAGGCTGAGTAGAGAAATTGCTT	46381		
QY	180	---CCAGAGAGTCAAAAGCTGCAGTAGTGCAGAACCCAGGCACCTGATTCAGCCTGGG	236		
Db	46382	GAACCCAGAGAGGCAGAGAGCTGCACATAGTCAAAATTGACACA--CTGCATCTCAACCTGGG	46440		

[illegible]

```

RESULT 3
US-11-293-697-1292
; Sequence 1292, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1292
; LENGTH: 2252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1292

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Query Match	8.4%	Score 134.6	DB 7	Length 2252
Best Local Similarity	72.1%	Pred. No. 1.2e-14		
Matches 204	Conservative 0	Mismatches 74	Indels 5	Gaps 2
Qy	2	CCTGTAATTCACGACTGTGAGAGTCCGAGGTCAAGAGACTGCTTTGAGCCGAGAGTTCA	61	
Db	1691	CCGTATATCCAGACACTTTGGGATTTGGAGGTGGCCGATCATTAGTGTCAGAGATTCA	1950	
Qy	62	AGAGCAGCCTTGACAACACAGGAGACCTGTCACTACAAAGATTAATTAATTAGCCAGG	121	
Db	1951	AGACACAGCTGGCCACATGTTAAACCCCGTCTCTACAAATATACAAAGATTAGCTGG	2010	
Qy	122	CTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGCAAGATGGA---CTGCTT	177	
Db	2011	TGTGTGGCACGGGCTGTATATCCACACCCCTTGAAAGGCCAAGCGAGAAATGCGCTC	2070	
Qy	178	GTCCACGAGGTCAAGACTGCAGTGAAGCTGAGCCAGCCACTGTCATTCCAGGCTGGG	237	
Db	2071	AACACTGAGGTGAGAGGTTCGACGTGACCTGAGATTGTGCCA-CTGCACTCCAGGCTGGC	2129	
Qy	238	AACAAAAAGAGACCCTGTCTCAAAAAATTAATTAAATTAATAA	280	
Db	2130	AATGAGCGAAGACCTGTCTTCAAAAAATTAATTAATTAATAA	2172	

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RESULT 4
US-11-293-697-441/C
; Sequence 441, Application US//11293697
; Publication No. US20060105376A1
;
GENERAL INFORMATION:
;
APPLICANT: HELIX RESEARCH INSTITUTE
;
TITLE OF INVENTION: Novel full length cDNA
;
FILE REFERENCE: H1-A0106
;
CURRENT APPLICATION NUMBER: US//11/293,697
;
CURRENT FILING DATE: 2005-12-05
;
PRIORITY APPLICATION NUMBER: US/10/108,260
;
PRIOR FILING DATE: 2002-03-28
;
NUMBER OF SEQ ID NOS: 5458
;
SOFTWARE: PatentIn Ver. 2.1
;
SEQ ID NO 441
;
LENGTH: 2374
;
TYPE: DNA
;
ORGANISM: Homo sapiens
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SOFTWARE: PatentIn 3.2
SEQ ID NO 433
LENGTH: 4987
TYPE: DNA
ORGANISM: Homo sapiens
US-10-505-928-433

Query Match
Best Local Similarity 71.5%; Pred. No. 8.4e-14;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTCTGAGAGTCCGAGGTCAGAGGACTCTTGAGGCCAGAGTTCA 61
DB 3805 CCTGTAATTCAGTCTGAGAGTCCGAGGTCAGAGGACTCTTGAGGCCAGAGTTT 3746
QY 62 AGAGCAGCCTTGAGCAACACAGGAGGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3745 AGAGCAGCCTTGAGCAACATGAGTGAACCTGTCTCTAATAAATAATTAGCCAG 3686
QY 121 GCTTAAGTGCATCCCTGTGTGTCCTGAGTCTGAGGAGCAGAGTGAAGA---CTGCT 176
DB 3685 GTGTGTGGGACACACCTGTATCCAGTACTTGGAGGCCAAGGAGGAAATATCACTT 3626
QY 177 TGTCCAGAGAGTCAAGACTGCACTGAGTGAAGACCAGCCACTGATTCAGCCTGGG 236
DB 3625 GAACCTGGTGTGAGAGTGTGACAGTGAAGGAGATTCACCA-CTGCATCTCAGCCTGGG 3567
QY 237 CAACAAAAGAGACCCCTGTCTCAAAAATAAATAAATAAATAAATAAATAA 294
DB 3566 TGACACAGTGAAGACTGTATCGCAAAAAAAGT 3509

RESULT 8

US-11-251-465-4/C
Sequence 4, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 4987
TYPE: DNA
ORGANISM: Homo sapiens
US-11-251-465-4

Query Match
Best Local Similarity 71.5%; Pred. No. 8.4e-14;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTCTGAGAGTCCGAGGTCAGAGGACTCTTGAGGCCAGAGTTCA 61
DB 3805 CCTGTAATTCAGTCTGAGAGTCCGAGGTCAGAGGACTCTTGAGGCCAGAGTTT 3746
QY 62 AGAGCAGCCTTGAGCAACACAGGAGGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3745 AGAGCAGCCTTGAGCAACATGAGTGAACCTGTCTCTAATAAATAATTAGCCAG 3686
QY 121 GCTTAAGTGCATCCCTGTGTGTCCTGAGTCTGAGGAGCAGAGTGAAGA---CTGCT 176
DB 3685 GTGTGTGGGACACACCTGTATCCAGTACTTGGAGGCCAAGGAGGAAATATCACTT 3626

QY 177 TGTCCAGAGAGTCAAGACTGCACTGAGTGAAGACCAGCCACTGATTCAGCCTGGG 236
DB 3625 GAACCTGGTGTGAGAGTGTGACAGTGAAGGAGATTCACCA-CTGCATCTCAGCCTGGG 3567
QY 237 CAACAAAAGAGACCCCTGTCTCAAAAATAAATAAATAAATAAATAAATAA 294
DB 3566 TGACACAGTGAAGACTGTATCGCAAAAAAAGT 3509

RESULT 9

US-11-251-465-5/C
Sequence 5, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 5014
TYPE: DNA
ORGANISM: Homo sapiens
US-11-251-465-5

Query Match
Best Local Similarity 71.5%; Pred. No. 8.4e-14;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTCTGAGAGTCCGAGGTCAGAGGACTCTTGAGGCCAGAGTTCA 61
DB 3832 CCTGTAATTCAGTCTGAGAGTCCGAGGTCAGAGGACTCTTGAGGCCAGAGTTT 3773
QY 62 AGAGCAGCCTTGAGCAACACAGGAGGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3772 AGAGCAGCCTTGAGCAACATGAGTGAACCTGTCTCTAATAAATAATTAGCCAG 3713
QY 121 GCTTAAGTGCATCCCTGTGTGTCCTGAGTCTGAGGAGCAGAGTGAAGA---CTGCT 176
DB 3712 GTGTGTGGGACACACCTGTATCCAGTACTTGGAGGCCAAGGAGGAAATATCACTT 3653
QY 177 TGTCCAGAGAGTCAAGACTGCACTGAGTGAAGACCAGCCACTGATTCAGCCTGGG 236
DB 3652 GAACCTGGTGTGAGAGTGTGACAGTGAAGGAGATTCACCA-CTGCATCTCAGCCTGGG 3594
QY 237 CAACAAAAGAGACCCCTGTCTCAAAAATAAATAAATAAATAAATAAATAA 294
DB 3593 TGACACAGTGAAGACTGTATCGCAAAAAAAGT 3536

RESULT 10

US-11-293-697-1324
Sequence 1324, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: Helix Research Institute
TITLE OF INVENTION: Novel Full Length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1

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/ SEQ ID NO 1324
/ LENGTH: 2682
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-293-697-1324

Query Match      8.1%; Score 129.4; DB 7; Length 2682;
Best Local Similarity 71.1%; Pred. No. 8.8e-14;
Matches 214; Conservative 0; Mismatches 81; Indels 6; Gaps 3;

QY      2 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACCTGTGAGGCGAGAGTTCA 61
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QY      62 AGAGCAGCCTGAGCAACACAGGAGA-CCTGTACTACAAAGATTAATTAATTAAGCCAG 120
DB      2150 AGAGCAGCCTGAGCAACATGTGTAACCCCGTCTTACTTAAATTAATTAAGCCAG 2209
QY      121 GCTTATGCTCATCTCCTGTGCTCCAGCTACTAGAGGAGCAGAAAGTAGACTGCTGT- 179
DB      2210 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2269
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RESULT 11
US-11-318-813-42/c
/ Sequence 42, Application US/11318813
/ Publication No. US20060105381A1
/ GENERAL INFORMATION:
/ APPLICANT: Ellipsis Biotherapeutics Corporation
/ APPLICANT: Peltekova, Yanya D
/ APPLICANT: Stiminovitch, Katherine A
/ APPLICANT: St George-Hyslop, Peter H
/ APPLICANT: Rubini, Laurence A
/ APPLICANT: Peltekova, Yanya D
/ APPLICANT: Winkle, Richard F
/ TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIAT
/ TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS
/ FILER REFERENCE: ELLP-020
/ CURRENT APPLICATION NUMBER: US/11/318,813
/ PRIOR FILING DATE: 2005-12-27
/ PRIOR APPLICATION NUMBER: US/10/327,188
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/362,700
/ PRIOR FILING DATE: 2002-03-08
/ PRIOR APPLICATION NUMBER: 60/343,338
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/427,529
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: 60/362,717
/ PRIOR FILING DATE: 2002-03-08
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 42
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Matches 208; Conservative 0; Mismatches 74; Indels 5; Gaps 3;

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DB 16640 AAGGAGAGCTGGAACAACAGGGAGA-CCTGTCTACTAATAAATTAATTAGCTG 16581
QY 120 GGCTTAGTGCTCATCTCTGTGTGCTCCAGCTACTAGGAGGAGAACTAGGA--CTGCT 176
DB 16580 GGCAGGTTGCAAGTGTCTGTATCCAGCTACTGGGAACCTGAGGAGAGATTGCT 16521
QY 177 TGTCCAGAGGTCAGAGTGCAGTGAAGTGAAGCCAGCACTGATTCAGGCTGGG 236
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DB 16461 CAACAAAAGAGACTCATCTCAACAAACAACAACAACACTATA 16415
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Sequence 1206, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1206
LENGTH: 3097
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-1206

Query Match 8.0%; Score 128.2; DB 7; Length 3097;
Best Local Similarity 72.5%; Pred. No. 1,4e-13;
Matches 208; Conservative 0; Mismatches 73; Indels 6; Gaps 3;

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DB 2323 CCTGTATTCACGACTGTGAGAGTCCGAGTCAAGAGCTGCTGAGGCCAGAGTTCA 2264
QY 62 AAGAGAGCTGGAACAACAGGGAGA-CCTGTCACTACAAGAAATTAATTAGCCAG 120
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Query Match 7.9%; Score 127.2; DB 7; Length 2140;
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 Matches 213; Conservative 0; Mismatches 83; Indels 6; Gaps 3;

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QY 62 AGAGCAGCTTGACACACAGGAGAG-CCTGTCACTACAAAGATTAATAATTAGCCAG 120
 DB 1774 AGACCAAGCTTGACACACAGGAGAGTGAACCTGTCTCTACTAATACATACAAAATTAGTCGG 1715

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	485	21.4	736	2	US-08-846-012A-1
4	485	21.4	736	2	US-09-100-297-1
5	170.4	7.5	601	3	US-09-949-016-176561
6	170.4	7.5	35493	3	US-09-949-016-15780
7	168.4	7.4	37292	3	US-09-949-016-15382
8	167.4	7.4	126237	3	US-09-949-016-16674
9	167.4	7.4	126237	3	US-09-949-016-16675
10	167.4	7.4	16230	3	US-09-949-016-14788
11	165.2	7.3	99370	3	US-09-949-016-17540
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15	164.2	7.2	63783	3	US-09-949-016-13576
16	164.2	7.2	24221	3	US-09-949-016-13576
17	163.8	7.2	601	3	US-09-949-016-63328
18	163	7.2	32594	3	US-09-949-016-12319
19	163	7.2	32594	3	US-09-949-016-15242
20	162.6	7.2	29171	3	US-09-949-016-12283
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32	161.4	7.1	17607	3	US-09-949-016-15968	Sequence 15968, A
33	161.2	7.1	56737	3	US-09-782-378A-17	Sequence 17, Appl
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38	160.8	7.1	52824	3	US-09-949-016-12116	Sequence 12116, A
39	160.6	7.1	8133	3	US-09-659-791A-10	Sequence 10, Appl
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41	160.6	7.1	61461	3	US-09-949-016-16419	Sequence 16419, A
42	160.4	7.1	40641	3	US-09-949-016-11376	Sequence 11376, A
43	160.4	7.1	55130	3	US-09-949-016-11850	Sequence 11850, A
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45	160	7.0	152583	3	US-09-949-016-17390	Sequence 17390, A

ALIGNMENTS

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US-09-949-016-14689
Sequence 14689, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14689
LENGTH: 39754
TYPE: DNA
ORGANISM: Human
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Qy 1805 GAGAAAGTGAATTAAGACAGGCGCGCGCTGACGCTTGTGAACACCGTCTGCTGGG 1864
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Db 29547 AAGGCAAGAGGTGTGTGACGTGACCAAGACTTGTGTGTGTGTGTGTGTGTGTGTGT 29606
Qy 1925 CAGAGGTTGGCGCGCGGAGAGTGTGAGGAGCGGAGGAGTGTGCAAGAGGAGTGAACA 1984
Db 29607 CAGAGGTTGGCGCGCGGAGAGTGTGAGGAGCGGAGGAGTGTGCAAGAGGAGTGAACA 29666
Qy 1985 TCTCGGAGAAACGAGAGTGAACGCGGTATGAGGAGCGACCGGAAACGCGAGTGTGAAGA 2044
Db 29667 TCTCGGAGAAACGAGAGTGAACGCGGTATGAGGAGCGACCGGAAACGCGAGTGTGAAGA 29726
Qy 2045 TCAATGAGAAACCTTAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2104
Db 29727 TCAATGAGAAACCTTAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 29786
Qy 2105 GCAACCAATAGAGAGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2164
Db 29787 GCAACCAATAGAGAGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 29846
Qy 2165 CCCCAGAGCTTAAAGCG 2224
Db 29847 CCCCAGAGCTTAAAGCG 29906
Qy 2225 GCGCTTGGGATTAAGTGTGTCAAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2270
Db 29907 GCGCTTGGGATTAAGTGTGTCAAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 29952

RESULT 2
US-09-949-016-15281
; Sequence 15281: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949.016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15281
LENGTH: 11808
TYPE: DNA
ORGANISM: Human
US-09-949-016-15281

Query Match 89.1%; Score 2022.8; DB 3; Length 11808;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 1; Gaps 1;

Matches 2035; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 233 GAGGCGACGACAGTGGCTCAACCTGTATTCAGTACTGTGAGAGTCCGAGGTCAAG 292
DB 1 GAGGCGACGACAGTGGCTCAACCTGTATTCAGTACTGTGAGAGTCCGAGGTCAAG 60
QY 293 GACTGCTTGAAGCCAGAGATTCAAGAGCAGCTTGAGCAACACAGGAGACCTGTCTAC 352
DB 61 GACTGCTTGAAGCCAGAGATTCAAGAGCAGCTTGAGCAACACAGGAGACCTGTCTAC 120
QY 353 AAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412
DB 121 AAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
QY 413 GGCAGAGTGAAGTGAAGTGTCTCCAGAGAGTCAAGAGTCAAGTCAAGTCAAGTCAAG 472
DB 181 GGCAGAGTGAAGTGAAGTGTCTCCAGAGAGTCAAGAGTCAAGTCAAGTCAAGTCAAG 240
QY 473 CCTGATTCAGCTGGGCAACAAAGAGACCTGTCTCAAAATTAATTAATTAATTAAT 532
DB 241 CCTGATTCAGCTGGGCAACAAAGAGACCTGTCTCAAAATTAATTAATTAATTAAT 300
QY 533 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 592
DB 301 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
QY 593 GACTTCATGCTGCGTCTGTGATCTCACTTCCCTTTTCAAGGCTCAACTTTTAA 652
DB 361 GACTTCATGCTGCGTCTGTGATCTCACTTCCCTTTTCAAGGCTCAACTTTTAA 420
QY 653 GTCTCTTTTGCAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 712
DB 421 GTCTCTTTTGCAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 713 GACAGCCAGGGGCAATTTTGTGTCGAGGCTTGTGATCTGCTGCTGCTGCTGCTGCTG 772
DB 481 GACAGCCAGGGGCAATTTTGTGTCGAGGCTTGTGATCTGCTGCTGCTGCTGCTGCTG 540
QY 773 CAATCTCAGCAAAATTTGCCGAGCTCTCCGAAATGACAGACAGACAGAGTCAAGGCG 832
DB 541 CAATCTCAGCAAAATTTGCCGAGCTCTCCGAAATGACAGACAGAGTCAAGGCG 600
QY 833 AAAAGCTAGAGAACTGGCGGAGGAGACTCAAGTGGCAAAAAAATTATCTTTTC 892
DB 601 AAAAGCTAGAGAACTGGCGGAGGAGACTCAAGTGGCAAAAAAATTATCTTTTC 660
QY 893 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 952
DB 661 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 720
QY 953 CTCTCTGCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 1012
DB 721 CTCTCTGCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 780

QY 1013 GCAGAAATTAATCTGCTTGAATCTTGTTCACGCTGCTTGTCCAGACCATGCGCTCG 1072
DB 781 GCAGAAATTAATCTGCTTGAATCTTGTTCACGCTGCTTGTCCAGACCATGCGCTCG 840
QY 1073 GCGGTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1132
DB 841 GCGGTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 900
QY 1133 TTCCCTGAGAGTCCCTTCTGCTGTGAAAACATATATGCGCCGAGCTGACAGAGTGA 1192
DB 901 TTCCCTGAGAGTCCCTTCTGCTGTGAAAACATATATGCGCCGAGCTGACAGAGTGA 960
QY 1193 AGTGTGAATATCAGAGAGATGACTGAAAGCTTTTGGAGTCCGTTTCTCATTTGAAA 1252
DB 961 AGTGTGAATATCAGAGAGATGACTGAAAGCTTTTGGAGTCCGTTTCTCATTTGAAA 1020
QY 1253 ATGAGGTTAATTAACAGCTTCTTCTAATCCCAAGCAGAGTGTGTCGCGGAGAG 1312
DB 1021 ATGAGGTTAATTAACAGCTTCTTCTAATCCCAAGCAGAGTGTGTCGCGGAGAG 1080
QY 1313 GGCCCAATTTGTGCTGTTTCAAGCATGTTACCCCAAGAGAGGAGTCAAGCAATTAA 1372
DB 1081 GGCCCAATTTGTGCTGTTTCAAGCATGTTACCCCAAGAGAGGAGTCAAGCAATTAA 1140
QY 1373 GGCAGAACAGCCCGGTTTCATCTCTGACGCTTTTCTCATCCAGGCTGAGACAGAG 1432
DB 1141 GGCAGAACAGCCCGGTTTCATCTCTGACGCTTTTCTCATCCAGGCTGAGACAGAG 1200
QY 1433 CTGGCTGGGCGCGGCTGTGCTTGTCAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1492
DB 1201 CTGGCTGGGCGCGGCTGTGCTTGTCAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
QY 1493 TGTAGAGCGTGAAGTCAAGCTGAGGCTCCCGCGCGGAGCTTTTATGTCCTCG 1552
DB 1261 TGTAGAGCGTGAAGTCAAGCTGAGGCTCCCGCGCGGAGCTTTTATGTCCTCG 1320
QY 1553 TCCTTAAACGCGAGCGCTTCACCGGAGGAGAGGCGGAAACCCAGCGAGCCCAACG 1612
DB 1321 TCCTTAAACGCGAGCGCTTCACCGGAGGAGAGGCGGAAACCCAGCGAGCCCAACG 1380
QY 1613 GCTGTGTCGAGTGGCGGAGCACTGTTGTCGAGTCTGATTTGTTCTTCCCGGACA 1672
DB 1381 GCTGTGTCGAGTGGCGGAGCACTGTTGTCGAGTCTGATTTGTTCTTCCCGGACA 1440
QY 1673 ACGCGGCGGCTGTAAACCAATGACAGCGAGGCGGCTGCGAGGCGCCAGTCCGCTGC 1732
DB 1441 ACGCGGCGGCTGTAAACCAATGACAGCGAGGCGGCTGCGAGGCGCCAGTCCGCTGC 1500
QY 1733 AGAGCCAGCGCGCGCTCGCTGCGAGAGGAGTGTGATTTGCCAGCGTAAAGGAGGCT 1792
DB 1501 AGAGCCAGCGCGCGCTCGCTGCGAGAGGAGTGTGATTTGCCAGCGTAAAGGAGGCT 1560
QY 1793 GGGCCCAATTAAGAGAGAGTGAACCTTAAGACAGGCGCGCGTGAAGCTTTTGAAGAC 1852
DB 1561 GGGCCCAATTAAGAGAGAGTGAACCTTAAGACAGGCGCGCGTGAAGCTTTTGAAGAC 1619
QY 1853 GTCTGCTGAGAGAGGAGAGGAGTGTGACTGAGCAAACTTTTCTGCGGCTGAGTC 1912
DB 1619 GTCTGCTGAGAGAGGAGAGGAGTGTGACTGAGCAAACTTTTCTGCGGCTGAGTC 1679
QY 1913 TTGCTATCTCTCAAGAGAGTGTGCGGCGCGGAGAGAGTGTGAGGAGAGGAGGAGGAG 1972
DB 1680 TTGCTATCTCTCAAGAGAGTGTGCGGCGCGGAGAGAGTGTGAGGAGAGGAGGAGGAG 1739
QY 1973 AGGAGAGTGAACATCTCGGAGAAAGAGAGTGAACAGGAGTGAATGAGAGCAGGAGAAAG 2032
DB 1740 AGGAGAGTGAACATCTCGGAGAAAGAGAGTGAACAGGAGTGAATGAGAGCAGGAGAAAG 1799
QY 2033 GAGTGAAGAAAGTCAAGAGAGAACTTAAGGAGGAGGAGGAGTCCCGGAGAAAGGAGGAG 2092
DB 1800 GAGTGAAGAAAGTCAAGAGAGAACTTAAGGAGGAGGAGGAGTCCCGGAGAAAGGAGGAG 1859

QY 2093 TCACAGGCTCTCCGACCCCAAGTAGAGAGCTGCGAGGCGCCGCGCCCGCGAGGCGCCAC 2152
DB 1860 TCACAGGCTCTCCGACCCCAAGTAGAGAGCTGCGAGGCGCCGCGCCCGCGAGGCGCCAC 1919
QY 2153 CCGCGGCGCCCGCGCGAGGCTTAAAGCGCGCGCGCGCTGCGCGAGGCGCCACTGCGAA 2212
DB 1920 CCGCGGCGCCCGCGCGAGGCTTAAAGCGCGCGCGCGCTGCGCGAGGCGCCACTGCGAA 1979
QY 2213 GCCCAGCTGCGCGCGCTTGGAGTTCAGCTGTCACAGCTGCGCGCGCTGCTCGAGCGCG 2270
DB 1980 GCCCAGCTGCGCGCGCTTGGAGTTCAGCTGTCACAGCTGCGCGCGCTGCTCGAGCGCG 2037

RESULT 3

US-08-846-012A-1
Sequence 1, Application US/08846012A
Patent No. 5807740
GENERAL INFORMATION:
APPLICANT: AMARAL, M. Catherine.
APPLICANT: CHEN, Jin-Long
TITLE OF INVENTION: Regulators of UCP2 Gene Expression
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,012A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 736 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-846-012A-1

Query Match 21.4%; Score 485; DB 2; Length 736;
Best Local Similarity 99.6%; Pred. No. 3.5e-100;
Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1762 GGGTGGTGTAGTTTGGCCAGCGTGAAGGGGGGCTGGGCCCATTAAGAGGAAGTGCATTAG 1821
DB 1 GGGTGGTGTAGTTTGGCCAGCGTGAAGGGGGGCTGGGCCCATTAAGAGGAAGTGCATTAG 60
QY 1822 ACACGCGCCCGCGTGAAGCGCTGTAGAAACCGTCTGGCTGGGGAAGCAAGAGGTGTGTG 1881
DB 61 ACACGCGCCCGCGTGAAGCGC-TGTTTAAACCGTCTGGCTGGGGAAGCAAGAGGTGTGTG 119
QY 1882 ACTGCAACAAGACTTTTCTGGCGGTCAAGTCTTGCCATCTCAAGAGGTTGGCGGCGCG 1941
DB 120 ACTGCAACAAGACTTTTCTGGCGGTCAAGTCTTGCCATCTCAAGAGGTTGGCGGCGCG 179
QY 1942 AAGAGTGTGAGGCAAGCGCGGGAAGTGGCAAGGAGTACCATCTTCGGGGAACAAGAA 2001
DB 180 AAGAGTGTGAGGCAAGCGCGGGAAGTGGCAAGGAGTACCATCTTCGGGGAACAAGAA 239

QY 2002 GTAAACGGGTGATGATGAGACGACCGGAACGGGAGTGTGAGAAAGTATGAGAGAACCTTA 2061
DB 240 GTAAACGGGTGATGATGAGACGACCGGAACGGGAGTGTGAGAAAGTATGAGAGAACCTTA 299
QY 2062 GCGCGGCGGTCTCCCGCGGAAGGCGGTGCTCCAGGCTCTCCGACCCCAAGTAAAGACT 2121
DB 300 GCGCGGCGGTCTCCCGCGGAAGGCGGTGCTCTCCAGGCTCTCCGACCCCAAGTAAAGACT 358
QY 2122 GCGCGGCGGTCTCCCGCGGAGGCGGTGCTCCAGGCTCTCCGACCCCGCGGCTTAAAGCGG 2181
DB 359 GCGCGGCGGTCTCCCGCGGAGGCGGTGCTCCAGGCTCTCCGACCCCGCGGCTTAAAGCGG 418
QY 2182 CCGCGGCGGTCTCCCGCGGAGGCGGTGCTCCAGGCTCTCCGACCCCGCGGCTTAAAGCGG 2241
DB 419 CCGCGGCGGTCTCCCGCGGAGGCGGTGCTCCAGGCTCTCCGACCCCGCGGCTTAAAGCGG 478
QY 2242 GTCCAGGCTGCGCGCGGTCTGTCGACGCG 2270
DB 479 GTCCAGGCTGCGCGCGGTCTGTCGACGCG 507

RESULT 4

US-09-100-297-1
Sequence 1, Application US/09100297
Patent No. 5849514
GENERAL INFORMATION:
APPLICANT: AMARAL, M. Catherine.
APPLICANT: CHEN, Jin-Long
TITLE OF INVENTION: Regulators of UCP2 Gene Expression
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,297
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,012
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 736 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-100-297-1

Query Match 21.4%; Score 485; DB 2; Length 736;
Best Local Similarity 99.6%; Pred. No. 3.5e-100;
Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1762 GGGTGGTGTAGTTTGGCCAGCGTGAAGGGGGGCTGGGCCCATTAAGAGGAAGTGCATTAG 1821
DB 1 GGGTGGTGTAGTTTGGCCAGCGTGAAGGGGGGCTGGGCCCATTAAGAGGAAGTGCATTAG 60

QY 1822 ACACGCCCCCGCTGAGACCTGTTTGAACCGTCTCTGCTGGGAAGCGAAGAGTGTGTG 1881
Db 61 ACACGCCCCCGCTGAGACCGT-TGTTTGAACCGTCTCTGCTGGGAAGCGAAGAGTGTGTG 119
QY 1882 ACTGACAAAGACTTGTCTTCTGAGCGGTCACTTGGCATCTTCAAGAGAGTTGGCGGCGG 1941
Db 120 ACTGACAAAGACTTGTCTTCTGAGCGGTCACTTGGCATCTTCAAGAGAGTTGGCGGCGG 179
QY 1942 AGAGAGTGTGAGCGAGAGCGGAGTGTGCAAGGAGTGTGACATCTCGGGGAACGAA 2001
Db 180 AGAGAGTGTGAGCGAGAGCGGAGTGTGCAAGGAGTGTGACATCTCGGGGAACGAA 239
QY 2002 GTAAACCGGTGTGATGTGAGCGAAGCGGAGTGTGAGAAAGTATGTAGAGAACCTTA 2061
Db 240 GTAAACCGGTGTGATGTGAGCGAAGCGGAGTGTGAGAAAGTATGTAGAGAACCTTA 299
QY 2062 GCGCGGCGGCTGCTCCCGCGGAAAGCGGCTGCTCCAGGCTTCCGACCCCAAGTAGAGCT 2121
Db 300 GCGCGGCGGCTGCTCCCGCGGAAAGCGGCTGCTCCAGGCTTCCGACCCCAAGTAGAG- 358
QY 2122 GCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2181
Db 359 GCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 418
QY 2182 GCGCGGCGGCTGCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2241
Db 419 GCGCGGCGGCTGCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 478
QY 2242 GTCCACGCTGCGCGGCGGCTGCTCCGACGCG 2270
Db 479 GTCCACGCTGCGCGGCGGCTGCTCCGACGCG 507

RESULT 5

US-09-949-016-176561/c
; Sequence 176561, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176561
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-176561

Query Match 7.5%; Score 170.4; DB 3; Length 601;

Best Local Similarity 74.7%; Pred. No. 4.2e-29; Matches 254; Conservative 0; Mismatches 81; Indels 5; Gaps 3;

QY 217 TTTAAGAGAAATTTCTTAGGCGCAGCAGTGTCTACACCTGTATTTCCAGTACTGTGA 276
Db 600 TTTAATAATATATATCGGGGCGAGCGCAGTGTCTACACCTGTATTTCCAGCATTGG 541
QY 277 GAGGCCAGGTGAGAGAGTGTCTTAGGCGGAGGTTCAAGAGAGTGTGACAAACAG 336
Db 540 GAGGCCAGGTGAGTGTCTTCACTGAGGCGGAGGTTCAAGAGAGTGTGACAAACAG 481
QY 337 GGAGA-CCTGTCACTAACAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 395

Db 480 CGAAACCCATCTCCATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 421
QY 396 GTCCAGTACTAGAGAGGAG 452
Db 420 ATCCAGTACTAGAGAGGAG 361
QY 453 AGTAGCTGAG 512
Db 360 ATTGAGCTGAGATCATGTCCA-CTGCGTTCCAGCGCTGGGCAACAAAGCAGACTCATCTC 302
QY 513 AAAAATAGTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 552
Db 301 AATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 262

RESULT 6

US-09-949-016-16780/c
; Sequence 16780, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16780
; LENGTH: 35493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(35493)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16780

Query Match 7.5%; Score 170.4; DB 3; Length 35493;

Best Local Similarity 74.7%; Pred. No. 1.8e-28; Matches 254; Conservative 0; Mismatches 81; Indels 5; Gaps 3;

QY 217 TTTAAGAGAAATTTCTTAGGCGCAGCAGTGTCTACACCTGTATTTCCAGTACTGTGA 276
Db 12792 TTTAATAATATATATCGGGGCGAGCGCAGTGTCTACACCTGTATTTCCAGCATTGG 12733
QY 277 GAGGCCAGGTGAGAGAGTGTCTTAGGCGGAGGTTCAAGAGAGTGTGACAAACAG 336
Db 12732 GAGGCCAGGTGAGTGTCTTCACTGAGGCGGAGGTTCAAGAGAGTGTGACAAACAG 12673
QY 337 GGAGA-CCTGTCACTAACAAGAAATTAATAATTAATTAATTAATTAATTAATTAATTA 395
Db 12672 CGAAACCCATCTCCATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 12613
QY 396 GTCCAGTACTAGAGAGGAG 452
Db 12612 ATCCAGTACTAGAGAGGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 12553
QY 453 AGTAGCTGAG 512
Db 12552 ATTGAGCTGAGATCATGTCCA-CTGCGTTCCAGCGCTGGGCAACAAAGCAGACTCATCTC 12494
QY 513 AAAAATAGTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 552
Db 12493 AATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 12454

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RESULT 7
US-09-949-016-15382/c
; Sequence 15382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15382
; LENGTH: 37292
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(37292)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15382

Query Match      7.4%; Score 168.4; DB 3; Length 37292;
Best Local Similarity 63.2%; Pred. No. 5.2e-28;
Matches 345; Conservative 0; Mismatches 186; Indels 15; Gaps 5;

QY      5 GATTCGCCCCGCTCAAGCTTCCCAAAAGTCTGGATTTGCGAGTCCACCTCACTTGG 64
DB      31797 GATTCGCCCCGCTCAAGCTTCCCAAAAGTCTGGATTTGCGAGTCCACCTCG 31738
QY      65 CTACAGTTTTCMAAATATCATTTATCTAGTACCATCATATCTCCAGTTTGTTCACAGA 124
DB      31737 C-----CCTAGACCTAGGGGTTTCAATTCACAGCTTCCCACTGTTTGGGGGGT 31685
QY      125 CATCTTATGACTTGTAGCAAGCTGTAAATCCAAAGGCTGACGCTTTGTATGTCTAAG 184
DB      31684 TGGCTGCAAGGGCTGTCACTGGGGAAAGATGTAGAAATGATC-TCAGTCCCCCTTTC 31626
QY      185 GATGTCTAGATGTGCCCCCACTTGAAGAATTAAAGAAATTTCTTAGAGCCAGGCAC 244
DB      31625 AAGTCCCTTCTATCTGGCTTCCCTATTTAGCACTTCTAAG--TCTTCAGGCTGGGCGT 31568
QY      245 AGTGGCTCACCTGTATTTCCAGTCTGTAGAGTCCGAGGTCAGAGGACTGCTTAGG 304
DB      31567 GGTGGCTCATGCTTATATTCAGCAGCTTTGGAGGCTGAGGTGGAAGATTTGCTTAGC 31508
QY      305 CCAGAGTTCAAGAGCAGCTGTGACAAACAGGAGACCTGTCTACTACAAAGATTAATA 364
DB      31507 CCTGAGATTTCAGACAGCTGTGGCAACATTAAGAGACCTGTCTCTACAAATAATTAATA 31448
QY      365 AATTAGCCAGGCTTAGTGTCTATCCCTGTGTCCAGCTACTAGGAGGAGGAGCAATAGG 424
DB      31447 AATGAGCCAGGATGTGTGTGCTGTGTGCTGTGCTCCAGCAACTCAGAGGCTGAGGTGG 31388
QY      425 A-----CTGCTGTCCAGAGAGTCAAGACTGAGTGAAGCAGCAGCCTTGCTATT 480
DB      31387 AGGACCGATTCAAGCTGTGGAGGTAGAGGCTGAGTGGCCATGATTTGTGCCA-CTGCACT 31329
QY      481 CCAGCTGTGGCAACAAAAGAGACCTGTGTCTCAAAAAATTAAGTTAATAATAATAATAATA 540
DB      31328 CCAGCTGTGGCAACAAAAGAGACCTGTGTCTCAAAAAATTAAGTTAATAATAATACTGAT 31269
QY      541 AAAATA 546
DB      31268 AAAATA 31263
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RESULT 8
US-09-949-016-16674/c
; Sequence 16674, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16674
; LENGTH: 126237
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16674

Query Match      7.4%; Score 167.4; DB 3; Length 126237;
Best Local Similarity 70.1%; Pred. No. 1.4e-27;
Matches 253; Conservative 0; Mismatches 106; Indels 2; Gaps 2;

QY      178 TCTATGAGATTGCTCAGATCTGCCCCCAACCTGAAAGATTTTAAAGAAATTTCTGAGGC 237
DB      21667 TCCTTTGAGAGATCAGGGGTGACCAAGCTATTATTCCTATTAAAAAGTAACATAGGC 21608
QY      238 CAGGACAGTGGCTCAACCTGTATTTCCAGTACTGTGAGAGTCCGAGTCCAGAGACTG 297
DB      21607 CAGGTGAGTGGCTCAACCTGTATTTCCAGCACTTTGGAGGCCAAGGCAAGAGATCA 21548
QY      298 CTGAGGCGCAGAGTTCAAGAGCAGCTGGAGCAACAGAGGAGA-CCTGTCACTCAAAAG 356
DB      21547 CATGAGCCCGGAGTTTGACAGCTGTGGCAACAGGAGACCCCATCTTCAAAAC 21488
QY      357 AATAAATAATTAAGCAGGCTTATGTGCTCATCCTGTGTGTCACGTTAAGGAGGCA 416
DB      21487 AAAAATAAATTAAGCTGGGCATAGTATGATGATGCTGTGTGTCACGTTAAGGAGG 21428
QY      417 GAATGAGACTGCTGTGTCACAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCTG 476
DB      21427 GAGGACAGACTGCTGTGAGCCCGAGGTCMAAGACTGCTGTGAGCTGTGATGCTGCA 21369
QY      477 CATTCAGCTGGGCAACAAAAGAGCCGTCTCAAAAAATTAAGTTAATAATAATA 536
DB      21368 CACTACAGCTGGGTGACAGAGTGAAGCCCTGTCTTGGAAAAAACAAAAAACCAAAAC 21309
QY      537 A 537
DB      21308 A 21308

RESULT 9
US-09-949-016-16675/c
; Sequence 16675, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16675
LENGTH: 126237
TYPE: DNA
ORGANISM: Human
US-09-949-016-16675

Query Match
Best Local Similarity 7.4%; Score 167.4; DB 3; Length 126237;
Matches 253; Conservative 0; Mismatches 106; Indels 2; Gaps 2;

QY 178 TCTATAGATTGCTCAGATCTGCCCCCACTGAAAGATTAAAGAAATTTCTTGAGGC 237
DB 21667 TCCTTTGGAAGCATCAGGGTGACCAAGCTATTATTCCTATTAAAAAGTACATAGGC 21608
QY 238 CAGGCACAGTGGCTCACAACCTGTAATTCAGTACTGTGAGATCCGAGGTCAAGAGACTG 297
DB 21607 CAGGTGAGTGGCTCACAACCTGTAATTCAGTACTGTGAGATCCGAGGTCAAGAGATCA 21548
QY 298 CTTGAGGCCAGAGATTCAAGAGACCTGAGCAACACAGGGAGA-CCTGTCACTACAAAG 356
DB 21547 CATGAGCCCGGAGATTGAGACCAAGCTGTGGCAACACAGGAGACCCATCTTACAAAC 21488
QY 357 AATAAATAATTAATCCAGGCTTAAGTGGCTATCCCTGTGTCCAGCTACTAGGAGAGCA 416
DB 21487 AAAAATAAATTAATCTGGGCTATGATGATGCTGTGTGTCCAGCTATGTGGGAGCT 21428
QY 417 GAATAGACTGCTTGTCCCAAGAGGTAAACATGCACTGAGTGAACCAACCACTG 476
DB 21427 GAGCAGAGACTGCTTGTGAGCCCGGAGGTCAAGACTGTGTGAGCTGTGCTGTGCCA-CTG 21369
QY 477 CATCCAGCTGTGGCAACAAAAGAGACCTGTCTCAAAAATAATTAATAATAAT 536
DB 21368 CACTACAGCTGTGGTGACAGTAGAGACCTGTCTGTGAAAAAACAACCAACCAAC 21309
QY 537 A 537
DB 21308 A 21308

RESULT 10
US-09-949-016-14788
Sequence 14788, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14788
LENGTH: 16230
TYPE: DNA
ORGANISM: Human
US-09-949-016-14788

Query Match
Best Local Similarity 7.4%; Score 167; DB 3; Length 16230;
Matches 254; Conservative 0; Mismatches 85; Indels 6; Gaps 3;

QY 213 AGAATTTAAGGAATTTCTTGAGCCAGGACAGTGGCTCACACCTGTATTTCCATCT 272
DB 11027 AGAATTTAAGGAATTTCTTGATTAACCTGGCAGGTACAGTGGCTCACACCTGTATTTCCAGCACT 11086
QY 273 GTGAGATCCGAGGTCAAGAGACTGTGAGGCGCAGGAGTTCAAGAGACCTGGAGAAC 332
DB 11087 TTGGAGAGCCAGGACAGAGAGATCACTTGACACTAGAGTTTGATAGATAGCTGGAGAAC 11146
QY 333 ACAGGAGA-CCTGTCACTACAAAGAAATTAATAATTAAGCCAGGCTTAGTGGCTATCC 391
DB 11147 ATGTGAGAGCCCTGTCTACAGAAAATTTAAATTAAGCCAGCTTAGTGGCTATCC 11206
QY 392 TGTGTCTCCAGCTACTGTGAGGAGCAAGTAGA-CTGTGTGTCCAGAGAGTCAAG 447
DB 11207 TGTGTCTCCAGCTACTGTGAGGAGTGAAGTAGAATCACTTGAAGCCAGAGAGTCAAG 11266
QY 448 ACTGACGTGAGCTGAGACCCAGGACCTGATTCACACCTGGGCAACAAAAGAGACCT 507
DB 11267 GCTGACGTGAGCTGAGTTGACCA-CTGCACTTCCAGCTTGGGTGACAGAGCAAGACCT 11325
QY 508 GTCTCAAAAATAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 552
DB 11326 GTTCAAAAATAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 11370

RESULT 11
US-09-949-016-12816
Sequence 12816, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12816
LENGTH: 99370
TYPE: DNA
ORGANISM: Human
US-09-949-016-12816

Query Match
Best Local Similarity 7.3%; Score 165.2; DB 3; Length 99370;
Matches 240; Conservative 0; Mismatches 83; Indels 5; Gaps 2;

QY 223 AGAATTTCTTGAGCCAGGACAGTGGCTCACACCTGTATTTCCAGTACTGTGAGTCC 282
DB 66639 AATATTTGACAGGCCAGGTGACAGTGGCTCACAGCTGTATTTCCAACTTTGGAGGCC 66698
QY 283 GAGGTGAGAGTCTGTTGAGGCGAGAGTTCAAGAGAGCTGTGAGCAACAGAGAGA- 341
DB 66699 AAGGTGACAGATCACATTAAGTCCAGAGAGTTCAAGAGAGCTGTGAGCAACAGAGAGA 66758
QY 342 CTTGTCACTACAAAGAAATTAATAATTAAGCCAGGCTTAGTGGCTATCCCTGTGCTCCA 401
DB 66759 CTTGTCTCTACAAATTAATAATAATAATAATTAAGCCAGGCTTAGTGGCTATCCCTGTGCTCCA 66818
QY 402 GCTACTAGGAGGACAGAGTAGGA-CTGTGTGTCCAGAGAGTCAAGAGTCAAGAGTCA 457
DB 66819 GCTACTAGGAGGCTGTGGTGGAGATCACTTGAACCCAGAGAGAGAGAGTGGACAGTGA 66878
QY 458 GCTGAGACCCAGCACCTGATTCAGGCTGTGGCAACAAAAGAGACCTGTCTCAAAA 517
DB 66879 GCTGAGATCATGCCCACTGCACTGTAGCTTGGGGAACAGAGCAAGACCTGTCTCAAAA 66938

Qy 518 ATAGTAAATTAATTAATTAATTAAT 545
Db 66939 AAAAAAAAAAACAACCCCAAAAT 66966

RESULT 12

US-09-949-016-17540
; Sequence 17540, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540

Query Match 7.3%; Score 165.2; DB 3; Length 99370;

Best Local Similarity 73.2%; Pred. No. 46-27; Indels 5; Gaps 2;
Matches 240; Conservative 0; Mismatches 83;

Qy 223 AGAATTTCTTGGAGCCAGGACAGTGGCTCAGACCTGTAATTCAGTACTGTGAGATCC 282
Db 66639 ATATTTTGACAGGCGAGGTGAGTGGCTCAGACCTGTAATTCAGTACTGTGAGAGCC 66698
Qy 283 GAGGTCAAGGACTGCTTGAAGCCAGGAGTTCAAGAGCCTTGACAAACAGAGGAGA- 341
Db 66699 AAGGTGGCAGATCATTAAGTCCAGGAGTTCAAGAGCCTTGACAAACAGAGGAGAA 66758
Qy 342 CCTGCTACTACAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 401
Db 66759 CCTGCTCTACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 66818
Qy 402 GCTACTAGGAGGAGGAGGAGTGA---CTGCTTGTCCAGAGGTCAGAGTGCAGTGA 457
Db 66819 GCTACTAGGAGGAGGAGTGAAGGATGATCACTTGAACCCAGAGAGAGGTTGAGTGA 66878
Qy 458 GGTGAGACCCAGCCAGCTGCTTCCAGCTTGGGCAACAAAAGAACCTGTCTCAAAA 517
Db 66879 GGTGAGATCATGCTCCAGCTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 66938
Qy 518 ATAGTAAATTAATTAATTAATTAAT 545
Db 66939 AAAAAAAAAAACAACCCCAAAAT 66966

RESULT 13
US-09-949-016-27232/c
; Sequence 27232, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 27232
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27232

Query Match 7.2%; Score 164.2; DB 3; Length 601;

Best Local Similarity 59.7%; Pred. No. 16-27; Indels 8; Gaps 3;
Matches 330; Conservative 1; Mismatches 214;

Qy 6 ATTCGCCGCTCAGCTTCCAAAGTGTGGATTGACGGGTGAGCCACCTCAGCTGAC 65
Db 588 ATTCGCTGCTCAGCTTCCAAAGTGTGGATTGACGGGTGAGCCACCTCAGCTGAC 529
Qy 66 TACAAGT---TTTCAAAATACATTATCTAGTACCCATACATCTCCAGTTGTCCACAG 122
Db 528 CCTCATGACTTTAAAAAACAATTAAAGAAATGAACTTTGTAATAATGTAATAATG 469
Qy 123 GACATCTATGACTTGACCAAGCTGCTAAATCCAAAGGTGACAGCTTTGATGTCTAT 182
Db 468 GACAGAAATTTGAATTAATGATTCATTAATTAATTAATTAATTAATTAATTAAT 409
Qy 183 AGGATTGCTCAGATCTGCCCCCAGCCCTGAAAGAAATTTAAGAAATTTCTTGAGCCAGGC 242
Db 408 TCAATGATTAATCTTACGATATGAAATTAATTTTAAATTAATTTATTTCTGCGCCAGGC 349
Qy 243 ACAGTGGCTCAGCTGTAATTCAGTACTGAGAGTCCAGAGTCCAGAGCTGCTTGA 302
Db 348 ACGGTGCTCAGCTGTAATTCAGCTGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAG 289
Qy 303 GGCAGGATTCAGAGAGCTGAGCAACACAGAGGAGCTGTCACTACAAAGATTA 362
Db 288 GGTCAAGATTCAGAGAGCTGATCAACATGACAAACCCCATCTGCTACAAAATATC 229
Qy 363 TAAATTAAGCTTGAATGCTCATCCCTGTGTGCTCCAGACTGAGGAGGAGGAGTGA 422
Db 228 AAAATTAAGCTGAGGAGTGTGAGCAATGCTGTAATCCAGCTGAGGAGGAGGAGGAG 169
Qy 423 GGA---CTGCTTGTCCAGAGGTCAGAGTGCAGAGTGCAGAGCCAGCA-CTGC 477
Db 168 GGAAGATGCTTGAACCCGAGGAGGAGGAGTGCAGAGTGCAGAGTGCAGAGTGC 109
Qy 478 ATTCAGCTGAGGCAACAAAAGAGACCTGTCTCAAAAATTAATTAATTAATTAAT 537
Db 108 ACTCAGCTGAGGCAACAGAGCAAGAACTCCATCTCAAAAATTAATTAATTAATTAAT 49
Qy 538 ATAAATTAATTT 550
Db 48 TTCTGAATTAATGT 36

RESULT 14
US-09-949-016-160756/c
; Sequence 160756, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 160756
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-160756

Query Match 7.2%; Score 164.2; DB 3; Length 601;
 Best Local Similarity 59.7%; Pred. No. 1e-27;
 Matches 330; Conservative 1; Mismatches 214; Indels 8; Gaps 3;

QY 6 ATCTGCCCCCTCAGCTCCCAAGTCTGGATTCAGGGCTGAGCCACTCCTACTGCG 65
 DB 588 ATCTGCCCCCTCAGCTCCCAAGTCTGGATTCAGGGCTGAGCCACTCCTACTGCG 529
 QY 66 TACAAGT---TTTCAAAATACATTTATCTAGTACCATACATTCCTCCAGTTTGTCCAG 122
 DB 528 CCCCCTCAGCTTTTAAATAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 469
 QY 123 GACATCTTATGACTTGAAGCAAGCTGCTAAATCCAGGGTGCAGCGTTTGTATGCTAT 182
 DB 468 GACAGAAATTTGAAT 409
 QY 183 AGGATTTGTCAGATCTGCCCCCAGCTTAAAGAAATTTAAGAAATTTTGAAGCCAGGC 242
 DB 408 TCAATATGATATCTTAAATGATATGATATGATATGATATGATATGATATGATATG 349
 QY 243 ACAGTGGCTCACCTGTATTTCCAGTACTGTGAGAGTCCAGAGTCCAGAGTCCAGTCTGA 302
 DB 348 ACAGTGGCTCACCTGTATTTCCAGTACTGTGAGAGTCCAGAGTCCAGAGTCCAGTCTGA 289
 QY 303 GGCAGAGGTTCAAGAGCAGCTGAGCAACAGGAGAGCTGTCTACTACAAAGAAATTA 362
 DB 288 GGTGAGAGGTTCAAGAGCAGCTGAGCAACAGGAGAGCTGTCTACTACAAAGAAATTA 229
 QY 363 TAAATTTGAGGCTTACTGCTCTATCCCTGTGCTCCAGTACTAGGAGGAGCAAGTA 422
 DB 228 AAAATTTGAGGCTTACTGCTCTATCCAGTACTAGGAGGAGCAAGTA 169
 QY 423 GGA---CTGCTTGTCCAGAGGTCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 477
 DB 168 GGAATTTGCTTGAACCCGAGAGGAGGAGTTCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 109
 QY 478 ATTCCAGCTTGGCAACAAAAGAGCCCTGTCTCAAAAATTAATTAATTAATTAATA 537
 DB 108 ACTCCAGCTTGGCAACAAAAGAGCCCTGTCTCAAAAATTAATTAATTAATTAATA 49
 QY 538 ATAAATTAATTT 550
 DB 48 TTCTGAATTAATGT 36

RESULT 15
 ; US-09-949-016-13576
 ; Sequence 13576, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 13576
 ; LENGTH: 63783
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-13576

Query Match 7.2%; Score 164.2; DB 3; Length 63783;
 Best Local Similarity 66.7%; Pred. No. 5.7e-27;
 Matches 266; Conservative 0; Mismatches 128; Indels 5; Gaps 2;

QY 205 ACCGTGAAGATTTTAAAGAAATTTCTTGAAGCCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 264
 DB 35918 ATCCACAGAAAGATTTAAATAAATGCAAAATCCAGCCGCGCCAGTGTCTACACCTGTAA 35977
 QY 265 CCACTACTGTGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 324
 DB 35978 CCAGCACTTTGGAGGCGGAGTGGTGGATCATTGAGTCCAGAGTCCAGAGTCCAGAGTCC 36037
 QY 325 TGAACAAACAGGAGAGCTGTCTACTACAAAGAAATTAATTAATTAATTAATTAATTA 384
 DB 36038 TGGCCAAACATGTGAACCCCATCTCTCTAATAAATAATTAATTAATTAATTAATTA 36097
 QY 385 TCATCCCTGTGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 440
 DB 36098 AGGCACTTGTATGCTTAAAGTCTGAGAGGCTGAAGAGGAAATCACTGAACCCAGAG 36157
 QY 441 GGTCAAGACTGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 500
 DB 36158 GGCAGAGGTTGCACTGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 36216
 QY 501 AGACCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 560
 DB 36217 AGACTTCATCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 36276
 QY 561 CACATCTTCTTTTCAAGAGACTTCTTAAGAGCTTCA 599
 DB 36277 TCTTATTTTACTTAATAAGTATTAATTAAGTTACTACA 36315

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846.8	37.3	9314	6	US-10-197-019-1 Sequence 1, Appl1
2	550.6	24.3	562	4	US-09-925-065A-566754 Sequence 566754
3	531.6	23.4	554	4	US-09-925-065A-177131 Sequence 177131
4	447.4	19.7	1161	6	US-10-265-689-27 Sequence 27, Appl1
5	364.2	16.0	5283	6	US-10-311-455-1865 Sequence 1865, Ap
6	312.4	13.8	5283	6	US-10-311-455-1866 Sequence 1866, Ap
7	188.4	8.3	44348	7	US-10-301-832-11 Sequence 11, Appl1
8	175	7.7	160556	8	US-10-719-993-6827 Sequence 6827, Ap
9	172.8	7.6	11172	3	US-09-764-878-231 Sequence 231, App
10	172.8	7.6	11172	5	US-10-079-854-231 Sequence 231, App
11	168	7.4	563	4	US-09-925-065A-770821 Sequence 770821
12	167.2	7.4	135005	8	US-10-723-860-2220 Sequence 2220, Ap
13	167.2	7.4	135005	9	US-10-756-149-1719 Sequence 1719, Ap
14	166.8	7.3	3030	5	US-10-027-632-115210 Sequence 115210
15	166.8	7.3	3030	5	US-10-027-632-115211 Sequence 115211
16	166.8	7.3	3030	5	US-10-027-632-115210 Sequence 115210
17	166.8	7.3	3030	6	US-10-027-632-115211 Sequence 115211
18	166.6	7.3	52242	7	US-10-052-482-172 Sequence 172, App
19	166	7.3	1614	4	US-09-925-065A-551304 Sequence 551304
20	165.6	7.3	1187	4	US-09-925-065A-71294 Sequence 71294, A
21	165.6	7.3	1187	4	US-09-925-065A-71295 Sequence 71295, A
22	164	7.2	1369	5	US-10-027-632-86881 Sequence 86881, A
23	164	7.2	1369	5	US-10-027-632-178961 Sequence 178961

24	164	7.2	1369	6	US-10-027-632-86881 Sequence 86881, A
25	164	7.2	1369	6	US-10-027-632-178961 Sequence 178961
26	164	7.2	186510	6	US-10-043-715-1 Sequence 1, Appl1
27	163.4	7.2	558	4	US-09-925-065A-822292 Sequence 822292
28	163.4	7.2	558	4	US-09-925-065A-839930 Sequence 839930
29	163.2	7.2	561515	8	US-10-741-600-15682 Sequence 5682, Ap
30	163.2	7.2	561515	8	US-10-741-600-17730 Sequence 17730, A
31	162.6	7.2	81099	5	US-10-087-192-1756 Sequence 1756, Ap
32	161.8	7.1	109906	5	US-10-087-192-1756 Sequence 31, Appl1
33	161.4	7.1	383432	9	US-10-235-192A-31 Sequence 34, Appl1
34	161.4	7.1	383432	9	US-10-737-082-34 Sequence 34, Appl1
35	161.2	7.1	56737	3	US-10-765-790-34 Sequence 17, Appl1
36	160.8	7.1	60815	5	US-09-782-378A-17 Sequence 52, Appl1
37	160.6	7.1	599	4	US-10-087-192-52 Sequence 875725
38	160.6	7.1	599	4	US-09-925-065A-875725 Sequence 905153
39	160.6	7.1	7739	6	US-09-764-877-3189 Sequence 3189, Ap
40	160.6	7.1	7739	6	US-10-242-515-3189 Sequence 3189, Ap
41	160.6	7.1	8133	7	US-10-380-124-10 Sequence 10, Appl1
42	160.4	7.1	87467	7	US-10-741-600-5634 Sequence 5634, Ap
43	160.4	7.1	87467	8	US-10-741-600-17624 Sequence 17624, A
44	160.4	7.1	136436	9	US-10-756-149-3773 Sequence 3773, Ap
45	160.2	7.1	492	5	US-10-027-632-84916 Sequence 84916, A

ALIGNMENTS

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RESULT 1
US-10-197-019-1
Sequence 1, Application US/10197019
Publication No. US20030207284A1
GENERAL INFORMATION:
APPLICANT: Chew, Anne
APPLICANT: Denton, R. Rex
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Nandabalan, Krishnan
APPLICANT: Parks, Katie E.
TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
FILE REFERENCE: MMH-004205
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: US/10197,019
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02485
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 9314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1283)..(1283)
OTHER INFORMATION: P81: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (1714)..(1714)
OTHER INFORMATION: P82: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2051)..(2051)
OTHER INFORMATION: P83: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (2124)..(2124)
OTHER INFORMATION: P84: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2287)..(2287)
OTHER INFORMATION: P85: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (2408)..(2408)
OTHER INFORMATION: P86: polymorphic base adenine or guanine

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FEATURE:
NAME/KEY: allele
LOCATION: (4768)..(4768)
OTHER INFORMATION: PS7: polymorphic base adenine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (4785)..(4785)
OTHER INFORMATION: PS8: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (4813)..(4813)
OTHER INFORMATION: PS9: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (4882)..(4882)
OTHER INFORMATION: PS10: polymorphic base adenine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (4976)..(4976)
OTHER INFORMATION: PS11: polymorphic base thymine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (5600)..(5600)
OTHER INFORMATION: PS12: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (5820)..(5820)
OTHER INFORMATION: PS13: polymorphic base thymine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (6536)..(6536)
OTHER INFORMATION: PS14: polymorphic base thymine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (6607)..(6607)
OTHER INFORMATION: PS15: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (6617)..(6617)
OTHER INFORMATION: PS16: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (6872)..(6872)
OTHER INFORMATION: PS17: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (6966)..(6966)
OTHER INFORMATION: PS18: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (7036)..(7036)
OTHER INFORMATION: PS19: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (7086)..(7086)
OTHER INFORMATION: PS20: polymorphic base adenine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (8100)..(8100)
OTHER INFORMATION: PS21: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (8221)..(8221)
OTHER INFORMATION: PS22: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (8677)..(8677)
OTHER INFORMATION: PS23: polymorphic base thymine or adenine
US-10-197-019-1

Query Match 37.3%; Score 846.8; DB 6; Length 9314;
Best Local Similarity 98.9%; Pred. NO. 2e-204;
Matches 874; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 1387 GGTCCATCTCTGAGCGCTTTTCTCATCCAGAGCTGACAGGCAAGCTGGCCCGC 1446
DB 1 GGTTCATCTCTGAGCGCTTTTCTCATCCAGAGCTGACAGGCAAGCTGGCCCGC 60
QY 1447 GCTTGCTCTGTCAGTGTGGGGGCGGCGCTTGTCTGTGTGTAGAGGCTGAG 1506
DB 61 GCTTGCTCTGTCAGTGTGGGGGCGGCGCTTGTCTGTGTGTAGAGGCTGAG 120
QY 1507 GTACGCTGGTGTCTCCGCGCCCGCGGCTTTAGTGTCTCTGTCTTAAAGCCAG 1566
DB 121 GTACGCTGGTGTCTCCGCGCCCGCGGCTTTAGTGTCTCTGTCTTAAAGCCAG 180
QY 1567 GCCGCTCCACCGGGGGAGAGAGGCGGAACCCAGCGAGCCCAAGGCTGTGTGGTTG 1626
DB 181 GCCGCTCCACCGGGGGAGAGAGGCGGAACCCAGCGAGCCCAAGGCTGTGTGGTTG 240
QY 1627 CCGAGCCACTGTGCTGCACTTGTGATTTGTTCTTCCCGAGACACCGGCGCTGTA 1686
DB 241 CCGAGCCACTGTGCTGCACTTGTGATTTGTTCTTCCCGAGACACCGGCGCTGTA 300
QY 1687 ACCAATCGACAGCGAGCGCGGTGCGAGGCGCCCAAGTCCCGCTGAGAGCCAGCGCG 1746
DB 301 ACCAATCGACAGCGAGCGCGGTGCGAGGCGCCCAAGTCCCGCTGAGAGCGCGCG 360
QY 1747 CGCTGCTCGCAGAGGCGGTGAGTTTGGCCAGCGGTAGGGGGGCTGGGCGCATAAAGA 1806
DB 361 CGCTGCTCGCAGAGGCGGTGAGTTTGGCCAGCGGTAGGGGGGCTGGGCGCATAAAGA 419
QY 1807 GGAAGTGACCTTAAGACACGCGCCCGCTGAGCGCTTGTGAACCGTCTGCTGGGAA 1866
DB 420 GGAAGTGACCTTAAGACACGCGCCCGCTGAGCGCTTGTGTGAACCGTCTGCTGGGAA 477
QY 1867 GCGAAGGTGTGTGATCTGACAAAGATTGTTCTTGTGCGCGGTACGTCTTCTCA 1926
DB 478 GCGAAGGTGTGTGATCTGACAAAGATTGTTCTTGTGCGCGGTACGTCTTCTCA 537
QY 1927 GAGGTTGGCGCCGAGAGAGTGTGAGCAGAGCGGGAGTGGCAAGGGAATGACATC 1986
DB 538 GAGGTTGGCGCCGAGAGAGTGTGAGCAGAGCGGGAGTGGCAAGGGAATGACATC 597
QY 1987 TCGGGGAACGAAGAGTAAACCGGTGATGGACGACGGAACCGGAGTGGAGAAATC 2046
DB 598 TCGGGGAACGAAGAGTAAACCGGTGATGGACGACGGAACCGGAGTGGAGAAATC 657
QY 2047 ATGAGAGAACCTTAGCGCGGCGGTCCCGCGGAAGCGGCTGTCTCAAGGTCTCCG 2106
DB 658 ATGAGAGAACCTTAGCGCGGCGGTCCCGCGGAAGCGGCTGTCTCAAGGTCTCCG 717
QY 2107 ACCCAAGTAGAGCTGGCAGGCGCGGCGCCGCGCCGAGAGCCCAAGCCCGGCGCCG 2166
DB 718 ACCCAAGTAGAGCTGGCAGGCGCGGCGCCGCGCCGAGAGCCCAAGCCCGGCGCCG 777
QY 2167 CCGAGGCTTAAGCCGCGCGCGCTGCGGAGAGCCCACTGCGAAGCCCACTGCGCGC 2226
DB 778 CCGAGGCTTAAGCCGCGCGCGCTGCGGAGAGCCCACTGCGAAGCCCACTGCGCGC 837
QY 2227 GCCTTGGATTGACTGTCCACGCTGCGCGGCTGTCTGTCCAGCGG 2270
DB 838 GCCTTGGATTGACTGTCCACGCTGCGCGGCTGTCTGTCCAGCGG 881

RESULT 2
US-09-925-065A-566754
Sequence 566754, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08


```

? PRIOR APPLICATION NUMBER: US 60/243,096
? PRIOR FILING DATE: 2000-10-24
? PRIOR APPLICATION NUMBER: US 60/252,147
? PRIOR FILING DATE: 2000-11-20
? PRIOR APPLICATION NUMBER: US 60/250,092
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/261,766
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/289,846
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 566754
? LENGTH: 562
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-925-065A-566754

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Query Match	Score	DB	Length
24.3%	550.6	4	562
Best Local Similarity	88.6%	1	120

Matches	561;	Conservative	1;	Mismatches	0;	Indels	1;	Gaps	1;
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[illegible]

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1 CURRENT FILING DATE: 2001-08-08
2 PRIOR APPLICATION NUMBER: US 60/243,096
3 PRIOR FILING DATE: 2000-10-24
4 PRIOR APPLICATION NUMBER: US 60/252,147
5 PRIOR FILING DATE: 2000-11-20
6 PRIOR APPLICATION NUMBER: US 60/250,092
7 PRIOR FILING DATE: 2000-11-30
8 PRIOR APPLICATION NUMBER: US 60/261,766
9 PRIOR FILING DATE: 2001-01-16
10 PRIOR APPLICATION NUMBER: US 60/289,846
11 PRIOR FILING DATE: 2001-05-09
12 NUMBER OF SEQ ID NOS: 957086
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 177131
15 LENGTH: 554
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 US-09-925-065A-177131

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Query Match	23.4%	Score 531.6	DB 4	Length 554
Best Local Similarity	99.5%	Pred. No. 9	8e-125	
Matches 553	Conservative	1	Mismatches 0	Indels 2
				Gaps 2

QY	1131	TGTTCCCTGGCAGTCCCTTCTGCTGTGGTGA	AAACAATATGGCGCGGCTGACCAAGGCTG	1190
Db	554	TGTTCCCTGGCAGTCCCTTCTGCTGTGGTGA	AAACAATATGGCGCGGCTGACCAAGGCTG	495
QY	1191	TAAGTGTGTATATATCAAGAAAGATGATGAA	ACGATTCCTTGGGACATCCGTTTCTCATTTGTA	1250
Db	494	TAACTGTGTAAATATCAAGAAAGATGATGAA	ACGATTCCTTGGGACATCCGTTTCTCATTTGTA	435
QY	1251	AAATGAGGTTAATATACAGGACCTTCTTCTACT	CCCCAACGACAGCTGTTTGTCCCGGCAG	1310
Db	434	AAATGAGGTTAATATACAGGACCTTCTTCTACT	CCCCAACGACAGCTGTTTGTCCCGGCAG	375
QY	1311	AGGGCCCAATTTGTTGGCTGTTCAAGCATCA	GTATACCCCCACAGACGGGTACGCCAATTA	1370
Db	374	AGGG-CCAAATTTGTTGGCTGTTCAAGCATCA	GTATACCCCCACAGACGGGTACGCCAATTA	316
QY	1371	AAGGCGAACCAGGCGCGGTCCATCTCTGAC	AGCCTTTTCTCATCCCAAGGCTTGACAAGCG	1430
Db	315	AAGGCGAACCAGGCGCGGTCCATCTCTGAC	AGCCTTTTCTCATCCCAAGGCTTGACAAGCG	256
QY	1431	AGCTGACCTGAGCCCGGCTCTGCTTGTCA	CGTGGGAGCGCGGCCCGGCTTGTCTG	1490
Db	255	AGCTGACCTGAGG-CCGGCTCTGCTTGTCA	CGTGGGAGCGCGGCCCGGCTTGTGTCTG	197
QY	1491	TGTGTGAGAACGTGAGGTCAACGCTGGGGTGC	CTCCCGCCCGCGGGGCTTTAGTGTCCCT	1550
Db	196	TGTGTGAGAACGTGAGGTCAACGCTGGGGTGC	CTCCCGCCCGCGGGGCTTTAGTGTCCCT	137
QY	1551	GGTTCCTTAAACGCGCAGGCGCCTCCA	CCGGGGGAGAAAGCGCGAACCCACGCGAGCCCA	1610
Db	136	GGTTCCTTAAACGCGCAGGCGCCTCCA	CCGGGGGAGAAAGCGCGAACCCACGCGAGCCCA	77
QY	1611	CGGCTGTTTGTCCGTTGCTCCGGGCAACG	TCTTGTCTGCAATTTGATTTGTTCTTCCCCGA	1670
Db	76	CGGCTGTTTGTCCGTTGCTCCGGGCAACG	TCTTGTCTGCAATTTGATTTGTTCTTCCCCGA	17
QY	1671	CAACGCGGCGGCGCTGTA	1686	
Db	16	CAACGCGGCGGCGCTGTA	1	
RESULT 4				
US-10-265-689-27				
; Sequence 27, Application US/10265689				
; Publication No. US20030119775A1				
; GENERAL INFORMATION:				
; APPLICANT: SURMIT, RICHARD S.				
; APPLICANT: COLLINS, SHEILA A.				
; APPLICANT: WARDEN, CRAIG H.				
; APPLICANT: SELDIN, MICHAEL F.				

```
APPLICANT: RICOIER, DANIEL
APPLICANT: BOULLAUD, FREDERIC
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
FILE REFERENCE: 1579-376
CURRENT APPLICATION NUMBER: US/10/265,689
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/353,645
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: PCT/US97/06864
PRIOR FILING DATE: 1997-04-22
PRIOR APPLICATION NUMBER: 60/034,960
PRIOR FILING DATE: 1997-01-15
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: "n" bases may be a, t, c, g, modified or unknown
US-10-265-689-27
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Query Match      19.7%; Score 447.4; DB 6; Length 1161;
Best Local Similarity 94.9%; Pred. No. 3.9e-103;
Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;
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QY 1733 AGGAGCCAGCCGCGCTGCTCGCAGAGGTTGGTATTGCCAGCGT--AGGGGGG 1790
DB 2 AAGAACCCAGCGCGCTTGTGTCAGAGGTTGGTATTGCCAGGGGTAAGGGGGG 61
QY 1791 CTGGGCGCATTAAGAGAGAGTGTC-ACCTAAGACACGCGCCCGCTGAGCGCTTTGTAAGA 1849
DB 62 CTGGGCGCATTAAGAGAGAGTGTC-ACCTAAGACACGCGCCCGCTGAGCGCTTTGTAAGA 121
QY 1850 ACCGTCCT-GGCTGGAGAGGCAAGAGTGTTGTCGACTGCAACAAGCTTTTCT-GGCGGT 1907
DB 122 ACCCTCTGGTGGGAGAGGCAAGAGTGTTGTCGACTGCAACAAGCTTTTCTGGCGCGGT 181
QY 1908 CAGCTCTGTCATCTTCACAGAGTTGGCGCGCCGAGAGAGTGTCGAGAGCGAGCGGGGAG 1967
DB 182 CAGCTCTGTCATCTTCACAGAGTTGGCGCGCCGAGAGAGTGTCGAGAGCGAGCGGGGAG 241
QY 1968 TGGCAAGGAGTGACCATCTCGGGGAAAGAGAGTAACGCGGTATGGAGCGACAG- 2026
DB 242 TGGCAAGGAGTGACCATCTCGGGGAAAGAGAGTAACGCGGTATGGAGCGACAG- 301
QY 2027 AAAAGGAGTGAGAAAGTCTATGAGAGAACTTAGCGCGGGCGGTCCCGCGGAAAGGC 2086
DB 302 AAAAGGAGTGAGAAAGTCTATGAGAGAACTTAGCGCGGGCGGTCCCGCGGAAAGGC 361
QY 2087 GGCTGCTCAGAGGTCCTCCGACCCCAAGTAGAGCTGGAGCGCGCGCCCGCCCGCCGACAG 2146
DB 362 GGCTGCTCAGAGGTCCTCCGACCCCAAGTAGAGCTGGAGCGCGCGCCCGCCCGCCGACAG 421
QY 2147 CCCCAAGGAGGAGCGCGCCCGCCCGGAGCTTAAGCGCGCGCGCGCTGCGAGAGCCCAAG 2206
DB 422 CCCCAAGGAGGAGCGCGCGCCCGCCCGGAGCTTAAGCGCGCGCGCGCTGCGAGAGCCCAAG 481
QY 2207 TGGCAAGCCAGCTGCGCGCGCTTGGAGATTGACTGTCCAGCGTGGCGCGGCTGTGCGA 2266
DB 482 TGGCAAGCCAGCTGCGCGCGCTTGGAGATTGACTGTCCAGCGTGGCGCGGCTGTGCGA 541
QY 2267 GCGG 2270
DB 542 GCGG 545
```

```
RESULT 5
US-10-311-455-1865
Sequence 1865, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
```

```
APPLICANT: PIERPENROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1865
LENGTH: 5283
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1865
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Query Match      16.0%; Score 364.2; DB 6; Length 5283;
Best Local Similarity 77.4%; Pred. No. 1.3e-81;
Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;
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QY 1668 CGACAAAGCGCGGCTGTAAACCAATCGACAGAGCCGTCGCGAGGCCCAAGTCCCGC 1727
DB 2 CGATACCGCGGCGGTGTAATTAATCAATGATAGAGAGTGTGCGCAAGTATTAGTTTGT 61
QY 1728 CCGCAGAGAGCCAGCGCGCGCTCGCTCGCAGAGAGTGAGTATTGCCCCAGCTAGAGG 1787
DB 62 TTTGTAAGAGTTAGTCGCGCGCTGCTGTGAGAGAGTGAGTATTGTTTAAAGCTA-GG 120
QY 1788 GGGCTGGGCCCATTAAGAGAGAGTGCACTTAAGACACGCGCCCGCTGAGCGCTTGTAG 1847
DB 121 GGGTGGGTTTAATAAGAGAGAGTGATTTAAGATAGCGTTAG--TGACGTGTAG 178
QY 1848 AACCGTCTGCTGTGGAGAGCAAGAGTGTCGTCGACAAAGCTTTCTGCGCGT 1907
DB 179 AATGTTGTTGTTGTTGAGAGGTAAGAGAGTGTCGTCGACAAAGCTTTCTGCGCGT 238
QY 1908 CAGCTCTGTCATCTTCACAGAGTTGGCGCGCCGAGAGAGTGTCGAGAGCGAGCGGAG 1967
DB 239 TAGTTTGTATTTTATTAAGAGTTGGCGGTTTCAAGAGAGTGTGAGAGAGCGGGAG 298
QY 1968 TGGCAAGGAGTGACCATCTCGGGGAAAGAGAGTAACGCGGTATGGAGCGACAG- 2027
DB 239 TGGTAAGGAGTGATTAATTCGGGGAGCAAGAGTAACGCGGTATGGAGCGACAG- 358
QY 2028 AACGGAGTGAGAAAGTCAATGAGAGAACTTAGCGCGGGCGGTCCCGCGGAAAGGGC 2087
DB 359 AACGGAGTGAGAAAGTCAATGAGAGAACTTTAGCGGGGCGGTTTTCGCGAAAGGGC 418
QY 2088 GCTGCTCAGAGGTCCTCCGACCCCAAGTAGAGCTGGAGCGCGCGCCCGCCCGCAGAGC 2147
DB 419 GTTGTTTAAGGTTTTCGATTTAAGTAGAGATTGTGAGTTTTCGTTTCGTAAGGT 478
QY 2148 CCCACCGCGGCGCGCCCGCCCGAGGCTTAAGCGCGCGCGCGCTGCGAGAGCCCACT 2207
DB 479 TTTATTTTGGGTTTGTGTTTTCGAGGTTTAAGTCGCGTCTTTTCGCGGAGTTTAT 538
QY 2208 GCGAAGCCAGCTGCGCGCGCTTGGAGATTGACTGTCCAGCGTGGCGCGGCTGTGCGA 2267
DB 539 GCGAAGTTTATGTCGCGCGGTTTGGAGATTGATTGTTTACGTTTCGTTTCGTTTCGAC 598
QY 2268 GCG 2270
DB 599 GCG 601
```

```
RESULT 6
US-10-311-455-1866/c
```

Db 8510 AGGACAAATATATAGATATAGTATATATAGATTTCTGCTGCTACTATGAGAACCTT 8451
Qy 181 ATAGATTGCTAGATCTGCCCCACCTGAAAGATTTTAAAGAAATTTCTTGAGGCCAG 240
Db 8450 TCCCTCAGACAAAGATGATATAAATTTGGGTTTTCTTTTAAAGATGAGGACCTGCCAG 8391
Qy 241 GCACAGTGGCTACACCTGTAATTCAGACTGTAGAGTCCGAGAGTCCAGAGACTGCTT 300
Db 8390 GCACAGTGGCTACACCTGTAATTCAGACTGTAGAGTCCGAGAGTGGGTGAGACACTT 8331
Qy 301 GAGGACAGAGTTCAGAGACAGCTGACCAACAGAGGAGA-CCTGTCACTCAAGAAAT 359
Db 8330 GAGGTACAGAGTTCAGAGACAGCTGACCAATATGTTAAACCCATCTCTAATAAAT 8271
Qy 360 AAATTAATTTAGCCAGGCTTAGTGCTCATCCTGTGCTCCAGCTACTAGAGGAGCAGAA 419
Db 8270 ACATAAATTTAGCCAGGCGCGGTGGCTACACTGTATGCTCCAGTACTAGAGGCTGAG 8211
Qy 420 GTAGAGCTGCTTGTCCAGAGAGTGA-AGACTGCACTAGAGTGAACCCAGCCTGCA 478
Db 8210 ACAGATTTGCTGAACCGGAAAGCAGAGTTTACAGCTTACATGTTGCTCCTGAC 8151
Qy 479 TTCCAGCTGGGCAACAAAGAGACCTGCTCAAAAAAATTAATTAATAATTAATTA 538
Db 8150 TCCAGCTAGGTGTGAGACAGAGTGAAGCTCTCTCAAAAAAATTAATAATAATAATA 8091
Qy 539 TAAAAATGTTAAACCTTAACACATCTTCTTTT 574
Db 8090 AAAAAAGTAGGAGCAGCATGACTTATATATTTGT 8055

RESULT 11

US-09-925-065A-770821/c
; Sequence 770821, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770821
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-770821

Query Match 7.4%; Score 168; DB 4; Length 563;
Best Local Similarity 74.6%; Pred. No. 4.1e-32;
Matches 252; Conservative 0; Mismatches 80; Indels 6; Gaps 3;

Qy 218 TTAAAGAAATTTCTTGAGGCCAGGACAGTGGCTACACCTGTATATTCAGTACTGTAG 277
Db 493 TTCAAAGCATATCTTGAGGCCAGGATGAGTGGCTACACCTGTATATTCAGTACTGTAG 434
Qy 278 AGTCGAGTCAAGAGACTGCTTGAGGCCAGGAGTTCAAGAGAGAGCTGAGCAACACAGG 337
Db 433 AGGTCAAGTGGTGGATCCTTGAGGCCAGGAGTTTGAACAGAGCTGGGCAACATGAT 374
Qy 338 GAGACCTGTCACTACAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 397

Db 373 GAAACTGTCTTATTTAAATAATACAAATAATTAATGCGGAGTGGGACATGCGCTGAT 314
Qy 398 CCCAGCTACTAGGAGGAGAGAGTGAAGTCTGCTTGT-----CCAGAGAGTCAAGACTCA 453
Db 313 CCCAGCTACTAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 254
Qy 454 GTGAGCTGAGACCCAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 512
Db 253 GTGAGCTGAGATTTGGGCA-TTGCAACAGAGCTGGGTGAGAGAGAGAGAGAGAGAGAGTCTCA 195
Qy 513 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 550
Db 194 AAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 157

RESULT 12

US-10-723-860-2320/c
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

Query Match 7.4%; Score 167.2; DB 8; Length 135005;
Best Local Similarity 80.3%; Pred. No. 9.3e-31;
Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

Qy 235 GCGCAGGACAGTGGCTTCACTGTAATTCAGTACTGTGAGTCCGAGGTGAGAGGA 294
Db 84840 GCGTGGACACAGTGGCTTCACTGTAATTCAGTACTGTGAGTCCGAGGTGAGAGGA 84781
Qy 295 CTGCTTGAAGGAGGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 352
Db 84780 TTGCTTGAAGGAGGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 84721
Qy 353 AAGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412
Db 84720 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 84661
Qy 413 GCGAAGATGAGTGTCTTG-TCGAGAGGTCAAGACTGAGTGAAGTGAAGTGAAGTGAAGTGA 471
Db 84660 GCGTGAAGTGAAGTGTCTTGAGTCAAGAGGTGAGGAGGAGGAGGAGTGAAGTGAAGTGA 84601
Qy 472 ACCGTCAATTCAGGCTGGGCAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 521
Db 84600 A-CTGACTCCAACTGGGCAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 84552

RESULT 13
US-10-756-149-1719/c
; Sequence 1719, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS &
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER


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; Sequence 1866, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1866
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1866

Query Match      13.8%; Score 312.4; DB 6; Length 5283;
Best Local Similarity 72.0%; Pred. No. 2e-68;
Matches 435; Conservative 0; Mismatches 166; Indels 3; Gaps 2;

OY 1667 CCGACAAAGGGGGCTGTGTAACCATCGACAGCGGCGGCTGGAGGCCCCCACTCCCG 1726
DB 5283 CCGACAAAGCGACGCTATTAACCAATCAACAGAACCGATCGGAAACCCCAATCCCG 5224
OY 1727 CCTGTCAGAGAGCAAGCCGCGCTGCTGCGAGAGGGTGGGTATTTGCCAGCGTAG 1786
DB 5223 CCTGTCAGAGAGCAAGCCGCGCTGCTGCGAGAGGGTGGGTATTTGCCAGCGTAG-A 5165
OY 1787 GGGGCTGGGCCCCATTAAGAGAGTGAATTAGACACGCGCCCGCTGACGCTTGTTA 1846
DB 5164 AAAACTAAACCATTAATAAATAAATACATTAACACGACCC--ATAAAGCTATTA 5107
OY 1847 GAAACCGCTGCTGGGAGGAGCAAGAGTGTGTAACGACATCTTTCTGGGCG 1906
DB 5106 AAAACCGCTGCTGGGAGGAGCAAGAGTGTGTAACGACATCTTTCTGGGCG 5047
OY 1907 TCAGTCTTGCATCTCTCAGAGAGTGGCGGCGGAGAGTGTGAGGAGAGCGGGA 1966
DB 5046 TCATCTTACCATCTCTCAGAGAGTGGCGGCGGAGAGTGTGAGGAGAGCGGGA 4987
OY 1967 GTGCGAAGAGTGAATCTCTGGGGAACGAAGAGTAAACGCGGTGATGGAGCGCAG 2026
DB 4986 ATAACTAAATAATCAATCTCTGAAAAACGAATAAATTAACGCGCTATTAACGCGA 4927
OY 2027 AAAGGAGTGAATAATCAATCTGAGAGACCTTGGGCGGCGCTCCCGCGGAAAGC 2086
DB 4926 AAAGGAGTGAATAATCAATCTGAGAGACCTTGGGCGGCGCTCCCGCGGAAAGC 4867
OY 2087 GGTGCTCTCAGAGTCTCCGCAACCAAGTAGAGTGGAGAGCCGCGCGCGCGAGG 2146
DB 4866 GACTACTCTCAAAATCTCCGCAACCAAGTAGAGTGGAGAGCCGCGCGCGAGG 4807
OY 2147 CCCCACCCCGGCGCGCGCGCGCGGAGGCTTAAAGCGCGCGCGCTGCGGAGCGCAC 2206
DB 4806 CCCCACCCCGGAGCCCGCGCGCGCGGAAATTAACCGCGCGCGCTGAGCAACCCAC 4747
OY 2207 TGGCAAGCCAGCTGCGGCGGCTTGGATTGACTGTCAGAGTGGCGCGGCTGTCGA 2266
DB 4746 TACGAAGCCCACTACGCGCGCTTAAATTAATCAATCAATCAATCAATCAATCA 4687
OY 2267 CGCG 2270
DB 4686 CGCG 4683
```

```
RESULT 7
US-10-301-832-11/c
; Sequence 11, Application US/10301832
; Publication No. US20040102390A1
; GENERAL INFORMATION:
; APPLICANT: Susan W. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF NOTCH3 EXPRESSION
; FILE REFERENCE: RTS-0414
; CURRENT APPLICATION NUMBER: US/10/301,832
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 155
; SEQ ID NO 11
; LENGTH: 44348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-301-832-11

Query Match      8.3%; Score 188.4; DB 7; Length 44348;
Best Local Similarity 63.7%; Pred. No. 2.2e-36;
Matches 354; Conservative 0; Mismatches 191; Indels 11; Gaps 4;

OY 5 GATCTGCCGCTCAGCCTCCCAAGTGTGGATGCGAGGCGTGAGCCACTCAGCTCG 64
DB 12725 GATCTGCCGCTCAGCCTCCCAAGTGTGGATGCGAGGCGTGAGCCACTCAGCTCG 12666
OY 65 CTACAGTTTCAAAATATCATTTA---TCTAGTACCATTAATCTCCAGTTGCCACA 121
DB 12665 CTTGTTGTTTATTAACCTTAAACAGATTTAGTACTGCTTTTATTCATTATTA 12606
OY 122 GGAATCTTATGACTGTGAGCAAGCTGTAAATCAAGAGTGTGAGCGCTTGATGCTA 181
DB 12605 TGAGAGCTATGAACATTAAGAGAGAGTGTGAGCAATTCACACACCTAGATTCAAC 12546
OY 182 TAGAATGCTCAGATCTGCCCCCAGCCTGAAAGAT--TTAAGAAATTTCTTGAGCC 238
DB 12545 TATGTTAGCTTATTAATCAATCTCTTTTCTTAAACATTTAAATAATGAGACAC 12486
OY 239 AGGACAGTGTGCTACACCTGTATTCAGTACTGTAGAGTCCGAGGTGAGAGACTGC 298
DB 12485 GGGCAGAGTGTGCTACACCTGTATTCAGTACTGTGAGAGTCCGAGGTGAGAGTGC 12426
OY 299 TTGAGGCGAGAGTTCAAGAGCAGCTGAGCAACAGAGAGAGCTGTCACTAACAGAA 358
DB 12425 TTGAGGCGAGAGTTCAAGAGCAGCTGAGCAATATAGTGAACCGCTCTTACAAAATA 12366
OY 359 TAAATTAATTAAGCAGAGCTTATGCTTATCTCTGTGCTGCTGCTGCTGCTGCTG 418
DB 12365 TACAAACCTTAAGCAGAGCTTATGCTTATCTCTGTGCTGCTGCTGCTGCTGCTG 12306
OY 419 AGTAGA-----CTGCTGTGCTCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 474
DB 12305 GGTGGAGAGTCACTTGAAGCCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 12247
OY 475 TGCAATTCAGAGCTGAGCAACAAAAGAGAGCTGTCTCAAAAATAATTAATTAATA 534
DB 12246 TGTAATTCAGAGCTGAGCAACAAAAGAGAGCTGTCTCTCAAAAATAATTAATAAT 12187
OY 535 ATAAATTAATTAATTTT 550
DB 12186 CAATCAATCAATTAATTT 12171

RESULT 8
US-10-719-993-6827/c
; Sequence 6827, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARBIL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
```

;; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: C1001496
;; CURRENT APPLICATION NUMBER: US/10/719,993
;; CURRENT FILING DATE: 2003-11-24
;; NUMBER OF SEQ ID NOS: 55342
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 6827
;; LENGTH: 160556
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(160556)
;; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6627

Query Match
Best Local Similarity 7.7%; Score 175; DB 8; Length 160556;
Matches 258; Conservative 2; Mismatches 117; Indels 4; Gaps 1;

QY 216 ATTTAAGAGATTCTTGAGCCAGGACAGAGTGGCTCAGACCTGTATTCAGTACTGTG 275
DB 30112 ATTCAAAATPAACATATTCAGCCGGGTGAGTGGCTCAVCGCTGTAATCTTAGCACTTTG 30053

QY 276 AGAGTCGAGGTGAGAGAGCTGTTGAGGCCAGAGTTCAAGAGCAGCTGAGCAACACA 335
DB 30052 GGAAGGCCAAGGAGAGGTGATTCGTAGAGTTCAGAGATTGAGAGCAGCTGGCCAAACAG 29993

QY 336 GGGAGACTGTCTCACTCAAAAGATTAATAATTAGCCAGGCTTAGTGCTCATCTCTGTG 395
DB 29992 GTGACACCTGTCTCTAATAAAATCAAAAATTAGCCAGGAGTGTGGCGGCTCTGA 29933

QY 396 GTCCCGACTACTAGGGAGGAGAGTAAGA---CTGCTTGTCCAGAGGTCAGACAG 451
DB 29932 GTCCCGACTACTAGGGAGGAGTGAAGAGATCTAGTAACCCAGAGGTGAGGTTA 29873

QY 452 CAGTAGCTGAGACCCAGCCACTGCTTCCAGCTTGGCCCAAAAAGAGACCTGTCT 511
DB 29872 CAGTAGCTGAGATTGGACACACTGCACTCCAGCCCTGGGTGACAGAGTCACTGTCT 29813

QY 512 CAAAAAATAGTTAATAATAATAATAATAATAAGTTTAAACCTTAAACACATCTTCT 571
DB 29812 CAAAAAATATATAAAACAATGTGAAAAAATAATAATAATATAGTAGAGAACAACTTGA 29753

QY 572 TTTCAAGAGAGACTTCTTAAG 592
DB 29752 TGACAAAAATGTGTTACTAAG 29732

RESULT 9
US-09-764-878-231/c
; Sequence 231, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior Application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 231
; LENGTH: 11172
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-231

Query Match
Best Local Similarity 7.6%; Score 172.8; DB 3; Length 11172;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

QY 1 AACGATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGACGGCTGAGCCACCTCAG 60

DB 8630 AAGTATCCGCTGCTTGGCTCCCAAGTGTAGATTACAGCAGAGCTACCGAC 8571
QY 61 CTGGCTACAGATTTCAAAATATCATTTATCTAGTACCATATCTCCAGTTTCCAC 120
DB 8570 CTGGCTCCCTCCCAAGATCTAACATTAATCCCGAGCTCCAAAACAATGAAACAA 8511

QY 121 AGGACATCTTATGACTTAGAGCAAGCTGTAAATAATCCAAAGGTGACGGTTGTATGCT 180
DB 8510 AGGACTTAATTTATAGATTATAGTTATTAATTTCTGTGTATCTATAGAGAGCTT 8451

QY 181 ATGAGATTCTCAGATCTCCGCCCACTGAAAGATTGAAGAAATTTTGAAGCCAG 240
DB 8450 TCCCTCAGACAAAGATGATTAATTTGGTTTCTTTTAAAGTAGAGGACTCGCAG 8391

QY 241 GCACAGTGTCTCACCTCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCT 300
DB 8390 GCACAGTGTCTCACCTCTGTAATTCAGTACTGTGAGAGTCCGAGTGTGAGCACCCT 8331

QY 301 GAGGCCAGAGTTCAAGAGCAGCTGACCAACACAGAGGAGA-CTGTCACTCAAGAAT 359
DB 8330 GAGGTCAAGAGTTCAAGACCACTGACCAATATGTAAACCCATCTTCTAATAAAT 8271

QY 360 AATTAATTTAGCCAGCTTATGCTCATCCCTGTGTCCAGTACTAGAGGAGCAGAA 419
DB 8270 ACAAATTTAGCCAGCGCGGGTGGCTACCTGTATGCCAGTACTAGGAGGCTGAG 8211

QY 420 GTAGAGCTGCTGTCCAGAGAGTCA-AGACTGAGTAGCTGAGAACCCAGCAGCTGCA 478
DB 8210 ACAGATTGCTTGAACCCGGAAGGAGGATTACGTAGACCTAATTTGTGCTGAC 8151

QY 479 TTCAGCCTGGGCACAAAAAGAGACCTGTCTCAAAAATTAATTAATAATAATA 538
DB 8150 TCCAGCTTAGTGTGAGACAGAGTGAAGTCTATCTCAAAAAAATTAATAATAATA 8091

QY 539 TAAAAATAGTTTAAACCTTAAACACATCTTCTTTT 574
DB 8090 AAAAAAGATGAGGACCATGACTTATTAATTTGT 8055

RESULT 10
US-10-079-854-231/c
; Sequence 231, Application US/10079854
; Publication No. US20030054368A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121C1
; CURRENT APPLICATION NUMBER: US/10/079,854
; CURRENT FILING DATE: 2002-02-22
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 231
; LENGTH: 11172
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-854-231

Query Match
Best Local Similarity 7.6%; Score 172.8; DB 5; Length 11172;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

QY 1 AACGATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGAGCGGTGAGCAGCTCAG 60
DB 8630 AAGTATCCGCTGCTTGGCTCCCAAGTGTAGATTACAGGAGGCTACCGCAG 8571

QY 61 CTGGCTACAGATTTCAAAATATCATTTATCTAGTACCATATCTCCAGTTTGTCCAC 120
DB 8570 CTGGCTCCCTCCCAAGATCTAACATTAATCCCGAGCTCCAAAACAATGAAACAA 8511

QY 121 AGGACATCTTATGACTTAGAGCAAGCTGTAAATAATCCAAAGGTGAGCGTTGTATGCT 180

Query Match 7.3%; Score 166.8; DB 5; Length 3030;
Best Local Similarity 61.8%; Pred. No. 1.9e-31;
Matches 336; Conservative 0; Mismatches 197; Indels 11; Gaps 4;

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OY 1 AACGATCTGCCCGCTCAGCTCCCAAGTGTGGATTGACAGGCTGAGCACCTCAC 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2458 AAGCATCTCTCTGCTCAGCTCAGCTTACCAAAATGCTGAGATTACAGGTTGATCACAGCAC 2399
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 CTGGCTACAAAGTTTCAAAATACATTATCTAGTACCAATCTCCAGTTTGTCCAC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2398 CTGGCCCCCTAAATTACTTTTGACATTGTATGTTTCTTGAAGTGACTCTTCTTA 2339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 AGGACATCTTATGACTTGAGCAAGCTGCTAAAAATCCAAAGGTGACGCTTGTATGCT 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2338 GACAAAGCCACATGGATCTTCAGGTTTAAAGGTTTATATGTAATACTTCTTAATGT 2279
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 ATAGGATTGCTCAGATCTGCCCGCTCAGCTCCCAAGTGTGGATTGACAGGCTGAGCACCTCAC 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2278 AAAGAAATGAATACAGATTTCTTGAGACTTGATTTCCAAATCATATTTAAAAAGCCTTGA 2219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 235 GGCCAGGACAGTGGCTCACACCTGTAATTCAGTACTGTGAGAGTCCGAGGTACAGAGA 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2218 GGCTAGGAGAGTGGCTCATGCTTGAATTCAGCAGCTTTAGAGGCCAAGGTGAGAAAG 2159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 295 CTGCTTGAGGCCAGAGATTCAAGAGCAGCTGGACACACAGGAGACC--TGTACTA 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2158 TGGTTGGGGCCAGAGATTGAGACAGCTGGGCAACCTAGTGAGACCCCGTTTCACA 2099
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 352 CAAGAATAAATAATTAAGCCAGGCTAGTGGCTATCCCTGTGTGCCAGCTACTAGGG 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2098 AAATTTTTTTAAATTAGCTGGGCAATGTTGAATGCTGTGCTCACTACTTGGG 2039
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 412 AGGCAAGATGAGACTGCTTG-TCCAGAGAGTCAAGACTGCAAGTGAAGTGAACCCAGC 470
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2038 AGGCAAGAGTGAATCACTTGAGGCCAAGATTGAGGTCGATGAGTATGATCGTGT 1979
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 471 CACCTGCATTCAGCTTGGGCAACAAAAGAGACCTGTCTCAAAAAATTAAGTTAAATPA 530
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1978 CA-CTGCACTCCAGCTGGGCAACAGATTAAGATCTGTCTCAAAAAAAAGGTCTTA 1920
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 531 ATAA 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1919 AAAA 1916
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: April 22, 2006, 16:00:00
Job time : 1636 secs

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QY 1025 TGCCTGACCTTGTGTTCCAGCGCTGCTTGCACGAGCATGCGCTCGGCTGTTTCT 1084
DB 121 TGCCTGACCTTGTGTTCCACGCTGCTTGTGCACGAGCATGCGCTCGG-GTGTTTCT 179
QY 1085 TTCCGCTAATATATATCAGAGCCCATCCAGCTCTGTGCTCCCTCACTGTTCCCTGAGCT 1144
DB 180 TTCCGCTAATATATATCAGAGCCCATCCAGCTCTGTGCTCCCTCACTGTTTCCCTGAGCT 239
QY 1145 CCCTTGTGCTGGAAGAAACATATGCGCGCCCTGACAGAGCTGTAGTGTGAAAT 1204
DB 240 CCCTTGTGCTGGAAGAAACATATGCGCGCCCTGACAGAGCTGTAGTGTGAAAT 299
QY 1205 TCAGAGATGACTGACGCTTTTGGAGCTCCGTTTCTCATTTGTAATGAGGTTAAT 1264
DB 300 TCAGAGATGACTGACGCTTTTGGAGCTCCGTTTCTCATTTGTAATGAGGTTAAT 359
QY 1265 ACCAGCTTCTTCTACTCCCAACGACGCTGTTTGTCCGCGCAGAGGCGCCCAATTGTT 1324
DB 360 ACCAGCTTCTTCTACTCCCAACGACGCTGTTTGTCCGCGCAGAGGCGCCCAATTGTT 419
QY 1325 GGCTGTTCAGCATGATGATACCCCAACAGAGCGGCTGACCAATTAAGCGCAACGAGC 1384
DB 420 GGCTGTTCAGCATGATGATACCCCAACAGAGCGGCTGACCAATTAAGCGCAACGAGC 479
QY 1385 CCGATCATCTCTGACGCTTCTTCTCATCCAGAGGCTGACAGGAGCTGAGCTGAGC 1444
DB 480 CCGATCATCTCTGACGCTTCTTCTCATCCAGAGGCTGACAGGAGCTGAGCTGAGC 539
QY 1445 CGGCTGTGCTTGTGTCAGTGC 1467
DB 540 CGGCTGTGCTTGTGTCAGTGC 562

RESULT 2

US-10-301-480-268288/c
; Sequence 268288, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268288
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-268288

Query Match 23.7%; Score 538.6; DB 10; Length 561;
Best Local Similarity 99.5%; Pred. No. 3.9e-05;

Matches 560; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1131 TGTTCCTGAGCATGCTTCTGCTGTGTAACATATGCGCGGCTGACAGAGTG 1190
DB 561 TGTTCCTGAGCATGCTTCTGCTGTGTAACATATGCGCGGCTGACAGAGTG 502
QY 1191 TAAAGTGTGAATATCAGAGATGACTGAAGCTCTTTGGAGCTCGTTTCTCATTTGA 1250
DB 501 TAAAGTGTGAATATCAGAGATGACTGAAGCTCTTTGGAGCTCGTTTCTCATTTGA 442
QY 1251 AATGAGGTTAATACAGGCTTCTTACTCCCAAGCAGAGTGTGTTGTCGCGCAG 1310
DB 441 AATGAGGTTAATACAGGCTTCTTACTCCCAAGCAGAGTGTGTTGTCGCGCAG 382
QY 1311 AGGCGCAATTGTGCTGTTCAGATCAGTTACCCCAAGAGAGGCTGACCAATTA 1370

DB 381 AGGG-CAATGTTGTGCTGTTTCCAGGCTCAAGTTACCCCAAGAGAGGAGTCAATTA 323
QY 1371 AAGGCAACCAAGCCCGGCTTCATCTCTGAGCGCTTTTCTCATCCAGAGGCTGACAGGC 1430
DB 322 AAGGCAACCAAGCCCGGCTTCATCTCTGAGCGCTTTTCTCATCCAGAGGCTGACAGGC 263
QY 1431 AGCTGAGCTGAGGCGCGGCTTGTGTCAGTGTGCGGAGGCGGAGCCGTTTCTGTCTG 1490
DB 262 AGCTGAGCTGAGG-CCGAGCTTGTGTCAGTGTGCGGAGGCGGAGCCGTTTCTGTCTG 204
QY 1491 TGTGTAGAGAGCTGAGATGACGCTGAGTGTCTCCGCGCGCGGAGCTTTAGTGTCT 1550
DB 203 TGTGTAGAGAGCTGAGATGACGCTGAGTGTCTCCGCGCGCGGAGCTTTAGTGTCT 144
QY 1551 GGTCTCTAAGCCCAAGCGCGCTTCCACCGGAGGAGAAAGCGGCAACCCCAAGCAGCCCA 1610
DB 143 GGTCTCTAAGCCCAAGCGCGCTTCCACCGGAGGAGAAAGCGGCAACCCCAAGCAGCCCA 84
QY 1611 CGGCTGTTGTGAGTGTGCGGAGCAGCTGTGCTGAGTTGATTGTTCTTCCCGCA 1670
DB 83 CGGCTGTTGTGAGTGTGCGGAGCAGCTGTGCTGAGTTGATTGTTCTTCCCGCA 24
QY 1671 CAACGCGGCGCTGTACCAATC 1693
DB 23 CAACGCGGCGCTGTACCAATC 1

RESULT 3

US-10-301-480-881697/c
; Sequence 881697, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 881697
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-881697

Query Match 23.7%; Score 538.6; DB 10; Length 561;
Best Local Similarity 99.5%; Pred. No. 3.9e-05;

Matches 560; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1131 TGTTCCTGAGCATGCTTCTGCTGTGTAACATATGCGCGGCTGACAGAGTG 1190
DB 561 TGTTCCTGAGCATGCTTCTGCTGTGTAACATATGCGCGGCTGACAGAGTG 502
QY 1191 TAAAGTGTGAATATCAGAGATGACTGAAGCTCTTTGGAGCTCGTTTCTCATTTGA 1250
DB 501 TAAAGTGTGAATATCAGAGATGACTGAAGCTCTTTGGAGCTCGTTTCTCATTTGA 442
QY 1251 AATGAGGTTAATACAGGCTTCTTACTCCCAAGCAGAGTGTGTTGTCGCGCAG 1310
DB 441 AATGAGGTTAATACAGGCTTCTTACTCCCAAGCAGAGTGTGTTGTCGCGCAG 382
QY 1311 AGGCGCAATTGTGCTGTTCAGATCAGTTACCCCAAGAGAGGCTGACCAATTA 1370
DB 381 AGGCG-CAATGTTGTGCTGTTCAGATCAGTTACCCCAAGAGAGGCTGACCAATTA 323
QY 1371 AAGGCAACCAAGCCCGGCTTCATCTCTGAGCGCTTTTCTCATCCAGAGGCTGACAGC 1430

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Db 322 AAGGGAACAGAGCCCGGCTCATCTCTGACGCTTTTCTCATCCAGGGCTGAGAGGC 263
Qy 1431 AGCTGAGCTGGAGCCCGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 1490
Db 262 AGCTGAGCTGGAGCCCGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 204
Qy 1491 TGTGAGAGGCTGAGAGTACAGTGGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 1550
Db 203 TGTGAGAGGCTGAGAGTACAGTGGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 144
Qy 1551 GGTCCCTAAACCCAGAGCCGCTCCACCGGGGAGAAAGGCGCAACCCAGCGAGCCCA 1610
Db 143 GGTCCCTAAACCCAGAGCCGCTCCACCGGGGAGAAAGGCGCAACCCAGCGAGCCCA 84
Qy 1611 CGGCTGTTGTGGTGGCGGGGCAACCTGTTGTGAGTTCTGATTGTTCTTCCCGCA 1670
Db 83 CGGCTGTTGTGGTGGCGGGGCAACCTGTTGTGAGTTCTGATTGTTCTTCCCGCA 24
Qy 1671 CAACGGGCGGCTGTACCAATC 1693
Db 23 CAACGGGCGGCTGTACCAATC 1
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RESULT 4

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US-09-925-065A-177131/C
; Sequence 177131, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177131
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-177131
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Query Match 23.4%; Score 531.6; DB 6; Length 554;

Best Local Similarity 99.5%; Pred. No. 5.5e-05;

Matches 553; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

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Qy 1131 TGTTCCTGAGAGTCCCTTCTGCTGTGTAACACATATGCGCGGCTGACAGGGTG 1190
Db 554 TGTTCCTGAGAGTCCCTTCTGCTGTGTAACACATATGCGCGGCTGACAGGGTG 495
Qy 1191 TAAAGTGTGAATATCAGAGATGACAGTCTTTGGAGCTCCGTTTCTCTCATTTGA 1250
Db 494 TAAAGTGTGAATATCAGAGATGACAGTCTTTGGAGCTCCGTTTCTCTCATTTGA 435
Qy 1251 AAATGAGGTAAATACAGAGCTTCTTCTACTCCCAAAAGCAGTGTGTCCGGCCAG 1310
Db 434 AAATGAGGTAAATACAGAGCTTCTTCTACTCCCAAAAGCAGTGTGTCCGGCCAG 375
Qy 1311 AGGCGCCCAATTTGGCTGTTTACGCGATGATGTTACCCCAAGAGGGGTGACCAATTA 1370
Db 374 AGGCGCCCAATTTGGCTGTTTACGCGATGATGTTACCCCAAGAGGGGTGACCAATTA 316
Qy 1371 AAGGGAACAGAGCCCGGCTCATCTCTGAGCCTTTTCTCATCCAGGGCTGAGACAGC 1430
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Db 315 AAGGGAACAGAGCCCGGCTCATCTCTGAGCCTTTTCTCATCCAGGGCTGAGACAGC 256
Qy 1431 AGCTGAGCTGGAGCCCGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 1490
Db 255 AGCTGAGCTGGAGCCCGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 197
Qy 1491 TGTGAGAGGCTGAGAGTACAGTGGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 1550
Db 196 TGTGAGAGGCTGAGAGTACAGTGGGCTCTGCTCTTGTACAGTGGGGGGGCGGCGCGTTTGTCTG 137
Qy 1551 GGTCCCTAAACCCAGAGCCGCTCCACCGGGGAGAAAGGCGCAACCCAGCGAGCCCA 1610
Db 136 GGTCCCTAAACCCAGAGCCGCTCCACCGGGGAGAAAGGCGCAACCCAGCGAGCCCA 77
Qy 1611 CGGCTGTTGTGGTGGCGGGGCAACCTGTTGTGAGTTCTGATTGTTCTTCCCGCA 1670
Db 76 CGGCTGTTGTGGTGGCGGGGCAACCTGTTGTGAGTTCTGATTGTTCTTCCCGCA 17
Qy 1671 CAACGGGCGGCTGTGA 1686
Db 16 CAACGGGCGGCTGTGA 1
```

RESULT 5

```
US-09-925-065A-770821/C
; Sequence 770821, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770821
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-770821
```

Query Match 7.4%; Score 168; DB 6; Length 563;

Best Local Similarity 74.6%; Pred. No. 3.9e+03;

Matches 252; Conservative 0; Mismatches 80; Indels 6; Gaps 3;

```
Qy 218 TTAAGAGATTTCTTGGAGCCAGGACAGTGGCTCACACCTGTATTTCACTAGTGTG 277
Db 493 TTCAAGCATATCTTTGAGGCGCAGGTACAGTGGCTCACACCTGTATTTCACTAGTGTG 434
Qy 278 AGTCCGAGTCAGAGAGCTGTTGAGGCGCAGAGTTCAAGAGAGCTGAGCAACACAG 337
Db 433 AGTCCGAGTCAGAGAGCTGTTGAGGCGCAGAGTTGAGAGAGCTGAGCAACATGAT 374
Qy 338 GAGAGCTGTCACTCAAGAATAATTAATTAATAGCAGAGCTTAAGTGGCTCATCCTGTGT 397
Db 373 GAAACCTGTCTTATTAATAATTAATAATTAATAGCAGAGCTTAAGTGGCTCATCCTGTGT 314
Qy 398 CCCAGTACTAGGAGGACAGAGTGTGCTTGT-----CCCAGAGGCTCAAGACTGCA 453
Db 313 CCCAGTACTAGGAGGCTGAGGAGAGAGTGTGCTTGTGAAACCCAGAGGAGGAGTGTGCA 254
```

[illegible]

RESULT 6
US-09-925-065A-551304/C

ORGANISM: Homo sapiens
US-09-925-065A-551304

```
RESULT 7
US-10-301-480-529254/C
; Sequence 529254, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
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1  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
2  ;
3  ; FILE REFERENCE: 108627.137
4  ;
5  ; CURRENT APPLICATION NUMBER: US/10/301,480
6  ;
7  ; CURRENT FILING DATE: 2002-11-21
8  ;
9  ; PRIOR APPLICATION NUMBER: US 10/215,598
10 ;
11 ; PRIOR FILING DATE: 2002-08-09
12 ;
13 ; PRIOR APPLICATION NUMBER: US 60/311,695
14 ;
15 ; PRIOR FILING DATE: 2001-08-10
16 ;
17 ; NUMBER OF SEQ ID NOS: 122618
18 ;
19 ; SOFTWARE: FastSeq for Windows Version 4.0
20 ;
21 ; SEQ ID NO 529254
22 ;
23 ; LENGTH: 1614
24 ;
25 ; TYPE: DNA
26 ;
27 ; ORGANISM: Homo sapien
28 ;
29 US-10-301-480-529254

```

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RESULT 8
US-10-301-480-1142663/c
; Sequence 1142663, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTOR: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1142663
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1142663

```

Query Match	7.3%	Score 166;	DB 10;	Length 1614;
Best Local Similarity	76.2%	Pred. No. 2.1e+03;		
Matches 244;	Conservative 0;	Mismatches 70;	Indels 6;	Gaps 3


```
APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172533
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-172533
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```
Query Match      7.3%; Score 165.6; DB 9; Length 1187;
Best Local Similarity 75.9%; Pred. No. 2.6e+03;
Matches 243; Conservative 1; Mismatches 70; Indels 6; Gaps 3;
```

```
QY 225 AATTTCTTGAGGCCAGGACAGTGGCTCAACCTGTAATTCCAGTACTGTGAGAGTCCGA 284
    |||
DB 419 AAAATCATGAGGCCAGGACAGTGGCTCATGCTGTAATTCAGACACTTTGGAGGCTTA 360

QY 285 GGTCAAGAGACTGCTTGAGGCCAGAGTTCAGAGAGCGCTGGAACAACAGGAGAGA-CC 343
    |||
DB 359 GCGAGGCAATGCTTGAGGCCAGGAGTTCAAGATAGCTGGGCGAGTGTGAAACCC 300

QY 344 TGTCACTACAAGATAATTAATTAATTAAGCCAGCTTAGTGGCTCATCCCTGTGGTCCAGC 403
    |||
DB 299 TGCCCTCCACAAAATAATACAAAATTAAGCAAGTGTGTGTGTGTCACACCTGTGTCCAGC 240

QY 404 TACTAGGAGGAGCAAGTAGAGTCTGTTGT---CCAGAGAGTCAAGACTGCAGTAGAC 459
    |||
DB 239 TACTTGGAGGCTGAGGTAGAGAAATTGATTGAGAGCCRAAGAGTCAAGGCTCCAGTAGAC 180

QY 460 TGAGACCCAGCCAGCTTCAGCTTCAGCTGGGCAACAAAAGAGCCCTGTCCAAAAT 519
    |||
DB 179 CGAGATCACACCA-CTGCACTCCAGCTGTGCAACAGAGTGAGACCTGTCTCAAAAAAT 121

QY 520 AAGTTAAATTAATTAATTAAT 539
    |||
DB 120 AAAAAATTAATTAATTAATCAT 101
```

```
RESULT 12
US-10-301-480-172534/c
; Sequence 172534, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172534
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-172534
```

```
Query Match      7.3%; Score 165.6; DB 9; Length 1187;
Best Local Similarity 75.9%; Pred. No. 2.6e+03;
Matches 243; Conservative 1; Mismatches 70; Indels 6; Gaps 3;
```

```
QY 225 AATTTCTTGAGGCCAGGACAGTGGCTCAACCTGTAATTCCAGTACTGTGAGAGTCCGA 284
    |||
DB 419 AAAATCATGAGGCCAGGACAGTGGCTCATGCTGTAATTCAGACACTTTGGAGGCTTA 360

QY 285 GGTCAAGAGACTGCTTGAGGCCAGAGTTCAGAGAGCGCTGGAACAACAGGAGAGA-CC 343
    |||
DB 359 GCGAGGCAATGCTTGAGGCCAGGAGTTCAAGATAGCTGGGCGAGTGTGAAACCC 300

QY 344 TGTCACTACAAGATAATTAATTAATTAAGCCAGCTTAGTGGCTCATCCCTGTGGTCCAGC 403
    |||
DB 299 TGCCCTCCACAAAATAATACAAAATTAAGCAAGTGTGTGTGTGTCACACCTGTGTCCAGC 240

QY 404 TACTAGGAGGAGCAAGTAGAGTCTGTTGT---CCAGAGAGTCAAGACTGCAGTAGAC 459
    |||
DB 239 TACTTGGAGGCTGAGGTAGAGAAATTGATTGAGGCTAAGAGTCAAGGCTTCAGTAGAC 180

QY 460 TGAGACCCAGCCAGCTTCAGCTTCAGCTGGGCAACAAAAGAGCCCTGTCCAAAAT 519
    |||
DB 179 CGAGATCACACCA-CTGCACTCCAGCTGTGCAACAGAGTGAGACCTGTCTCAAAAAAT 121

QY 520 AAGTTAAATTAATTAATTAAT 539
    |||
DB 120 AAAAAATTAATTAATTAATCAT 101
```

```
RESULT 13
US-10-301-480-785942/c
; Sequence 785942, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 785942
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-785942
```

```
Query Match      7.3%; Score 165.6; DB 10; Length 1187;
Best Local Similarity 75.9%; Pred. No. 2.6e+03;
Matches 243; Conservative 1; Mismatches 70; Indels 6; Gaps 3;
```

```
QY 225 AATTTCTTGAGGCCAGGACAGTGGCTCAACCTGTAATTCCAGTACTGTGAGAGTCCGA 284
    |||
DB 419 AAAATCATGAGGCCAGGACAGTGGCTCATGCTGTAATTCAGACACTTTGGAGGCTTA 360

QY 285 GGTCAAGAGACTGCTTGAGGCCAGAGTTCAGAGAGCGCTGGAACAACAGGAGAGA-CC 343
    |||
DB 359 GCGAGGCAATGCTTGAGGCCAGGAGTTCAAGATAGCTGGGCGAGTGTGAAACCC 300

QY 344 TGTCACTACAAGATAATTAATTAATTAAGCCAGCTTAGTGGCTCATCCCTGTGGTCCAGC 403
    |||
DB 299 TGCCCTCCACAAAATAATACAAAATTAAGCAAGTGTGTGTGTGTCACACCTGTGTCCAGC 240

QY 404 TACTAGGAGGAGCAAGTAGAGTCTGTTGT---CCAGAGAGTCAAGACTGCAGTAGAC 459
    |||
DB 239 TACTTGGAGGCTGAGGTAGAGAAATTGATTGAGGCTCAAGGCTTCAGTAGAC 180

QY 460 TGAGACCCAGCCAGCTTCAGCTTCAGCTGGGCAACAAAAGAGCCCTGTCCAAAAT 519
    |||
DB 179 CGAGATCACACCA-CTGCACTCCAGCTGTGCAACAGAGTGAGACCTGTCTCAAAAAAT 121
```

OY 520 AAGTTAAATAATAAT 539
Db 120 AAAAAATAATAATCAT 101

RESULT 14

US-10-301-480-785943/C
; Sequence 785943, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 785943
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-785943

Query Match 7.3%; Score 165.6; DB 10; Length 1187;
Best Local Similarity 75.9%; Pred. No. 2.6e+03;
Matches 243; Conservative 1; Mismatches 70; Indels 6; Gaps 3;

OY 225 AATTTCTTGAGGCCAGCAGCTGCTCAACCTTAATTCAGTACTGTGAGAGTCCGA 284
Db 419 AAAATCATGAGGCCAGCAGCTGCTCATGCTTAATTCAGCAGCTTTGGAGGCTTA 360
OY 285 GGTGAGAGAGCTCTTGAGGCCAGAGTTCAAGAGAGCTTGAACAACAGGAGGA-CC 343
Db 359 GGCAGGAGAGTGGCTTGAGGCCAGAGTTCAAGAGTGGAGAGTGTGAAACCC 300
OY 344 TGTCACTACAAGATTAATAATTAATAGCCAGGCTTAGTGGCTATCCCTGTGCTCCAGC 403
Db 299 TCCCTCCACAAAAAATACAAAAATTAAGCAAGTGTGTGTGTCACACCTGTGTCCAGC 240
OY 404 TACTGAGGAGGAGAGTAGAGCTGCTGT-CCAGAGAGTCAAGACTGCACTGAGC 459
Db 239 TACTTGGAGGCTGAGTAGAGATTAATGAGGCTCAAGGCTCAAGTCACTGAGC 180
OY 460 TGAGACCCAGCAGCTGCTTCCAGCTGGGCAAAAAAGAGACCTGTCTCAAAAAAT 519
Db 179 CGAGATCACACCA-CTGCACTCCAGCTGTGCAACAGAGTGAACCTGTCTCAAAAAAT 121
OY 520 AAGTTAAATAATAAT 539
Db 120 AAAAAATAATAATCAT 101

RESULT 15

US-10-301-480-576542/C
; Sequence 576542, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 576542
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-576542

Query Match 7.3%; Score 165.4; DB 10; Length 809;
Best Local Similarity 74.2%; Pred. No. 3.5e+03;
Matches 250; Conservative 0; Mismatches 81; Indels 6; Gaps 3;

OY 211 AAAGATTTAAGAAATTTCTTGAGGCCAGCAGTGGCTCACACCTGTAATTCAGTA 270
Db 474 AAAAAAAGAAATGCTATCTGAGGCCAGCAGTGGCTCACACCTGTAATTCAGTA 415
OY 271 CTGTGAGAGTCCAGAGTCCAGAGAGCTGCTTGAAGCCAGAGTTCAGAGAGCTGAGCA 330
Db 414 CTTTGGAGAGGCCAGAGCGAGAGATTAAGTCAAGAGTTCAGAGAGCTGAGCA 355
OY 331 ACACAGGAGAC-CTGTCACTACAAAGATTAATTAATTAATTAATTAATTAATTAAT 389
Db 354 ACATAGTGAACACCATCTCTACTAAAAATTAATTAATTAATTAATTAATTAATTAAT 295
OY 390 CCTGTGTCCTCAGCTACTAGGAGAGCAAGTAGA---CTGCTTGTCCAGAGAGTCA 445
Db 294 CTTTAATCCAGTACTCAGAGAGCTGAGGAGAGATGCTGAGCCCAAGAGGAG 235
OY 446 AGACTGAGTGAAGTGAAGCCAGCCAGCTGCTTCCAGCTGGGCAAAAAAGAGAGC 505
Db 234 AGCTTGAAGTGAAGTGAAGTGTGCGCA-CTACACTCAAGCTTGGGCAAGAGAGACT 176
OY 506 CTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 542
Db 175 CTGTCTCAAAAAAAGATGTCAA 139

Search completed: April 22, 2006, 13:06:02
Job time : 947 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2005, 16:16:22 : Search time 11039 Seconds
(without alignments)
11688.979 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1_2270
Perfect score: 2270
Sequence: 1 aacgacatcgccgcgcacg.....cgccgcgtcgccgcacg 2270

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_in:*
- 3: gb_env:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pr:*
- 9: gb_ro:*
- 10: gb_atc:*
- 11: gb_ey:*
- 12: gb_un:*
- 13: gb_vl:*
- 14: gb_ptg:*
- 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2270	100.0	3505	E54511	E54511 UCP-2 promo
2	2238.8	98.6	199384	AF003531	AP003531 Homo sapi
3	2237.2	98.6	3270	AF306570	AF306570 Homo sapi
4	2226.8	98.1	156370	AP003717	AP003717 Homo sapi
5	2196.8	96.8	197031	AC019121	AC019121 Homo sapi
6	2189.2	96.4	156668	AC024029	AC024029 Homo sapi
7	2052.8	90.4	12177	DD087219	DD087219 Homo sapi
8	1820	80.2	3301	AF208500	AF208500 Homo sapi
9	519	22.9	2131	AK025742	AK025742 Homo sapi
10	485	21.4	736	AR039137	AR039137 Sequence
11	485	21.4	736	AR065267	AR065267 Sequence
12	485	21.4	736	BD061651	BD061651 Regulator
13	364.2	16.0	5283	AX346795	AX346795 Sequence
14	312.4	13.8	5283	AX346795	AX346795 Sequence
15	190.8	8.4	179222	AC090270	AC090270 Homo sapi
16	188.4	8.3	41150	AC004663	AC004663 Homo sapi
17	184.4	8.1	178344	AC067846	AC067846 Homo sapi
18	181.2	8.0	189723	AC090952	AC090952 Homo sapi

19	178.2	7.9	168274	AL954859	AL954859 Homo sapi
20	176.2	7.8	82827	AC079395	AC079395 Homo sapi
21	175.8	7.7	66188	AL391136	AL391136 Homo sapi
22	175.8	7.7	162820	AL138765	AL138765 Homo sapi
23	174.6	7.7	144848	AL592165	AL592165 Homo sapi
24	174.2	7.7	122552	CNS01DRS	AL118555 Homo sapi
25	173.6	7.6	87350	AC009752	AC009752 Homo sapi
26	173.6	7.6	137960	AC103889	AC103889 Homo sapi
27	173.6	7.6	169214	AC092720	AC092720 Homo sapi
28	173.6	7.6	170264	AC137640	AC137640 Homo sapi
29	173.6	7.6	208236	AC010536	AC010536 Homo sapi
30	173.4	7.6	193604	AL603832	AL603832 Homo sapi
31	173	7.6	84166	AC009095	AC009095 Homo sapi
32	173	7.6	139514	AC010530	AC010530 Homo sapi
33	172.8	7.6	128805	HS339A18	HS339A18 Homo sapi
34	172.8	7.6	167078	HS339A18	HS339A18 Homo sapi
35	172.6	7.6	185511	AC093414	AC093414 Homo sapi
36	172.4	7.6	123943	AC006208	AC006208 Homo sapi
37	172.2	7.6	206943	AC138848	AC138848 Homo sapi
38	172	7.6	168133	AC093622	AC093622 Homo sapi
39	171.4	7.6	191598	AC144362	AC144362 Homo sapi
40	171.4	7.6	199310	AC112215	AC112215 Homo sapi
41	171.4	7.6	217029	AC105934	AC105934 Homo sapi
42	171.2	7.5	255952	AL513473	AL513473 Homo sapi
43	171	7.5	163339	AC096533	AC096533 Homo sapi
44	171	7.5	184041	AC093496	AC093496 Homo sapi
45	171	7.5	187159	AC090941	AC090941 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS E54511 3505 bp DNA linear PAT 31-JAN-2002
DEFINITION UCP-2 promoter and use thereof.
ACCESSION E54511
VERSION E54511.1 GI:18629692
KEYWORDS JP 2000236886-A/1.
SOURCE JP 2000236886-A/1.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Toyota, Y., Kobayashi, M. and Igaki, S.
TITLE UCP-2 promoter and use thereof
JOURNAL Patent: JP 2000236886-A 1 05-SEP-2000;
TAKEDA CHEM IND LTD
COMMENT OS Homo sapiens (human)
PN JP 2000236886-A/1
PD 05-SEP-2000
PR 22-DEC-1999 JP 1999364724

PI YUKIO TOYOTA, MAKOTO KOBAYASHI, SHIGERU IGAKI
PC C12N15/09, A61K45/00, A61P3/04, A61P3/06, A61P3/10, A61P12, PC
A61P29/00, C12N1/21,
PC C12N5/10, C12Q1/02, G01N33/15, G01N33/50, A61K31/711, A61K38/00,
PC A61K48/00,
PC C12N15/09, C12R1/19, (C12N15/09, C12R1/21, C12R1/19),
PC (C12N15/10, C12R1/91), C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
PC C12R1/19),
PC (C12N15/00, C12R1/91), (C12N5/00, C12R1/91)

FT Key Location/Qualifiers
FT source 1. 3505 Location/Qualifiers
FT 1. 3505 Location/Qualifiers

FEATURES
source
1. 3505 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match	100.0%;	Score 2270;	DB 6;	Length 3505;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2270; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

QY	1021	AATCGCTTGA	CACTTCGTTTCC	ACGCTGCTTC	GCACAGAAC	CAATGCGCTCGCGTGT	1080
Db	1021	AATCGCTTGA	CACTTCGTTTCC	ACGCTGCTTC	GCACAGAAC	CAATGCGCTCGCGTGT	1080
QY	1081	TTCTTTCCGCA	TAAATTAAT	CCAGGACCC	ACAGCTCG	GTGCTCCCTCAGCTGT	1140
Db	1081	TTCTTTCCGCA	TAAATTAAT	CCAGGACCC	ACAGCTCG	GTGCTCCCTCAGCTGT	1140
QY	1141	CAGTCCCTT	CTGCTGTGAAAA	CA	CATATGCGCG	CGCTGACCAAGGAGTAA	1200
Db	1141	CAGTCCCTT	CTGCTGTGAAAA	CA	CATATGCGCG	CGCTGACCAAGGAGTAA	1200
QY	1201	AATATCAGAA	AAGATGACT	GAACGCTT	TGGGAC	CTCGCTTCTCATTTGTAAAT	1260
Db	1201	AATATCAGAA	AAGATGACT	GAACGCTT	TGGGAC	CTCGCTTCTCATTTGTAAAT	1260
QY	1261	TAAATCAGAG	CTTCTTCACT	CCCAACGAG	AGTGTGTC	CCCGGCACAGAGGCC	1320
Db	1261	TAAATCAGAG	CTTCTTCACT	CCCAACGAG	AGTGTGTC	CCCGGCACAGAGGCC	1320
QY	1321	TGTTGCTGT	TCACGCAT	CAGTTA	CCCCCA	CAGGACGGGTCA	1380
Db	1321	TGTTGCTGT	TCACGCAT	CAGTTA	CCCCCA	CAGGACGGGTCA	1380
QY	1381	AGCGCCGGT	CCATCTCT	GAACGCTT	TTCTCAT	TCCACAGGCTGGA	1440
Db	1381	AGCGCCGGT	CCATCTCT	GAACGCTT	TTCTCAT	TCCACAGGCTGGA	1440
QY	1441	GGCCCGGCT	CGCCTT	GCACGTC	GGGGGG	CGGGCCGTTTGCTGTG	1500
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Db	2041	AAAGTCAT	GAGAGAA	CCCT	TAGCGGGG	CGGTTCC	2100
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AUTHORS	Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.						
TITLE	Published Only in Database (2001)						
JOURNAL	2 (bases 1 to 199384)						
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TITLE	Direct Submission						
COMMENT	Submitted (18-APR-2001) Masahito Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22, Sukenri-chou, Tsukuba, Ibaraki, Japan, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsr.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/), Tel: 81-45-503-9111, Fax: 81-45-503-9170						
FEATURES	On Apr 26, 2002 this sequence version replaced gi:13699094.						
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	/map="11g"						
	/clone="RP11-535C12"						
ORIGIN							
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Matches 2262; Conservative 0; Mismatches 2; Indels 2; Gaps 2;							
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REFERENCE  1
            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Direct Submission
            Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22 Suehiro-Chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp-gsc.riken.go.jp/,
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DEFINITION Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT
ACCESSION AC019121
VERSION   AC019121.3 GI:8440022
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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          Hominoidea; Homo.
          1 (bases 1 to 197031)
          Waterston,R.H.
          The sequence of Homo sapiens clone
          Unpublished
          2 (bases 1 to 197031)
          Waterston,R.H.
          Direct Submission
          Submitted (30-DEC-1999) Genome Sequencing Center, Washington
          University School of Medicine, 4444 Forest Park Parkway, St. Louis,
          MO 63108, USA
          On Jun 10, 2000 this sequence version replaced gi:7105573.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0535C12
----- Summary Statistics -----
Sequencing vector: M13; 535
Sequencing vector: plasmid; 45%
Chemistry: Dye-primer ET; 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182418 bases at least Q40
Consensus quality: 187565 bases at least Q30
Consensus quality: 190012 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 194831; sum-of-contigs
Quality coverage: 4.10 in Q20 bases; agarose-fp
Quality coverage: 4.05 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 5764: contig of 2693 bp in length
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* 12865: gap of unknown length
* 12866
* 12965: gap of unknown length

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* 116913
* 117013
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* 60200 60300: gap of unknown length
* 60300 71424: contig of 11125 bp in length
* 71425 71524: gap of unknown length
* 71525 86218: contig of 14694 bp in length
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RESULT 7
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LOCUS
DEFINITION Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier)
 (UCP2) gene, complete cds; nuclear gene for mitochondrial product.
ACCESSION DQ087219
VERSION DQ087219.1 GI:67515418
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
REFERENCE
 1 (bases 1 to 12177)
 Livingston, R.J., Rieder, M.J., Shaffer, T., Bertucci, C., Baier, C.N.,
 Rajkumar, N., Wills, H.T., Daniels, M., Downing, T.K., Stanaway, I.B.,
 Nguyen, C.P., Gilderbieve, H., Cassidy, C.M., Johnson, B.J.,
 Swanson, D.E., McFarland, I., Yool, B., Park, C. and Nickerson, D.A.
 Direct Submission
TITLE
 Submitted (07-JUN-2005) Genome Sciences, University of Washington,
 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT
 To cite this work please use: NIEHS-SNPs, Environmental Genome
 Project, NIEHS S15478, Department of Genome Sciences, Seattle, WA
 (URL: <http://esp.gs.washington.edu>).
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7952

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Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 1; Gaps 1;

Matches 2065; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 361 CATCTTCTTTTCAAGAGACTTCTTAAGGACTCATGTGCGCTCTGTGATCTCCAG 420
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RESULT 8
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DEFINITION Homo sapiens uncoupling protein 2 (UCP2) gene, promoter and exon 1.
ACCESSION AF208500
VERSION AF208500.1 GI:6684000
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 3301)
Lentjes,K.U.
Molecular cloning and functional characterization of the promoter
region of the human uncoupling protein-2 gene
Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)
2 (bases 1 to 3301)
Tu,N., Chen,H., Winnikes,U., Reinert,I., Marmann,G., Pirke,K.M. and
Lentjes,K.-U.
Functional characterization of the 5'-flanking and promoter regions
of the human UCP2 gene
Biochem. Biophys. Res. Commun. (2000) In press
3 (bases 1 to 3301)
Lentjes,K.-U., Tu,N. and Chen,H.
Direct Submission
Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics,
Center for Psychobiological and Psychosomatic Research, University
of Trier, Friedrich-Wilhelm-Strasse 23, Trier D-54290, Germany
FEATURES
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Db 1184 CATCTTATGACTTGAGCAAGCTGCTAAATCCAAAGGTGACGCTTGTATGCTATAG 1243

Qy 185 GATTGCTCAGATCTGCCCCACCCTGTGAAGAATTTAAGAGATTTCTTGAGGCCAGGCAC 244
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Qy 245 AGT-ggctcagacct-gtaattccagtactgtgagagt--ccagagtcagagactgctt 300
Db 1304 ANTGGGCTCACACCTGGTAAATCCAGTACGTGAMAATCCGAGTCAAGAGACTGCTT 1363

Qy 301 GAGGCCAGAGTTTCAAGAGCAGCTGGACACAACAGGAGAGACCTGTCACTACAAAGATA 360
Db 1364 GAGGCCAGAGTTTCAAGANANCTGGACACATAGGAABA-ctgtcactcacaagaata 1422

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Qy 418 AAGTAGACCTGTGTCGCCAGAGTCAACATCTGACGTGAGCTGAAGCCAG-CCACCTG 476
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RESULT 9
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 LOCUS AK025742 2131 bp mRNA linear PRI 13-SEP-2003
 DEFINITION Homo sapiens cDNA: FLJ22089 fis, clone HEP16080, highly similar to
 HSU94592 Human uncoupling protein homolog (UCPH) mRNA.

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ACCESSION AK025742
VERSION AK025742.1 GI:10438354
KEYWORDS oligo capping, fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isoagi,T. and Sugano,S.
TITLE NEBO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2131)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isoagi,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEBO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan: cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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Best Local Similarity 99.8%; Pred. No. 1.5e-98;
Matches 530; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 1 AGCGCGCGCTCGTCCGAGAGGAGTGGTGTGTTGCCCGACGTTAGGGGGCTGGGCCCA 60
Qy 1800 TAAAGGAGAGTCACTTAAGACAGCGCGCGCGTGTGTAAGAACCGTCCG 1859
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QY							
Db							

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DEFINITION	Sequence 1 from patent US 5807740.	736 bp	DNA
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VERSION	AR039137.1	GI:5958500	
KEYWORDS			
SOURCE	Unknown.		

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REFERENCE      1 (bases 1 to 736)
AUTHORS       Amaral, M. Catherine, and Chen, J.-L.
TITLE         Regulators of UCP2 gene expression
JOURNAL       Patent: US 5807740-A 15-SEP-1998;
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Db	1	GGGTGGAGTAGTTTGCCCAAGCGTAGGGGGGCTGGGCCCATTAAGAGGAAAGTGACATTAG	60
OY	1822	ACAACGGCCCCGCTGGACCGCTTGTAAGAAACCGTCTCTGGCTGGGAAGGCAGAAGGTGTGTG	1881
Db	61	ACAACGGCCCCGCTGGACCGC-TGTTAGAAACCGTCTCTGGCTGGGAAGGCAGAAGGTGTGTG	119
OY	1882	ACTGGACAAAGACTTGTTCTTGGCGGGTCAGTCGTGGCAATCTCACAAGAGTTGGCGGGCCG	1941
Db	120	ACTGGACAAAGACTTGTTCTTGGCGGGTCAGTCGTGCATCTTCACAGAAGTTGGCGGGCCG	179
OY	1942	AGAGAGTGTGAGGCGAAGAGCGGGGAGTGGCAAGAGAGTGACCATCTCGGGGAAACGAAGAA	2001
Db	180	AGAGAGTGTGAGGCGAGAGCGGGGAGTGGCAAGAGAGTGACCATCTCGGGGAAACGAAGAA	239
OY	2002	GTAAGCGGGGTGATGGGACGCAACGGGAAACGGGAATGGAGAAAGTACATGAGAGAAACCTTA	2061
Db	240	GTAAGCGGGGTATATGAGACGCAACGGGAAACGGGAGTGGAGAAAGTATGAGAGAAACCTTA	299
OY	2062	GGCGGGGCGGTCCCGCGGAAAGCGCGCTGTCCAGGGGTCTTCGCAACCCAGTAGAGACT	2121
Db	300	GGCGGGGCGGTCCCGCGGAAAGCGCGCTGTCCAGGGGTCTTCGCAACCCAGTAGAGAG-T	358
OY	2122	GGCAGAGCCCGGCCCCCGGCTCCGAGAGGCCCAACCCCGGGGCCCGCCCCGAGGCTTTAAGCCG	2181
Db	359	GGCAGAGCCCGGCCCCCGGCTCCGAGAGGCCCAACCCCGGGGCCCGCCCCGAGGCTTTAAGCCG	418
OY	2182	CGCCGCGCGCTTGCGCGGAGGCCCACTGGGAAAGCCAGCTGCGCGCGCTTGGAGATTGACT	2241
Db	419	CGCCGCGCGCTTGCGCGGAGGCCCACTGGGAAAGCCAGCTGCGCGCGCTTGGAGATTGACT	478
OY	2242	GTCCACGCTCTCGCCCGGCTCTTCCAGCGG	2270
Db	479	GTCCACGCTCTCGCCCGGCTCTTCCAGCGG	507

RESULT	11		
LOCUS	AR065267	736 bp	DNA
DEFINITION	Sequence 1 from patent US 5849514.	linear	PAT 29-SEP-1999
ACCESSION	AR065267		
VERSION	AR065267.1	GI:5995483	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 736)		
TITLE	Amaraal,M.Catherine. and Chen,J.-L.		
JOURNAL	Method of identifying agents that modulate UCP2 promoter activity		
FEATURES	Patent.: US 5849514-A 1 15-DEC-1998;		
SOURCE	Location/Qualifiers		
	1..736		

ORIGIN

Query Match	21.4%	Score 485;	DB 6;	length 736;
Best Local Similarity	99.6%	Pred. No. 1.8e-91;		
Matches 507; Conservative	0;	Mismatches	0;	Indels 2; Gaps 2;

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 Db 1 GGGTGGGTGATTTGCCACAGCGTAGGGGGGCTGGGCGCCATTAAGAGGAAGTGCATTAG 60

Oy 1822 ACACGGCCCCGCTGGACGCTGTATTAGAAACCGCTCTTGCCTGGAAAGCAGAGAGGTGTGTG 1881
 Db 61 ACACGGCCCCGCTGGACGC-TGTAGAAACCGTCTCTGCTGGGAAGCAGAAGGTGTGTG 119

1002 ACATGACCAAGACCTTCTCTGGCGGTCACTTCCATCTCTCAAGAGGTTGGCGCCCG 179

1572 AGAAGAGTGTGAGGAGCGGAGAGTGGCAAGGAGAGTGCATCTCGGAGAAAGAAAGA 239
 180 AGAAGAGTGTGAGGAGCGGAGAGTGGCAAGGAGAGTGCATCTCGGAGAAAGAAAGA 239

240 GTAAACGCGGTGATGGACGACACGAAACGGGAGTGGAGAAAGTCATGGAGAGAACCTTA 299

300 GGCGGGCGCTCCCGCGAAGCGGCTGCTCCAGGCTCTCCGCACCCAGTAGGAG-T 358

Db 359 GGCAGGCCCGCCCGCCCCCGCAGGCCCGCCCGCCCCCGCCCGAGGCTTAAGCCG 418

419 CGCGCGCGCTGGCGCGGAGCCCACTGGCAGAGCCCAAGCTGGCGCGGCTTGGGATTGACT 478

Db 479 GTCCACGCTGCCCCGCTGTCCTCCGACGGC 507

LOCUS	BD061651	736 bp	DNA	linear	PAT 27-AUG-2002
DESCRIPTION	Regulator of Wnt3 gene expression				
RESULT 12					
BD061651					

ACCESION BD061651 GI:22607256
 VERSION BD061651.1
 KEYWORDS JP 2001507943-A/1.
 SOURCE synthetic construct

ORGANISM
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 736)

AUTHORS Amaral, C.M. and Chen, J.L.
 TITLE Regulators of UCP2 gene expression
 JOURNAL Patent: JP 2001507943-A 1 19-JUN-2001;
 COMMENT TULARIK INC
 PN JP 2001507943-A/1
 PD 19-JUN-2001
 PF 22-APR-1998 JP 1998547120
 PR 25-APR-1997 US 08/846012
 PI CATHERINE M AMARAL, JIN LONG CHEN
 PC C12N1/00, C12N5/10, C12N15/11, C12N15/63, C12Q1/02, C12Q1/68 CC
 Strandedness: Double;
 CC Topology: Linear;
 FH Key

FEATURES
 source Location/Qualifiers
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ORIGIN

Query Match 21.4%; Score 485; DB 6; Length 736;
 Best Local Similarity 99.6%; Pred. No. 1.8e-91;
 Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1762 GGGTGGAGTATTTGCGCAGCGTAGGGGGCTGGCCCATAAAGAGAGTCACTTAG 1821
 1 GGGTGGAGTATTTGCGCAGCGTAGGGGGCTGGCCCATAAAGAGAGTCACTTAG 60
 1822 ACACGGCCCGCTGAGCGCTTTGTAAGAACCGTCTGCGTGGAGAGGAGAGTGTGTG 1881
 61 ACACGGCCCGCTGAGCGCTTTGTAAGAACCGTCTGCGTGGAGAGGAGAGTGTGTG 119
 1882 ACTGGAACAAGCTTTCTGCGCGCTCACTGCTTCATCTTCAAGAGTGTGTGTGTG 1941
 120 ACTGGAACAAGCTTTCTGCGCGCTCACTGCTTCATCTTCAAGAGTGTGTGTGTG 179
 1942 AGAGAGTGAAGGAGAGAGCGGGAGTGGCAAGAGAGTGAACCATTCGCGGAGAGAGGA 2001
 180 AGAGAGTGAAGGAGAGCGGGAGTGGCAAGAGAGTGAACCATTCGCGGAGAGAGGA 239
 240 GTAAACGCGGTGATGGAGCGCAACGGAACGGAAGTGAAGAAATCATGAGAGAGAGCT 299
 2002 GTAAACGCGGTGATGGAGCGCAACGGAACGGAAGTGAAGAAATCATGAGAGAGCT 2061
 240 GTAAACGCGGTGATGGAGCGCAACGGAACGGAAGTGAAGAAATCATGAGAGAGCT 299
 2062 GCGCGCGCGCTGCGCGGAGAGCGGCTGCTCCAGGCTTCGCAACCCAGTAGAGCT 2121
 300 GCGCGCGCGCTGCGCGGAGAGCGGCTGCTCCAGGCTTCGCAACCCAGTAGAGAG-T 358
 2122 GCGAGCGCGCGCGCGCGCGGAGAGCGGCTGCTCCAGGCTTCGCAACCCAGTAGAGCG 2181
 359 GCGAGCGCGCGCGCGCGCGGAGAGCGGCTGCTCCAGGCTTCGCAACCCAGTAGAGCG 418
 2182 GCGCGCGCGCTGCGCGGAGAGCGGCTGCTCCAGGCTTCGCAACCCAGTAGAGCT 2241
 419 GCGCGCGCGCTGCGCGGAGAGCGGCTGCTCCAGGCTTCGCAACCCAGTAGAGCT 478
 2242 GTCCACGCTCGCGCGGCTGCTCCAGCGG 2270
 479 GTCCACGCTCGCGCGGCTGCTCCAGCGG 507

RESULT 13
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 DEFINITION Sequence 1865 from Patent WO0200928.
 ACCESSION AX346794
 VERSION AX346794.1 GI:18494680
 KEYWORDS
 SOURCE
 ORGANISM
 other sequences; artificial sequences.
 REFERENCE
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.

TITLE Diagnose of diseases associated with the immune system
 JOURNAL Patent: WO 0200928-A 1865 03-JAN-2002;
 EpiGenomics AG (DE)
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 /note="chemically treated genomic DNA (Homo sapiens)"

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Query Match 16.0%; Score 364.2; DB 6; Length 5283;
 Best Local Similarity 77.4%; Pred. No. 5.1e-66;
 Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

1668 CGACAGCGCGCGCTGTACCAATCGACAGCGCGCGCTGCGAGGCCCACTCCGC 1727
 2 CGATTAAGCGCGCGCTGTAAATTAATCAATGCGAGTGGTCCGAGGTTTACGTTTGT 61
 1728 CCGCAGAGCGCGCGCGCGCTGCTGCGAGAGGAGGTTGTTGCCAGGTTAGG 1787
 62 TTTGTAGAGTGAATCGCGCGCTGCTGTAAGAGAGGTTGTTTACGTA-GG 120
 1788 GGGCTGGGCCCATTAAGAGAGAGTGAATTAAGACAGCGCGCTGAGCGTTGTAG 1847
 121 GGGTTGGTTTAAAGAGAGAGTGAATTAAGATACGTTAG--TGAACGTTGTAG 178
 1848 AACCGTCTGCTGCGAGAGAGAGAGTGTGAATGAGACAGACTTTGTCGCGCT 1907
 179 AATCGTTTGTGGAGAGAGTGAAGAGTGTGAATGAGATTAAGTTTGTGGCGCT 238
 1908 CAGCTTGCATCTCTCAAGAGTGGCGCGCGCGAGAGTGAAGAGAGGCGGAG 1967
 239 TAGTTTGTATTTTATAGAGTTGGGTTCAAGAGTGAAGAGAGGCGGAG 298
 1968 TGGCAAGAGTGAACCATCTCGGGAGAGAGAGTGAACCGCTGATGAGAGCGACGGA 2027
 239 TGTGAAGAGTGAATTTTCGGGAGAGAGAGTGAACCGCTGATGAGAGCGACGA 358
 2028 AACGGAGTGAAGAGTGAAGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGCG 2087
 359 AACGGAGTGAAGAGTGAAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGCG 418
 2088 GCTGCTCAAGGCTTCGCGACCAAGTAGAGTGGAGCGCGCGCGCGCGCGCGAGCG 2147
 419 GTTGTATTAAGGTTTGTATTAAGTAGAGTGGAGTGGTTCGTTTCGTTAGAGT 478
 2148 CCCACCGCGCGCGCGCGCGCGGAGGCTTAAGCGCGCGCGCTGCGAGAGCGCCACT 2207
 479 TTTATTTGCGGTTTCGTTTGAAGTTTAAGTCCGCTGCTGTTGCGGAGATTATTT 538
 2208 GCGAAGCCAGCTGCGCGCGCTTGGAGTTGATGATGCTGCGCGCTGCTGCGAGC 2267
 539 GCGAAGTTAGTGGCGCGCTTGGAGTTGATGATGATGATGATGATGATGATGATGAT 598
 2268 GCG 2270
 599 GCG 601

RESULT 14
 LOCUS AX346795/c 5283 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 1866 from Patent WO0200928.
 ACCESSION AX346795
 VERSION AX346795.1 GI:18494681
 KEYWORDS
 SOURCE
 ORGANISM
 other sequences; artificial sequences.
 REFERENCE
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
 TITLE Diagnose of diseases associated with the immune system

JOURNAL Patent: WO 020928-A 1866 03-JAN-2002;
 Epigenomics AG (DB)
 FEATURES Location/Qualifiers
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ORIGIN

Query Match 13.8%; Score 312.4; DB 6; Length 5283;
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 Qy 1727 CCCTGACAGAGCCGCGCGCTGCTCGACAGAGGGTGGTGTGTTGCCAGCGTAGG 1786
 Db 5223 CCCTACAAAACCAACCGCGCTGCTCGCAAAAATAATTAATTAACCAAGTA-A 5165
 Qy 1787 GGGGCTGGGCGCCATTAAGAGAGTGAATTAAGACCGGCCCGCTGACGCTGTGTA 1846
 Db 5164 AAAAATAAACCAATTAATAATTAATTAATTAATTAATTAATTAATTAATTA 5107
 Qy 1847 GAAACCGCTCTGCTGAGAGGAGAGTGTGTGACAGAGCTGTGTTCTGCGCG 1906
 Db 5106 AAAACCGCTCTACTATAAAAACAAAATAATTAATTAATTAATTAATTAATTA 5047
 Qy 1907 TCAGCTTTGCTCATCTCAGAGGTTGCGCGCGCGAGAGTGTGAGGAGCGCGGGA 1966
 Db 5046 TCAATCTTACCATCTCTCAAAAATAATTAATTAATTAATTAATTAATTAATTA 4987
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 Db 4686 CGCG 4683

RESULT 15
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 LOCUS Homo sapiens chromosome 15 clone RP11-16R3 map 15, WORKING DRAFT
 DEFINITION
 AC090270
 ACCESSION AC090270.3 GI:22123606
 VERSION
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 179222)

AUTHORS JOURNAL REFERENCE AUTHORS

Barren, B., Nussbaum, C. and Lander, E.
 Homo sapiens chromosome 15, clone RP11-16R3
 Unpublished
 2 (bases 1 to 179222)

Barren, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barren, N., Bastien, V., Boguslavsky, L., Bouhagalter, B., Brown, A.,
 Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,
 Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J.,
 Gadyana, S., Glinde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hago, B., Hearford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
 Jones, C., Karatas, A., Labocque, K., Lamazares, R., Landers, T.,
 Lhoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P.,
 Marquis, N., Matthews, C., McCarthy, M., McGowan, P., McKernan, K.,
 McPheters, R., Meldrum, J., Menues, L., Mihova, T., Mlenga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunhahng, P., Pierre, N., Pollara, V., Raymond, C., Retter, R.,
 Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
 Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
 Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tsafaye, S., Theodore, J.,
 Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,
 Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 179222)

REFERENCE
 AUTHORS
 Barren, B., Nussbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barren, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhagalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
 Gadyana, S., Gode, S., Graham, L., Grand-Pierre, N., Hago, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrum, J., Menues, L., Mihova, T., Mlenga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunhahng, P., Pierre, N., Raymond, C., Retter, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
 Tsafaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 6, 2002 this sequence version replaced gi:113273418.
 All repeats were identified using RepeatMasker:
 Smit, A.P.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L12470
 Center clone name: 16.E.3
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 172707 bases at least Q40
 Consensus quality: 175660 bases at least Q30
 Consensus quality: 176790 bases at least Q20
 Insert size: 176000; agarose-fp
 Insert size: 177722; sum-of-contigs
 Quality coverage: 9.4 in Q20 bases; agarose-fp
 Quality coverage: 9.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 21865: contig of 21865 bp in length
* 21866 21965: gap of 100 bp
* 21966 22685: contig of 720 bp in length
* 22686 22785: gap of 100 bp
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* 23347 23446: gap of 100 bp
* 23447 24108: contig of 662 bp in length
* 24109 24208: gap of 100 bp
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* 45273 57290: contig of 12018 bp in length
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* 122263 151672: contig of 29410 bp in length
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Matches 295; Conservative 0; Mismatches 227; Indels 8; Gaps 2;

QY 1 AACGATGCGCGCTCAGCCTCCAAAGCTGAGATTGACGCGTACCTCAC 60
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QY 61 CTGGCTACAGCTTTTCAAAATATCATTTATAGTACCATTCATTCAGTTGTCCAC 120
DB 72891 CGAGCCAGTT 72832
QY 121 AGGACATCTTATGACTTGAGCAAGCTGTAAAAATCCAAAGGTGACGCTTGTATGCT 180
DB 72831 NNNCT 72772
QY 181 ATAGGATGCTCAGATGCGCCCAACCTGAAAGATTTAGAGATTTCTTGAGCCAG 240
DB 72771 TGGCATCATATGATTTATTTTCTTATCTTAGAATTTCTATTAATTT-----GCCAG 72717
QY 241 GCACAGTGGCTCACACTGTATTTACCTAGTGTGAGAGTCCGAGTCCAGAGACTGCTT 300
DB 72716 GCATGTGGCTCATTCCTGTATCCAGCACTTTGGAGGCTGAGCGGTGATTTCTT 72657
QY 301 GAGGCGAGAGTTTCAAGAGCAGCTTGACACACAGGAGACCTGTCTCAAAAGATA 360
DB 72656 GGGGTGAGAGTTTCAAGAGCAGCTTGACACAGGAGAACCCGTCTCTCAAAAGATA 72597
QY 361 AATAATGACGAGCTTAGTGGCTCATCCCTGTGTGCTCCAGCTTACGAGAGGAGAGA-- 418

Db 72596 CAAAAATTAGCTGTGCA CAGTGGCGCA CGTCTGTATCCACGCTACTTGGGAGCTGAGG 72537
Qy 419 -AGTAGGACTGCTTGTGTCGCCAGAGGTCAAGA CTGCAGTGAGTGAGACCCAGCCACTGC 477
Db 72536 CAGGAGAAATCCCTTGAAACGAGAGGCGAGAGGTTGCAGTAAAGTGAAGCTGTGCCACTGC 72477
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Db 72476 ACTCCAGTCTGGGTGACAGAGCGAAGTCTGTCTCAAAAAA 72427

Search completed: December 21, 2005, 21:08:07
Job time : 11049 secs

ORIGIN (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 26.1%; Score 593.2; DB 2; Length 941;
Best Local Similarity 95.3%; Pred. No. 9.9e-74;
Matches 667; Conservative 0; Mismatches 23; Indels 10; Gaps 5;

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QY GCGAAGACATGCGCTGCGGCGGTTTCTTTCCGCTATA-TTATCCAGGCGCATGCCA 1113
DB GCGAAGACATGCGCTGCGGCGGTTTCTTTCCGCTATA-TTATCCAGGCGCATGCCA 344
QY GCTCTGTCCTCCCTCAGCTGTTTCCCTGCGAGTCCCTTCTGCTGTGAAAAACATATGCG 1173
DB GCTCTGTCCTCCCTCAGCTGTTTCCCTGCGAGTCCCTTCTGCTGTGAAAAACATATGCG 284
QY CCGGCTTCAACAGGCTGTAAGTGTGTAATATCAGAAAGATGACTGAACGTTTGGGAC 1233
DB CCGGCTTCAACAGGCTGTAAGTGTGTAATATCAGAAAGATGACTGAACGTTTGGGAC 224
QY TCCGTTCTCTATTTGTAATAATGAGAGTTAATACAGCCTTCTCTACCTCCCAACGAC 1293
DB TCCGTTCTCTATTTGTAATAATGAGAGTTAATACAGCCTTCTCTACCTCCCAACGAC 164
QY GTGTTTGTCCGCGCAGAGGCGCCAAATGTTGCTGTTCAGCATCACTTACCCCAAG 1353
DB GTGTTTGTCCGCGCAGAGGCGCCAAATGTTGCTGTTCAGCATCACTTACCCCAAG 104
QY GACGAGTCAAGCAATTAAGGCAACAGGCGCGGTCACTCTCTGACGCTTTTTCAT 1413
DB GACGAGTCAAGCAATTAAGGCAACAGGCGCGGTCACTCTCTGACGCTTTTTCAT 44
QY CCCAGGCTGAGCAGGAGCTGAGCTGAGGCGCGGCTGCG 1453
DB CCCAGGCTGAGCAGGAGCTGAGCTGAGGCGCGGCTGCG 4

RESULT 2
AA903751 314 bp mRNA linear EST 09-JUN-1998
LOCUS OK64C05.81 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518728 3'
DEFINITION similar to gb:K17360_rnal HOMOBBOX PROTEIN HOX-D4 (HUMAN); mRNA
sequence.
ACCESSION AA903751
VERSION AA903751.1 GI:3038874
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 314)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Brenner-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert Length: 521 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 297.

FEATURES
Source location/Qualifiers
1..314
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1518728"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_id="NCI_CGAP GC4"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bernaldo."

ORIGIN

Query Match 13.3%; Score 303; DB 1; Length 314;
Best Local Similarity 99.7%; Pred. No. 7.5e-33;
Matches 314; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY TTTCTTCT 966
DB TTTCTTCT 60
QY TTCT 1026
DB TTCT 120
QY CTTGACTTCTGTTTCCAGCTGCTTGTGCGAGAACATGCGCTGCTTTTCTTT 1086
DB CTTGACTTCTGTTTCCAGCTGCTTGTGCGAGAACATGCGCTGCTTTTCTTT 180
QY CCGCTATTAATATCAGAGCCCATCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146
DB CCGCTATTAATATCAGAGCCCATCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY CTTCTGCTGTGAAGAACATATGCGCGGCTGACAGGCTGTAAGTGTGTAATATC 1206
DB CTTCTGCTGTGAAGAACATATGCGCGGCTGACAGGCTGTAAGTGTGTAATATC 299
QY AGGAAGATGACTGAA 1221
DB AGGAAGATGACTGAA 314

RESULT 3
B1222607 427 bp mRNA linear EST 11-JUL-2001
LOCUS B1222607 602940387F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5103573 5'
DEFINITION mRNA sequence.
ACCESSION B1222607
VERSION B1222607.1 GI:14676051
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 427)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMW, at:
<http://image.lnl.gov>
Plate: L14M1249 row: n column: 22
High quality sequence stop: 348.
Location/Qualifiers
1..427
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5103573"
/issue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN
Query Match 13.1%; Score 296.4; DB 2; Length 427;
Best Local Similarity 93.0%; Pred. No. 5.8e-32;
Matches 333; Conservative 0; Mismatches 21; Indels 4; Gaps 2;
QY 1785 GGGGGGCTGGGCGCCATATAAGAGAGTGCATTAAAGACAGGCGCCCTGAGCGCTTGT 1844
DB 1 GGGGGGCTGGGCGCCATATAAGAGAGTGCATTAAAGACAGGCGCCCTGAGCGCTTGT 60
QY 1845 TAGAAACCGCTCTGAGTGGAGGCAAGGCTGTGCTGAGCAAGACTTGTTCCTGGC 1904
DB 61 AAGAAACCGCTCTGAGTGGAGGCAAGGCTGTGCTGAGCAAGACTTGTTCCTGGC 120
QY 1905 GGTGAGTCTTGCATCTCACAAGAGTGGCGGCCCGGAGAGTGTGAGGAGAGGCGCG 1964
DB 121 GGTGAGTCTTGCATCTCACAAGAGTGGCGGCCCGGAGAGTGTGAGGAGAGGCGCG 180
QY 1965 GAGTGGCAAGGAGTGCATCTCGGGGAGCAAGAGAGTAAACCGCGTGTGAGGAGCGAC 2024
DB 181 GAGTGGCAAGGAGTGCATCTCGGGGAGCAAGAGAGTAAACCGCGTGTGAGGAGCGAC 240
QY 2025 GAAACCGGAGTGGAGAGTGCATGAGAGAACCTTAGCGGGGCGTCCCG--CGGA 2082
DB 241 GAAACCGGAGTGGAGAGTGCATGAGAGAACCTTAGCGGGGCGTCCCGGAGGAAA 300
QY 2083 AGGCGGCTGCTCCA--GGGTCTCCGCAACCAAGTAGAGTGGAGGCGCCGCGCGC 2138
DB 301 GTGGCGGCTGCTCCAAGTGGGTCTCTGCAACCAAGTAGAGTGGAGGCGCAAGTGGCAC 358

RESULT 4
BX486310 592 bp mRNA linear EST 04-SEP-2003
LOCUS BX486310
DEFINITION DKFZP686B08251_r1 686 (synonym: hlc3) Homo sapiens cDNA clone
ACCESSION BX486310
VERSION BX486310.1 GI:31949871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Ansoerger, W., Krieger, S., Regier, T., Rittmuller, C., Schwager, B.,
Mewes, H. W., Weill, B., Amid, C., Oanger, A., Fodor, G., Han, M. and
Wiemann, S.
TITLE EST (Ansoerger, W., Krieger, S., Regier, T., Rittmuller, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
Sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZP686B08251) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcententrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..592
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686B08251"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlc3)"
/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI;
cDNA collection"

ORIGIN
Query Match 7.1%; Score 161; DB 5; Length 592;
Best Local Similarity 74.8%; Pred. No. 5.2e-13;
Matches 228; Conservative 0; Mismatches 75; Indels 2; Gaps 2;
QY 234 AGGCGAGCACAGTGGCTCACACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGG 293
DB 308 AGGCGAGCGAGGCGGCTTACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGG 249
QY 294 ACTGCTGAGGCGAGGCTTCAAGAGAGCTGAGCAACACAGGAGACCT-GTCACTAC 352
DB 248 ATCACTGAGTCCAGGAGTTCAGACCAAGCTGAGCAACATGAGCACTCATCTTAC 189
QY 353 AAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412
DB 188 AAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 129
QY 413 GGCAGAGTAGAGACTGCTTGTCCAGAGTCAAGACTGACAGTGTGAGAGCCAGCA 472
DB 128 GACTCAGTGTGATCACTTGAAGCCCGGAGAGAGGTTACAGTGTGAGTGTGATCA 69
QY 473 CTGTCATTCAGAGCTGTGGCAACAAAGAGACCTGTCTGAAATTAATTAATTAAT 532
DB 68 -CTGTCATTCAGAGCTGTGGCAACAGATGAGACCTGTCTGAAATTAATTAATTAAT 10
QY 533 AATA 537
DB 9 AATA 5

RESULT 5
BM556801 1033 bp mRNA linear EST 20-FEB-2002
LOCUS BM556801
DEFINITION AGENCOURT_6540722 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737964
ACCESSION BM556801
VERSION BM556801.1 GI:18798321
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1033)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHM12748 row: 0 column: 21
High quality sequence stop: 606.
Location/Qualifiers
1. 1033
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737964"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC library."

ORIGIN

Query Match 7.1%; Score 160.6; DB 3; Length 1033;
Best Local Similarity 77.0%; Pred. No. 5e-13;
Matches 235; Conservative 0; Mismatches 64; Indels 6; Gaps 3;

231 TTGAGGCGAGGACAGTGGCTCAGACCTGTATTCAGTACTGTGAGAGTCCGAGTCAAG 290
Db TTTAGGCGAGGAGTGGTGGCTGGCGCTTATTCAGACCTTTGGAGGCGAGAGTGGG 282
291 AGGACTGCTTGAAGCCAGAGATTCAAGAGCAGCTGTGACACACAGGAGAG-CTGTTCAC 349
Db AGATGAGCTTGAAGTCCAGTGTTCAGAGCCAGCTGGGCAACATAGGAGAGCCTGATC 222
281 AGATGAGCTTGAAGTCCAGTGTTCAGAGCCAGCTGGGCAACATAGGAGAGCCTGATC 222
291 AGGACTGCTTGAAGCCAGAGATTCAAGAGCAGCTGTGACACACAGGAGAG-CTGTTCAC 349
Db TACCAAAATTAATTAATTTAGCCAGGCTTGTGCTATCCCTGTGCTCCAGCTTACTAG 409
350 TACCAAAATTAATTAATTTAGCCAGGCTTGTGCTATCCCTGTGCTCCAGCTTACTAG 409
221 TACCAAAATTAATTTAAATTCCTGTGGGTGTGTGACATACCTGTGCTCCAGCTTACTAG 162
410 GGAAGCGAGAGTATAGA----CTGCTTGTCCAGAGAGGTCAAGATGTGAGTGTGAGAC 465
Db GGAAGCGAGAGCGAGAGATGTGCTTGTGAGCCAGAGAGGTCAAGATGTGAGTGTGAGT 102
161 GGAAGCGAGAGCGAGAGATGTGCTTGTGAGCCAGAGAGGTCAAGATGTGAGTGTGAGT 102
466 CGAGCGCAGCTGTGATTCAGAGCTTGTGGCAACAAAAGAGACCTGTGCTCAAAAATTAAGTTA 525
Db CTGGGCA-CTGGCACTCCAGCTGTGGCAACAGAGCCCTGTCTCAAAAACAAAAAC 43
526 AATA 530
42 AAAAA 38

RESULT 6
LOCUS BC029972
DEFINITION Homo sapiens clusterin (complement lysin inhibitor, SP-40/40,
unlabeled glycoprotein 2, testosterone-repressed prostate message 2,
apolipoprotein J), mRNA (CDNA clone IMAGE:4939961).
ACCESSION BC029972
VERSION BC029972.1 GI:20455818
KEYWORDS HTC.

SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 2821)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Halsh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stepleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Umed, T.B., Tshiyuki, S.,
Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McGwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shvachenko, Y.,
Bouffard, G.G., Rodriguez, A.C., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalske, U., Smalins, D.S.,
Schmeckel, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2821)
NIH MGC Project
Direct Submissions
Submitted (06-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louis, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAK Plate: 42 Row: h Column: 7
this clone has the following problem: no 5' EST match.
Location/Qualifiers
1. 2821
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4939961"
/tissue_type="Brain, anaplastic oligodendroglioma with
1p/19q loss"
/clone_id="NCI CGAP_Brn67"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 7.1%; Score 160.6; DB 4; Length 2821;
Best Local Similarity 71.0%; Pred. No. 3.6e-13;
Matches 255; Conservative 0; Mismatches 99; Indels 5; Gaps 3;

219 TAAAGAAATTTCTTGAAGCGAGGACAGTGGCTCAGACCTGTATTCAGTACTGTGAGA 278
|||||

220 AAGAAATTCTTGAGGCCAGGCACAGTGGCTCACACTGTAAATTCAGTACTGTGAGAG 279

223 AGAATTCTTGAAGCCAGGCAAGTGGCTCACACTGTAAATTCAGTACTGTGAGAGTCC 282

Db	35	ACAAAAACAGGTGGCCAGGTGTGTGGCTCAACCTGTAAATCCGACACCTGTGGAGA3CC	238
Qy	283	GAAGTCAGAGGA-CTGCTTGAAGGCCAGGAATTCAAGAGAGCGCTGGACAACAAGGGAGAC	342
Db	297	ACGGTAGTGGACAGCGCTTGAAGCCCAAGAACTCAAGAACGCTTGGCAACATACCAAAAC	238
Qy	343	CT-GTCACTACAAAGATAAATAATTAGCCAGGCTTAGTGCCTATCCCTGTGGTCCA	401
Db	237	TTGATCTCTACAAAAAATGAAAAAATTAGCTAGGACAAGTGGTGTGATCGCTGTGGTCCA	178
Qy	402	GCTACTAGGGAGGCAGAGTAAGGA-----CTGCTTGTCCCAAGAGGTCAAGA-CTGACGTGA	45
Db	177	GCTACTCTGGAGACTGAGGTTGGAGGATCACTTGAACCAAGAGGTCAAGGCTTCAAGTGA	118
Qy	458	GCTGAGACCCAGCCACCTGATTTCCAGCCTTGGGCAACAAAAAGAGACCCCTGTCTCAAAA	517
Db	117	GCTGTGATCAACAACCC-ACATTGCAAGCTGTGGGTAAACAGATGGAACCTGTGCCAAAAA	59
Qy	518	ATTAAGTTAAATTAATTAATTAATAAATGTTTAACCTTAACCAACA	564
Db	58	AAAAAAAAAAAAAAAAAAAAAAAAATTGAAAAAAAAAAAAAAAAATA	12

RESULT	9
LOCUS	AG014791
DEFINITION	Homo sapiens genomic DNA, 21q region, clone: 76Z01SN19, genomic survey sequence.
ACCESSION	AG014791 AG006506
VERSION	AG014791.1 GI:3650009 GSS.
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1
REFERENCE	Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y. Homo sapiens genomic DNA, chromosome 21q Published Only in Database (1998) 2 (bases 1 to 749) Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y. Direct Submission Submitted (23-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences Center, RIKEN Yokohama Institute, Yokohama Research Promotion Division; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gs.c.riken.jp, Tel:81-45-503-9111, Fax:81-45-503-9113) On Feb 6, 1999 this sequence version replaced gi:2992384. AG006506; Submitted (27-Mar-1998).
AUTHORS	JOURNAL
TITLE	
COMMENT	

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FEATURES
SOURCE
Location/Qualifiers
1..749
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="762015N19"

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	Query Match	Similarity	Score	157.6	DB 10	Length	749
	Best Local	Similarity	71.9%	Pred. No.	1,5e-12		
	Matches	241	Conservative	0	Mismatches	88	Indels 6; Gaps 3,
QY	233	GAGGCCAGGACAGTGGCTCA	CACCTCTTAATTCAGTCTGTGAGATCCGAGGTCA	GAG	292		
Db	246	GAGACCTTGGACACAGTGGCTCATGCTGTAA	TTCCAGGACATTTGGAGAGTCCAGGACGCA		305		
QY	293	GACTGCTTTGAGGCCACGAGATTCA	GAGCAGCCTTGACAACA	CAAGGAGA	-CCTGTCACTA	351	
Db	306	AATGGCTTGAAGGCCACAGAGTTG	AGACACAGCCTTGGAANA	CAATGGCA	AAACCCACCTCTTA	365	
QY	352	CAGAAGATTAATTAATTTAGCCAGGCTT	ATGTGGCTATATCCCTGTGTGCCAGGTACTA	GAGG	411		

Db 366 CAAAAAATTGCAAAATTATGCGAGGATATATGGCATATGCTCTGTAGTCTCAGCTACTGGGG 425

Qy 412 AGCAGAAATGAGACTGCTCTGT ----CCAGAGAGTCAAGACTGCACTGAGTGAAGCC 467

Db 426 AGGCTGAGTGGGAGAGGCTTCTTTAGGCCAGAGAGCCAGGCTGCACTGAGCTGAATCA 485

Qy 468 AGCAGCTTGATTCAGAGCTGGGCAACAAAAAGAGAGCCCTGCTCAAAAAATATAGTTAA 527

Db 486 CGCCA-CTGTACTCCAGGCTGGGTGACAGAGCCAGAGCCCTGTCTTAAAAAAGAAAAAG 544

Qy 528 TAAATTAATTAATTAATTAATAGTTTAAACCTTAACA 562

Db 545 TAAATTAATTAAGCGNTTANNANNCTCAGAGTNTTCCA 579

RESULT 10	LOCUS	DEFINITION
BX504185/c	476 bp	linear
BX504185	476 bp	linear
DKR2p8686G1812_g1	686 (synonym: h1cc3)	Homo sapiens cDNA clone
DKR2p8686G1812_3		mRNA sequence.

SOURCE ORGANISM	Homo sapiens (human) Homo sapiens Bakaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 476)
AUTHORS	Poustka, A., Albert, R., Moosmayer, P., Schnupp, I., Wellenreuther, R., Mewes, H. W., Weill, B., Amid, C., Osaenger, A., Fodor, G., Han, M. and Mleamann, S.
TITLE	EST (Poustka, A., Albert, R., Moosmayer, P., Schnupp, I., Wellenreuther, R., et al.)
JOURNAL	Unpublished (2003)
COMMENT	Contact: MIPS

Ingo Isolaedter Landster, I, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
ri sequence also available.
This clone (DKFZp686G1812) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcententrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES	Source	Location/Qualifiers
1.	.476	
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	/mol_type="mRNA"	
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	/dev_stage="adult"	
	/lab_host="DH10B"	
	/clone_lib="866 (synonym: hlec3)"	
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	ncna-collection"	

ORIGIN		6.9%	Score 157,	DB 5,	Length 476,
	Query Match	Best Local Similarity	69.7%	Pred. No. 2e-12;	
	Matches 242;	Conservative	0;	Mismatches 100;	Indels 5; Gaps 2;
QY	211 AAAAATTTAAGAGAAATTTCTTGAAGCCAGGACAAGTGGCTTCACCTGTAAATTCAGTA	270			
DB	400 AGAAGATTAAGAAATGTCTCCCTTGGGCGGATGGGTGGCTTCAGCCCTGTATCCACACA	341			
QY	271 CTGTGAGAGTCCGAGGCTCAGAGGACGTGGTGAAGCCAGGAATTCGAAGGACGCTGGACA	330			
DB	340 CTTTGGGATTCGAGGTGGCGGATTCATTAGGTCAAGAAATTCAGAGCCAGCCTGGCCA	281			

QY 331 ACACAGGAGACCTGCTACTACAAAGATTAATTAATAGCAGGCTTAGTGGCTCATTCC 390
 DB 280 ACATGATTAACCCCTCTTACTTAACATACAAAGATTAGCTGTGTGGTGGACGGCC 221
 QY 391 CTGTGCTCCAGCTACTAGGAGGAGAGTAGA----CTGCTGTGCTCCAGAGGTCA 446
 DB 220 CTGTATATGACGCCCCCTTGGAAAGGCAAGGAGAGATTCGCTCAACACTGGAGTGA 161
 QY 447 GACTGAGTGAAGCTAGAGCCAGCAGCTGCTTCCAGCTGGGCAACAAAAAGAGACC 506
 DB 160 GATTGACAGTGAAGCTAGATTGGCCA-CTGCACCTCAGCTGGGCAATGAGCAAGACC 102
 QY 507 TGCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 553
 DB 101 TGCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 55
 RESULT 11
 LOCUS AO780044
 DEFINITION HS_3169_A1_B09_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=17 Row=C, genomic survey sequence.
 ACCESSION AO780044
 VERSION AO780044.1 GI:5683004
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 680)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 3169 row: C column: 17
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 680.
 Location/Qualifiers
 1..680
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3169 Col=17 Row=C"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
 ORIGIN
 Query Match 6.9%; Score 157; DB 9; Length 680;
 Best Local Similarity 74.8%; Pred. No. 1.8e-12;
 Matches 237; Conservative 0; Mismatches 75; Indels 5; Gaps 3;
 QY 219 TAAGAGATTTCTTGAAGCCAGGACAGTGGCTCACACTGTAAATTCAGTACTGTAGA 278
 DB 215 TAACAAATAATTAATTTGGGGCCAGGACAGTGGCTCACACTGTAAATTCAGTACTGTAGA 274

QY 279 GTCCAGAGTCAGAGGACTGCTTGAAGCCAGAGTTCAGAGCAGCTGGAACAACAGAGG 338
 DB 275 GCTTGAAGCAAGCAGACACACTTGAAGTTCAGAGATTGAGACTAGCTGGTAACTATGTG 334
 QY 339 AGACC-TGTCACTACAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 397
 DB 335 AAACCTGTCTCTACAAAATAACAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 394
 QY 398 CCCAGCTACTAGGAGAGCAGAAAT---AGACTGCTTTTCCAGAGAGTCAAGACTGCA 454
 DB 395 CCCAGCTACTCCGAGGCTGAGGTGGAGAGATTGCTTGAAGCCACAGCTGAGGAGTTGCA 454
 QY 455 TGAGTGAAGCCAGCCAGCTGCTTCCAGCTGGGCAACAAAAGAGACCCTGCTCA 514
 DB 455 TGAGCCGAGATTGTCTCA-TTGCCCTCCAGCTGGACAACTAAGAGACCTGTCTCA 513
 QY 515 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 531
 DB 514 AAACAAACAAACAAACA 530
 RESULT 12
 LOCUS BC015230
 DEFINITION Homo sapiens chromosome 9 open reading frame 115, mRNA (CDNA clone IMAGE:3899552), containing frame-shift errors.
 ACCESSION BC015230
 VERSION BC015230.1 GI:21955365
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1638)
 Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M.E., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Udell,T.B., Toshtaykly,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Muller,J.S., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Hellon,E., Kettelman,M., Madan,A., Young,A.C., Shcherchenko,Y., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shcherchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Gilmwood,J., Schmutz,J., Myers,R.M., Butcherfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.E., Schermer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1638)
 Director MGC Project.
 Direct Submission
 Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapdb-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.W.A.G.E. Consortium (LINT)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>

REMARK

COMMENT

Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLAST at: <http://image.llnl.gov>
Series: IRAX Plate: 14 Row: 1 Column: 12
This clone has the following problem: frame shifted.
Location/Qualifiers

FEATURES

source

1. 1638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:389552"
/class_type="Pancress", epithelioid carcinoma"
/clone_id="NH MGC_70"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 6.9%; Score 156.8; DB 4; Length 1638;
Best Local Similarity 70.2%; Pred. No. 1.5e-12;
Matches 254; Conservative 0; Mismatches 102; Indels 6; Gaps 3;
QY 208 CTGAAGAGATTAAAGAAATTTCTTGAAGCCAGCAGCACTGCTTAATTCCTCA 267
DB 1230 CTGTAAGATTAAAGATCTGCTTGAAGCCGGGTGCTCACACTTAATTCCTCA 1289
QY 268 GTACTGTGAAGTCCGAGAGTCAAGAGACTGCTTGAAGCCAGGCTTAAGTGTCTC 327
DB 1290 GCACTTGGAGAGCCGAGAGCTGGGGATTGCTTGAAGTCAAGAGTTCAGACCAAGCTCG 1349
QY 328 ACAACACAGAGAGA-CCTGTCACTACAAGATTAATTAATTAATTAATTAATTAATTA 386
DB 1350 CCAACATGATGAACCCCTGTCTCTACTAATAAATTAAGTAAGCAGCATGTGTGTC 1409
QY 387 ATCCCTGTGTCCCACTACTAGAGAGCAGAGATGAGA---CTGCTTGTCCAGAGAG 442
DB 1410 ATGCTCTTAATCCCTGCTACTTGTGAGAGCTGAGCAGAGATCACTGAACCTGGAGAG 1469
QY 443 TCAAGACTGAGTGAAGTGAAGCCAGCAGCTGATTCAGCCCTGGGCAACAAAAGAG 502
DB 1470 CGAAGTGTGCTGAGTGAAGTGTGAGC-CTGACCTCAGTCTGGGTGAAGAAGTAG 1528
QY 503 ACCCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 562
DB 1529 ACTGTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1588
QY 563 CA 564
DB 1589 AA 1590

RESULT 13

AQ088791/c

LOCUS AQ088791 444 bp DNA linear GSS 26-AUG-1998
DEFINITION HS 3002 AI P05 MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.

ACCESSION AQ088791
VERSION AQ088791.1 GI:3457702
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 444)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Sequence Tagged Connector
Plate: 3002 row: K column: 9
Class: BAC ends
High quality sequence stop: 444.
Location/Qualifiers

FEATURES

source

1. 444
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3002 Col=9 Row=K"
/sex="male"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in E-coli DH10B"

ORIGIN

Query Match 6.9%; Score 156.4; DB 9; Length 444;
Best Local Similarity 70.3%; Pred. No. 2.5e-12;
Matches 239; Conservative 0; Mismatches 96; Indels 5; Gaps 2;
QY 233 GAGCCAGGACAGTGTCTCAACCTTAATTCAGTACTGTGAGAGTCCGAGTCAAG 292
DB 359 GGGCCCGGTGAGTGTCTCATGTCTTAATCCAGACCTTGGAGAGCTGAAGCGGGTG 300
QY 293 GACTGCTTGAAGCCAGAGATTCAAGAGCAGCTGAGCAACAGAGAGAGCTGTCACTAC 352
DB 299 GATCTCTGAGCTCAGAGATTCAAGCTAGCTGGCTGAACATGTGTAACCTGTCTTAC 240
QY 353 AAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 412
DB 239 TAAATTAACAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180
QY 413 GGCAGAGTGA---CTGCTGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCA 468
DB 179 GGTGAAGCAGAGAGATCGCTTGAAGCTTGAAGGTGAAGTGAAGAGAGTGAAGTCT 120
QY 469 GCCACCTGATTCAGAGCTGGGCAACAAAAGAGACCTGTCTCAAAAATTAATTAAT 528
DB 119 GCCA-CTGCACTCCAGCTGGGCAACAGCCGACAGATTTTCAAAAAAAAAAATT 61
QY 529 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 568
DB 60 AGATTAATAAATAAAGTTTAAAGAGCTGGAAGAGTCT 21

RESULT 14

AQ313572/c

LOCUS AQ313572 675 bp DNA linear GSS 04-MAY-1999
DEFINITION RPI111-101F17.TV RPI11-11 Homo sapiens genomic clone RPI11-1101F17, genomic survey sequence.

ACCESSION AQ313572
VERSION AQ313572.1 GI:4045035
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 675)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSs: RPI111-101F17.TV

Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (peter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://info@resgen.com>). BAC end search page: http://www.ligr.org/cdb/hungen/bac_end_search/bac_end_search.html
Seq primer: 17
Class: BAC ends.

FEATURES

Location/Qualifiers
1..675
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7538536"
/db_xref="taxon:9606"
/clone="RPCI-11-101F17"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN

Query Match 6.9%; Score 156.4; DB 9; Length 675;
Best Local Similarity 69.6%; Pred. No. 2,2e-12;
Matches 256; Conservative 0; Mismatches 106; Indels 6; Gaps 3;
228 TTCTTGGAGCCAGGACAGTGGCTCAACCTGTAATTCAGTCTGTGAGAGTCCGAGT 287
471 TTGTTCTAGGCTGGCATGCTGGCTCAACCTGTAATTCAGTCTGTGAGAGTCCGAGT 412
288 CAGAGAGCTGCTTGGAGCCAGAGAGTTCAGAGAGCTGAGAGAGAGAGAGAGAGAGT 346
411 AGGTGATTCACCTGAGAGTCAAGAGTTCAGAGAGCTGAGAGAGAGAGAGAGAGAGT 352
347 CACTCAAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 406
351 CTCTACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 292
407 TAGGAGGAG 462
291 TTGGAGAGTCTGAG 232
463 GAGCCAGGACCTGCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
231 GATCGTGCCTGAT 173
523 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 582
172 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 113
583 ACTTCTTA 590
112 CCATATTA 105

RESULT 15

BE349022 444 bp mRNA linear EST 18-JUL-2000
LOCUS ht48a11.x1 NCI CGAP Mel15 Homo sapiens cDNA clone IMAGE:3149948 3'
DEFINITION similar to contains Alu repetitive element; contains element MER35
repetitive element "", mRNA sequence.
ACCESSION BE349022
VERSION BE349022.1 GI:9260875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 444)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL, send email to: info@image.llnl.gov
Seq primer: -40UP from G1bco
High quality sequence stop: 414.
Location/Qualifiers
1..444
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3149948"
/issue_type="malignant melanoma, metastatic to lymph node"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mel15"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

FEATURES

Location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3149948"
/issue_type="malignant melanoma, metastatic to lymph node"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mel15"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

ORIGIN

Query Match 6.9%; Score 155.8; DB 2; Length 444;
Best Local Similarity 74.8%; Pred. No. 3.1e-12;
Matches 237; Conservative 0; Mismatches 72; Indels 8; Gaps 3;
233 GAGGCCAGGACAGTGGCTCAACCTGTAATTCAGTCTGTGAGAGTCCGAGTCAAG 292
107 GGGCCAGGAGAGAGTGGCTCAACCTGTAATTCAGTCTGTGAGAGTCCGAGTCAAG 166
293 GAGCTTGAAGCCAGAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 351
167 GATGCTTGAAGCCAGAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 226
352 CAAGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 411
227 CAAAATTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 286
412 AGGAGAGATGAGA---CTGCTGTCCAGAGAGTCAAGCTGAGTGAAGAGCC 467
287 AGGCTGAGTGGAGAAATTTGTTGGGCCCAAGAAATTAAGAGTGAAGAGCGTGAGC- 345
468 AGGCACTGCACTTCAGAGTGGGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 527
346 --ACGAGTCACTTGAAGTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
528 TAAATTAATTAATTAATAA 544
404 AAAAAAAAAAATGAGA 420

Search completed: December 21, 2005, 23:23:02
Job time : 8092 secs

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Thu Dec 22 05:48:00 2005

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2005, 09:39:26 ; Search time 1254 Seconds
(without alignments)
12064.475 Million cell updates/sec

Title: US-09-869-098A-1_COPY_1_2270
Perfect score: 2270
Sequence: 1 aacgacatcgccgcctccag.....cgccgcgctcgccgacgcg 2270

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001s:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2270	100.0	3505	AAA62932	Aaa62932 DNA cont.
2	846.8	37.3	9314	ADG65405	Adg65405 Human unc
3	485	21.4	736	AAV44874	Aav44874 UCP2 gene
4	485	21.4	736	AAV08879	Aav08879 UCP2 prom
5	447.4	19.7	1161	AAV44599	Aav44599 Human unc
6	364.4	16.0	5283	ABL33892	Ab133892 Human imm
7	312.4	13.8	5283	ABL33893	Ab133893 Human imm
8	188.4	8.3	41150	ADL13819	Adl13819 Osteocarth
9	188.4	8.3	44348	ADN48556	Adn48556 Human Not
10	172.8	7.6	11172	AAS29967	Aas29967 Human lun
11	172.8	7.6	11172	ADB33304	Adb33304 Human nov
12	168.4	7.4	25825	ABA19375	Abal9375 Human ner
13	167.2	7.4	135005	ADQ19501	Adq19501 Human sof
14	166.6	7.3	52242	ADA02666	Ada02666 Human MDM
15	166.6	7.3	52242	ADB72404	Adb72404 Human MDM
16	166.6	7.3	52242	ADE95914	Ade95914 Human MDM
17	164	7.2	186510	ADE24797	Ade24797 Human end
18	162.6	7.2	81099	ACN45018	Acn45018 Human gen
19	162.2	7.1	46275	ABR10145	Abt10145 Human bre

c 20	162.2	7.1	46275	10	ADL13621	Adl13621 Osteocarth
c 21	162	7.1	125910	3	AAC64370	Aac64370 Human KCN
c 22	161.8	7.1	7759	4	AAK77916	Aak77916 Human imm
c 23	161.8	7.1	109906	6	ABK94411	Abk94411 DNA encod
c 24	161.8	7.1	109906	12	ADL08112	Adl08112 Human gen
c 25	161.6	7.1	10899	5	ABA15344	Abal5344 Human ner
c 26	161.6	7.1	12758	5	ABA15345	Abal5345 Human ner
c 27	161.4	7.1	93500	13	ADT77142	Adt77142 Type II d
c 28	161.4	7.1	110000	14	AEA61124	Aea61124 Human SLIC
c 29	161.2	7.1	56737	6	ABS69895	Abs69895 Human hyp
c 30	160.8	7.1	60815	11	ACN43882	Acn43882 Human gen
c 31	160.8	7.1	110000	12	ADN06353_0	Adn06353 Human FLA
c 32	160.8	7.1	110000	13	ADS94372_0	Ads94372 Human 5-1
c 33	160.6	7.1	7739	4	AAL36824	Aal36824 Human mus
c 34	160.6	7.1	7739	8	ABX59812	Abx59812 cDNA enco
c 35	160.6	7.1	7739	12	ADJ30562	Adj30562 Human mus
c 36	160.6	7.1	8133	6	ABN99663	Abn99663 Human clu
c 37	160.6	7.1	20000	14	ADZ70132	Adz70132 Human clu
c 38	160.4	7.1	31749	4	AAK72959	Aak72959 Human can
c 39	160.4	7.1	78925	3	AAc89888	Aac89888 Human FN
c 40	160	7.0	110000	10	ADG70447_0	Adg70447 Human ANG
c 41	160	7.0	110000	10	ABZ79565_0	Abz79565 CLID8 and
c 42	160	7.0	169659	12	ADQ59434	Adq59434 Human can
c 43	160	7.0	187851	14	ADZ13735	Adz13735 Human can
c 44	159.8	7.0	563	14	ACL58953	Ac158953 Human col
c 45	159.8	7.0	30030	11	ACN44714	Acn44714 Human gen

ALIGNMENTS

RESULT 1

AAA62932 ID AAA62932 standard; DNA, 3505 BP.

AC AAA62932;

DT 02-NOV-2000 (first entry)

DE DNA containing human uncoupling protein-2 (UCP-2) promoter region.

KW Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;
hypotension; hyperlipidaemia; anti-pyretic; de.

XX Homo sapiens.

OS WO200039315-A1.

PD 06-JUL-2000.

PF 22-DEC-1999; 99WO-JP007198.

PR 24-DEC-1998; 98JP-00366719.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Toyoda Y, Kobayashi M, Igaki S;

DR WPI; 2000-452407/39.

PT DNA with promoter region containing regulator sequence of uncoupling protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in therapy.

PS Claim 4; Fig 1-6; 43pp; Japanese.

XX This invention relates to DNA comprising a promoter region containing the regulatory sequences of human uncoupling protein-2 (UCP-2). Included in the invention are a recombinant vector containing the DNA sequence, cells transformed by the vector, and a method for screening for compounds or salts that can promote or inhibit the UCP-2 promoter activity using the transformants. The DNA and cells transformed using it can be used to

CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic
CC and anti-pyretic drugs. The present sequence represents DNA containing
XX the UCP-2 promoter sequences

Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 2270; DB 3; Length 3505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 AACGATCTGCGCGCTCAGCCTCCCAAAGTCTGGGATTTGACAGCGTGAAGCCACTCAC 60
Db 1 AACGATCTGCGCGCTCAGCCTCCCAAAGTCTGGGATTTGACAGCGTGAAGCCACTCAC 60
Qy 61 CTGGCTCAAGTTTCAAAATACATTTATCTAGTACCATCATCTTCCAGTTTGTCCAC 120
Db 61 CTGGCTCAAGTTTCAAAATACATTTATCTAGTACCATCATCTTCCAGTTTGTCCAC 120
Qy 121 AGGACATCTTATGACTTGAGCAAGCTGTAAAAATCCAGGGTGCAGCGTTGTATGCT 180
Db 121 AGGACATCTTATGACTTGAGCAAGCTGTAAAAATCCAGGGTGCAGCGTTGTATGCT 180
Qy 181 ATAGGATTTGCTCAATCTGCGCCGACCCCTGAAGAATTTAGAATTTCTTGAGGCGAG 240
Db 181 ATAGGATTTGCTCAATCTGCGCCGACCCCTGAAGAATTTAGAATTTCTTGAGGCGAG 240
Qy 241 GCACAGTGGCTCACAACCTGTAAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGCT 300
Db 241 GCACAGTGGCTCACAACCTGTAAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGCT 300
Qy 301 GAGGCGAGAGTTCAAGAGCAGCTGACAAACAAGGAGACCTGTCTACAAAGATA 360
Db 301 GAGGCGAGAGTTCAAGAGCAGCTGACAAACAAGGAGACCTGTCTACAAAGATA 360
Qy 361 AATAAATTAAGCAGGCTTATGAGCTCAATCCCTGTGCTCCAGTACTAGAGGAGGAGAG 420
Db 361 AATAAATTAAGCAGGCTTATGAGCTCAATCCCTGTGCTCCAGTACTAGAGGAGGAGAG 420
Qy 421 TAGGACTGCTTGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGCAAT 480
Db 421 TAGGACTGCTTGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGCAAT 480
Qy 481 CCAGCTTGGGCAAAAAAGAGCCCTGTCTCAAAAAATTAATTAATTAATTAATTA 540
Db 481 CCAGCTTGGGCAAAAAAGAGCCCTGTCTCAAAAAATTAATTAATTAATTAATTA 540
Qy 541 AAAATAGTTAAACCTTAAACACATCTTTCTTTCAAGAGGACTTCTTAAGACTTCAT 600
Db 541 AAAATAGTTAAACCTTAAACACATCTTTCTTTCAAGAGGACTTCTTAAGACTTCAT 600
Qy 601 GCTGCGTCTGTGATCTCACTTCCCTTTTTCAGCGTCCACACTTTTAAAGACTCTTT 660
Db 601 GCTGCGTCTGTGATCTCACTTCCCTTTTTCAGCGTCCACACTTTTAAAGACTCTTT 660
Qy 661 TGCAGAGATTAATAATATATAGTTTCTGAATCCAGATCTTCCCTGTGGAACAGCA 720
Db 661 TGCAGAGATTAATAATATATAGTTTCTGAATCCAGATCTTCCCTGTGGAACAGCA 720
Qy 721 GGGGGAACAATTTTGTGTGAGAGGCTTGAATCTGTCTGCTGCTGCTGCAATCTCA 780
Db 721 GGGGGAACAATTTTGTGTGAGAGGCTTGAATCTGTCTGCTGCTGCAATCTCA 780
Qy 781 CAGCAAAATTTGCGAGCTCTCCGGAATGCAACGCGAGACAGACTCAGCCCAAAAGTA 840
Db 781 CAGCAAAATTTGCGAGCTCTCCGGAATGCAACGCGAGACAGACTCAGCCCAAAAGTA 840
Qy 841 GAGAACTGCGAGAGGAGACTCAGAGTGCACAAAAAACTTTATCTTTCTTTT 900
Db 841 GAGAACTGCGAGAGGAGACTCAGAGTGCACAAAAAACTTTATCTTTCTTTT 900
Qy 901 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 960
Db 901 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 960
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Qy 961 CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1020
Db 961 CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1020
Qy 1021 AATCTGCTTGAATCTGTGTTTCCAGCTGCTGTTTCTGCGAGAGACATGCGCTCGCTTT 1080
Db 1021 AATCTGCTTGAATCTGTGTTTCCAGCTGCTGTTTCTGCGAGAGACATGCGCTCGCTTT 1080
Qy 1081 TTTCTTCCGCTAATTAATATCCAGGACCATCCAGCTCTGCTGCTCCCTCAGCTTTCCCTGG 1140
Db 1081 TTTCTTCCGCTAATTAATATCCAGGACCATCCAGCTCTGCTGCTCCCTCAGCTTTCCCTGG 1140
Qy 1141 CAGTCCCTTCTGCTGTGAAACAATATGCGCGCGCTGACAGAGGTGAATGTGTG 1200
Db 1141 CAGTCCCTTCTGCTGTGAAACAATATGCGCGCGCTGACAGAGGTGAATGTGTG 1200
Qy 1201 AATATCAGAAATGACTGAACGTTCTTGGGACTCGGTTTCTCTATTGTAATATGAGGT 1260
Db 1201 AATATCAGAAATGACTGAACGTTCTTGGGACTCGGTTTCTCTATTGTAATATGAGGT 1260
Qy 1261 TAATACAGGCTTCTTCTACTCCGCAAGCAGTGTGTTGCTCCGCGCAGAGGCGCCAT 1320
Db 1261 TAATACAGGCTTCTTCTACTCCGCAAGCAGTGTGTTGCTCCGCGCAGAGGCGCCAT 1320
Qy 1321 TGTGCTGTTCAAGCATCAGTTAACCCCAAGAGACGAGTCAAGCAATTAAGCGCAACC 1380
Db 1321 TGTGCTGTTCAAGCATCAGTTAACCCCAAGAGACGAGTCAAGCAATTAAGCGCAACC 1380
Qy 1381 AGGCGCGCTCAATCTCTGACGCTTTTCTCATCTCCAGGCTGAGACAGGCTGCGCTG 1440
Db 1381 AGGCGCGCTCAATCTCTGACGCTTTTCTCATCTCCAGGCTGAGACAGGCTGCGCTG 1440
Qy 1441 GGCCCGGCTCTGCTTGTCAAGTACGCGGAGGCGGAGCGGCTTGTGCTGTGTATGAGAG 1500
Db 1441 GGCCCGGCTCTGCTTGTCAAGTACGCGGAGGCGGAGCGGCTTGTGCTGTGTATGAGAG 1500
Qy 1501 CGTAGAGTCAAGCTGAGTGTCTCCGCGCGCGGAGCTTTAGTGTCTTGTCTCTTAA 1560
Db 1501 CGTAGAGTCAAGCTGAGTGTCTCCGCGCGCGGAGCTTTAGTGTCTTGTCTCTTAA 1560
Qy 1561 CGCAGGCGCTCTCAACGCGGAGAGAAAGGCGGAAACCCAGCCAGCCAAAGCTGTGT 1620
Db 1561 CGCAGGCGCTCTCAACGCGGAGAGAAAGGCGGAAACCCAGCCAGCCAAAGCTGTGT 1620
Qy 1621 CGGTTGCGGAGCACTGTGCTGCAAGTTCTGATTTGCTTCCCGCAAGCGGAG 1680
Db 1621 CGGTTGCGGAGCACTGTGCTGCAAGTTCTGATTTGCTTCCCGCAAGCGGAG 1680
Qy 1681 GCTGTAAACAATGACAGCGAGGCGGCTCGAGAGCCCGAGTCCCGCTGAGAGAGCA 1740
Db 1681 GCTGTAAACAATGACAGCGAGGCGGCTCGAGAGCCCGAGTCCCGCTGAGAGAGCA 1740
Qy 1741 GCGCGCGCTGCTCGAGAGAGGAGGTGTTGTTGCCAGCGTAAAGGAGGCTGAGCCAT 1800
Db 1741 GCGCGCGCTGCTCGAGAGAGGAGGTGTTGTTGCCAGCGTAAAGGAGGCTGAGCCAT 1800
Qy 1801 AAAAGAGAAAGTGCATTAAGACACGAGCCCGCTGAGCGCTGTTAGAAAACGCTGTGGC 1860
Db 1801 AAAAGAGAAAGTGCATTAAGACACGAGCCCGCTGAGCGCTGTTAGAAAACGCTGTGGC 1860
Qy 1861 TGGAGAGCAAGAGTGTGACTGACAAAGACTTGTCTTGGCGGTCACTTTGCCATC 1920
Db 1861 TGGAGAGCAAGAGTGTGACTGACAAAGACTTGTCTTGGCGGTCACTTTGCCATC 1920
Qy 1921 CTCAAGAGGTTGGCGGCGCCGAGAGAGTGTGAGGCAAGGCGGAGATGTGCAGAGGAGTG 1980
Db 1921 CTCAAGAGGTTGGCGGCGCCGAGAGAGTGTGAGGCAAGGCGGAGATGTGCAGAGGAGTG 1980
Qy 1981 ACCATCTCGGAGAAAGAAAGATTAACGCGAGTGTGAGGCAAGGAGAGGAGAG 2040
Db 1981 ACCATCTCGGAGAAAGAAAGATTAACGCGAGTGTGAGGCAAGGAGAGGAGAG 2040
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Oy 2041 AAGTCATGAGAGAACCTTAGGCGGGCGGTCCTCCAGAGGT 2100
    |||
Db 2041 AAAGTCATGAGAGAACCTTAGGCGGGCGGTCCTCCAGAGGT 2100
    |||
Oy 2101 CTCGCGACCAAGTAGAGTGGCAGAGCCCGCCCGCCGACAGCCCAACCCCGAGCC 2160
    |||
Db 2101 CTCGCGACCAAGTAGAGTGGCAGAGCCCGCCCGCCGACAGCCCAACCCCGAGCC 2160
    |||
Oy 2161 CCGCGCCCGGAGGCTTAAGCCGCGCCGCTCGCGGAGGCCCACTGCGAAGCCAGCT 2220
    |||
Db 2161 CCGCGCCCGGAGGCTTAAGCCGCGCCGCTCGCGGAGGCCCACTGCGAAGCCAGCT 2220
    |||
Oy 2221 GCGCGCGGCTTGAGATGACTGTCCAGCGTCCGCGCTGTCGAGCGG 2270
    |||
Db 2221 GCGCGCGGCTTGAGATGACTGTCCAGCGTCCGCGCTGTCGAGCGG 2270
    |||

RESULT 2
ADG65405
ID ADG65405 standard; DNA; 9314 BP.
XX AC ADG65405;
XX DT 11-MAR-2004 (first entry)
XX DE Human uncoupling protein 2 (UCP2) gene.
XX KW anorectic; antidiabetic; immunomodulator; gene therapy; haplotyping;
KW uncoupling protein 2; mitochondrial; proton carrier; UCP2;
KW polymorphic site; haplotype; haplotype pair; obesity; diabetes;
KW immunological disorder; body mass defect; thermoregulation defect; human;
KW gene; ds; SNP; single nucleotide polymorphism.
XX OS Homo sapiens.
XX FH Key
FH FT Location/Qualifiers
FT FT 1283
FT FT /tag= a
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 1714
FT FT /tag= b
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 2051
FT FT /tag= c
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 2124
FT FT /tag= d
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 2287
FT FT /tag= e
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 2408
FT FT /tag= f
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 4768
FT FT /tag= g
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 4785
FT FT /tag= h
FT FT /standard_name= "Single nucleotide polymorphism"
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FT FT /tag= i
FT FT /standard_name= "Single nucleotide polymorphism"
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FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 4976
FT FT /tag= k
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 5281.8649
FT FT /tag= m
FT FT /product= "Uncoupling protein 2"
FT FT 5281.5406
FT FT exon

FT FT /tag= l
FT FT /number= 1
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FT FT /tag= o
FT FT /number= 2
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FT FT /tag= q
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FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 7019.7984
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FT FT 7086
FT FT /tag= ac
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FT FT 7985.8165
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FT FT /tag= af
FT FT /number= 5
FT FT 8221
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FT FT 8535.8649
FT FT /tag= ah
FT FT /number= 6
FT FT 8677
FT FT /tag= ai
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT exon
FT FT US2003207284-A1.
FT FT 06-NOV-2003.
FT FT exon
```

PF 16-JUL-2002; 200205-00197019.
 XX 25-JAN-2001; 2001WO-US002485.
 XX
 PA (CHEW/) CHEW A.
 PA (DENT/) DENTON R. R.
 PA (GILS/) GILSON C. R.
 PA (NAND/) NANDABALAN K.
 PA (PARK/) PARKS K. E.
 PI Chew A, Denton RR, Gilson CR, Nandabalan K, Parke KE.
 XX
 DR WPI; 2004-051505/05.
 DR P-PSDB; ADG65407.
 XX
 PT Haployping Uncoupling Protein 2 gene of an individual comprises
 PT identifying the phased sequence of nucleotides at polymorphic sites of
 PT the gene and assigning a haplotype or haplotype pair consistent with the
 PT phased sequence.
 XX
 PS Claim 1; SEQ ID NO 1; 64bp; English.

CC The invention describes haployping the uncoupling protein 2
 CC (mitochondrial, proton carrier) (UCP2) gene of an individual comprising
 CC identifying the phased sequence of nucleotides at polymorphic sites (PS) 1
 CC -23 for at least one copy of the individual's UCP2 gene and assigning to
 CC the individual a UCP2 haplotype or haplotype pair that is consistent with
 CC the phased sequence. The composition and methods are useful in
 CC haployping and/or genotyping the UCP2 gene in an individual to e.g.
 CC screen for drugs targeting the UCP2 protein to treat a condition or
 CC disease predicted to be associated with UCP2 activity. The disease or
 CC condition may include obesity, diabetes, immunological disorders and
 CC other diseases associated with defects in body mass and thermoregulation.
 CC This sequence represents the human uncoupling protein 2 (UCP2) gene.
 XX
 SQ Sequence 9314 BP; 1904 A; 2619 C; 2371 G; 2397 T; 0 U; 23 Other;

Query Match 37.3%; Score 846.8; DB 12; Length 9314;
 Best Local Similarity 98.9%; Pred. No. 7.5e-156;
 Matches 874; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 1387 GGTTCATCTCTGAGAGGCTTTCTCATCCGAGGCTGAGACAGGAGCTGGGCGCG 1446
 DB 1 GGTTCATCTCTGAGAGGCTTTCTCATCCGAGGCTGAGACAGGAGCTGGGCGCG 60
 QY 1447 GCTCTGCTTGTCACTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1506
 DB 61 GCTCTGCTTGTCACTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
 QY 1507 GTCAAGCTGAGTGTCTCCGCGCCGCGGAGCTTTAGTGTCTGTCCTTAAACGCCAG 1566
 DB 121 GTCAAGCTGAGTGTCTCCGCGCCGCGGAGCTTTAGTGTCTGTCCTTAAACGCCAG 180
 QY 1567 GCGCGCTCCACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1626
 DB 181 GCGCGCTCCACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 QY 1627 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1686
 DB 241 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 QY 1687 ACCAATGACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1746
 DB 301 ACCAATGACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 1747 GCGTCCGCTCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1806
 DB 361 GCGTCCGCTCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 419
 QY 1807 GGAAGTGCATTAAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1866
 DB 420 GGAAGTGCATTAAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477

QY 1867 GGCAGAGAGTGTGTGACTGAGCAAGACTTGTCTGCGCGGTAGCTTGCATCTCACA 1926
 DB 478 GGCAGAGAGTGTGTGACTGAGCAAGACTTGTCTGCGCGGTAGCTTGCATCTCACA 537
 QY 1927 GAGGTGAGCGGCGCCGAGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1986
 DB 538 GAGGTGAGCGGCGCCGAGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597
 QY 1987 TCGGAGGAGCAAGAGAGTAAACGCGGTGATGGACGACAGGAAACGAGGAGTGAAGAAAGTC 2046
 DB 598 TCGGAGGAGCAAGAGAGTAAACGCGGTGATGGACGACAGGAAACGAGGAGTGAAGAAAGTC 657
 QY 2047 ATGAGAGAAACCTTAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2106
 DB 658 ATGAGAGAAACCTTAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 717
 QY 2107 ACCCAATAGAGCTGAGACG 2166
 DB 718 ACCCAATAGAGCTGAGACG 777
 QY 2167 CCGAGGCTTAAGCG 2226
 DB 778 CCGAGGCTTAAGCG 837
 QY 2227 GCTTGGAGATTGACTGTGCACGCTCGCGCGGCTGTCTCGACGCG 2270
 DB 838 GCTTGGAGATTGACTGTGCACGCTCGCGCGGCTGTCTCGACGCG 881

RESULT 3
 AAV4974
 ID AAV4974 standard; cDNA; 736 BP.
 XX
 AC AAV4974;
 XX

DT 16-NOV-1998 (first entry)
 XX
 XX UCP2 gene transcriptional promoter sequence.

XX Uncoupling protein 2; UCP2 gene; transcriptional promoter; mouse;
 KM mitochondrial protein; cis transcriptional regulatory activity; therapy;
 KM expression modulator screening; fat feeding; diabetes; obesity; de.

OS Mus sp.

PN US5807740-A.

XX 15-SEP-1998.

XX 25-APR-1997; 97US-00846012.

XX 25-APR-1997; 97US-00846012.

XX (TTLA-) TULARIK INC.

XX Chen J, Amaral MC;

XX WPI; 1998-520130/44.

PT Mouse UCP2 gene promoter - useful for forming transfected cell lines
 PT employed in drug screening assays.

PS Claim 1; Col 7-8; 9p; English.

XX This sequence represents the mouse mitochondrial uncoupling protein 2

XX (UCP2) gene transcriptional promoter of the invention. The promoter has

XX cis transcriptional regulatory activity. Cells containing the promoter

XX attached to a non-UCP2 gene, in which the non-UCP2 gene is a reporter

XX gene can be used in screening assays for modulators of UCP2 gene
 XX expression, which may be useful for treating disorders in which the UCP2
 XX gene is upregulated in response to fat feeding, e.g. diabetes and obesity
 SQ Sequence 736 BP; 119 A; 236 C; 235 G; 146 T; 0 U; 0 Other;

Query Match 21.4%; Score 485; DB 2; Length 736;
Best Local Similarity 99.6%; Pred. No. 2.8e-85;
Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1762 GGGTGGGTAAGTTTCCAGCGTGAAGGGGGCTGGGCCATTAAGAGAGAGTGCATTAAAG 1821
1 GGGTGGGTAAGTTTCCAGCGTGAAGGGGGCTGGGCCATTAAGAGAGAGTGCATTAAAG 60

1822 ACAGGGCCCCCTGAGCGCTTGTGAAACCGTCTGGCTGGAGAGGCAAGAGTGTGTG 1881
61 ACAGGGCCCCCTGAGCGCTTGTGAAACCGTCTGGCTGGAGAGGCAAGAGTGTGTG 119

1882 ACTGGACAAGACTTGTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 1941
120 ACTGGACAAGACTTGTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 179

1942 AGAGAGTGTGAGGAGGAGGCGGAGTGGCAAGAGAGTGCATCTCCGAGAGCAAGAGA 2001
180 AGAGAGTGTGAGGAGGAGGCGGAGTGGCAAGAGAGTGCATCTCCGAGAGCAAGAGA 239

2002 GTAAACGCGGTGATGGACGCAACGGAACGCGAGTGAAGAAAGTCATGAGAGAACCTTA 2061
240 GTAAACGCGGTGATGGACGCAACGGAACGCGAGTGAAGAAAGTCATGAGAGAACCTTA 299

2062 GGGCGGGGGGTCCCGCGGAAAGGGGCTGCTCCAGGGGTCTCCGACCCAGTAGAGACT 2121
300 GGGCGGGGGGTCCCGCGGAAAGGGGCTGCTCCAGGGGTCTCCGACCCAGTAGAGAG-T 358

2122 GGCAGGCCCCCGGCCCCCGGAGGCCCCACCCCGGGCCCCCGCCCGAGGCTTAAAGCG 2181
359 GGCAGGCCCCCGGCCCCCGGAGGCCCCACCCCGGGCCCCCGCCCGAGGCTTAAAGCG 418

2182 CGCGCGCGCTGCGCGGAGGCCCACTGCGAAGCCCAAGCTGGCGCGCTTGGATTGACT 2241
419 CGCGCGCGCTGCGCGGAGGCCCACTGCGAAGCCCAAGCTGGCGCGCTTGGATTGACT 478

2242 GTCCACGCTCGCGCGGCTGCTCCGACGCG 2270
479 GTCCACGCTCGCGCGGCTGCTCCGACGCG 507

RESULT 4
AAV08879 standard; cDNA; 736 BP.

AAV08879;
20-MAR-2003 (revised)
25-FEB-1999 (first entry)

UCP2 promoter.
UCP2; promoter; transcription factor; modulator; diabetes; obesity;
therapy; ds.

Homo sapiens.
US5849514-A.
15-DEC-1998.
19-JUN-1998; 98US-00100297.
25-APR-1997; 97US-00846012.
(TULAR-) TULARIK INC.
Chen J, Amaral MC;
WPI; 1999-069722/06.
Screening assay for modulators of UCP2 gene expression - based on

Interaction of transcription factor and defined UCP2 promoter sequence.
Claim 1; Col 7-8; 9pp; English.

This sequence represents the UCP2 promoter, and is used in the method of the invention. The method is a screening assay for agents that modulate the effect of a transcription factor on a UCP2 promoter comprises combining the promoter and transcription factor in the presence and absence of a candidate agent and determining any change in the effect of the transcription factor on the promoter. The promoter comprises at least 50 nucleotides of a sequence comprising nucleotides 1-460 of the UCP2 promoter. The method is used to identify agents that modulate UCP2 gene transcription (agents that upregulate UCP2 are potentially useful for treating diabetes and obesity). (Updated on 20-MAR-2003 to correct PF field.)

Sequence 736 BP; 119 A; 236 C; 235 G; 146 T; 0 U; 0 Other;

Query Match 21.4%; Score 485; DB 2; Length 736;
Best Local Similarity 99.6%; Pred. No. 2.8e-85;
Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1762 GGGTGGGTAAGTTTCCAGCGTGAAGGGGGCTGGGCCATTAAGAGAGTGCATTAAAG 1821
1 GGGTGGGTAAGTTTCCAGCGTGAAGGGGGCTGGGCCATTAAGAGAGTGCATTAAAG 60

1822 ACAGGGCCCCCTGAGCGCTTGTGAAACCGTCTGGCTGGAGAGGCAAGAGTGTGTG 1881
61 ACAGGGCCCCCTGAGCGCTTGTGAAACCGTCTGGCTGGAGAGGCAAGAGTGTGTG 119

1882 ACTGGACAAGACTTGTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 1941
120 ACTGGACAAGACTTGTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 179

1942 AGAGAGTGTGAGGAGGAGGCGGAGTGGCAAGAGAGTGCATCTCCGAGAGCAAGAGA 2001
180 AGAGAGTGTGAGGAGGAGGCGGAGTGGCAAGAGAGTGCATCTCCGAGAGCAAGAGA 239

2002 GTAAACGCGGTGATGGACGCAACGGAACGCGAGTGAAGAAAGTCATGAGAGAACCTTA 2061
240 GTAAACGCGGTGATGGACGCAACGGAACGCGAGTGAAGAAAGTCATGAGAGAACCTTA 299

2062 GGGCGGGGGGTCCCGCGGAAAGGGGCTGCTCCAGGGGTCTCCGACCCAGTAGAGACT 2121
300 GGGCGGGGGGTCCCGCGGAAAGGGGCTGCTCCAGGGGTCTCCGACCCAGTAGAGAG-T 358

2122 GGCAGGCCCCCGGCCCCCGGAGGCCCCACCCCGGGCCCCCGCCCGAGGCTTAAAGCG 2181
359 GGCAGGCCCCCGGCCCCCGGAGGCCCCACCCCGGGCCCCCGCCCGAGGCTTAAAGCG 418

2182 CGCGCGCGCTGCGCGGAGGCCCACTGCGAAGCCCAAGCTGGCGCGCTTGGATTGACT 2241
419 CGCGCGCGCTGCGCGGAGGCCCACTGCGAAGCCCAAGCTGGCGCGCTTGGATTGACT 478

2242 GTCCACGCTCGCGCGGCTGCTCCGACGCG 2270
479 GTCCACGCTCGCGCGGCTGCTCCGACGCG 507

RESULT 5
AAV44599 standard; DNA; 1161 BP.

AAV44599;
24-NOV-1998 (first entry)

Human uncoupling protein-2 UCP2 gene clone hUCP2-g2 sequence 2.
Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
obesity; hyperinulinaemia; glucose intolerance; diabetes; syndrome X;
hypothermia; wasting; cachexia; anorexia; inflammation; fever;
hyperthermia; gene therapy; diagnosis; ds.

XX Homo sapiens.
OS
XX MO831396-A1.
XX
XX 23-JUL-1998.
XX
XX 22-APR-1997; 97WO-US006864.
XX
XX 15-JAN-1997; 97US-0034960P.
XX
XX (UYDU-) UNIV DUKE.
XX (REGC) UNIV CALIFORNIA.
XX (CMRS) CENT NAT RECH SCI.
XX
XX Surwit RS, Collins SA, Warden CH, Seidin MF, Riquier D;
PI Boulland F;
XX WPI; 1998-413823/35.
XX
XX Method for treating disease associated with altered UCP-2 expression - by
PT administering agent which enhances or inhibits UCP-2 activity,
PT effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
PT etc.
XX
XX Example II; Fig 10b; 98pp; English.
XX
XX This is the nucleotide sequence of a region (sequence 1) of the human
XX uncoupling protein-2 (UCP2) gene present in genomic clone hUCP2-g2 (I-
XX 1867). 4 Regions (see V44598-601) of hUCP2-g2 are provided. The hUCP2-g2
XX clone was isolated from a human placenta genomic DNA library constructed
XX in lambda EMB3 phage using a partial genomic fragment as probe. Sequence
XX 2 corresponds to DNA from positions bp -511 to +650 and includes the
XX putative proximal human UCP2 promoter. The UCP2 gene maps to a
XX chromosome 1 region (11q13) linked to obesity and hyperinsulinaemia. The
XX invention provides methods for the treatment of disorders associated with
XX diminished or elevated UCP2 expression or activity. An agent which
XX enhances UCP2 expression (e.g. an expression construct comprising a UCP2
XX encoding sequence) can be used to treat obesity, diabetes, syndrome X,
XX hyperthermia, hyperinsulinaemia, or glucose intolerance. An inhibitor of
XX UCP2 (e.g. an antisense construct) is used to treat wasting, anorexia,
XX inflammation, cachexia, fever or hyperthermia (all claimed). The
XX invention also relates to diagnostic and drug screening methodologies
XX
XX Sequence 1161 BP; 209 A; 346 C; 323 G; 234 T; 0 U; 49 Other;
SQ
Query Match 19.7%; Score 447.4; DB 2; Length 1161;
Best Local Similarity 94.9%; Pred. No. 76-78;
Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;
QY 1733 AGGAGCCAGCCGCGCTCGCTCGCAGAGGAGTGGTGTAGTTGCCAGCGT--AGGGGGG 1790
DB 2 ANGAACCAACCGCGGCTTCGTCGAGAGGTGTGTTAGTTGCTCCAGGGGTAAAGGGGG 61
QY 1791 CTGGGCCCATAAAGAGAGAGTGC-ACCTTAAGACACGGCCCGCTGACGGCTTGTAA 1849
DB 62 CTGGGCCCATAAAGAGAGAGTGCACCTTAAGACACGGCCCGCTGACGGCTTGTAA 121
QY 1850 ACCGTCCT-GGCTGGAGAGGCAAGAGGTGTGATGACAGAACTTGTCTTCT-GGCGGT 1907
DB 122 ACCTTCCTGGGTGGAGAGGCAAGAGGTGTGATGACAGAACTTGTCTTCTGGCGGT 181
QY 1908 CAGTCTTCATCTCCACAGAGTGTGGCGCCCGAGAGAGTGTGAGCAGAGCGGGAG 1967
DB 182 CAGTCTTCATCTCCACAGAGTGTGGCGCCCGAGAGAGTGTGAGCAGAGCGGGAG 241
QY 1968 TGGCAAGGAGTACCATCTCGGGAGCAAGAGAGTAAACCGGTGATGGAGCGACGG- 2026
DB 242 TGGCAAGGAGTACCATCTCGGGAGCAAGAGAGTAAACCGGTGATGGAGCGACGA 301
QY 2027 AAAAGGAGTGAAGAAATTCATGAGAGAACCTTAGCGGGCGGTCCCGCGAGAAAGC 2086
DB 302 AAAAGGAGTGAAGAAATTCATGAGAGAACCTTAGCGGGCGGTCCCGCGAGAAAGC 361

QY 2087 GAGTGTCCAGAGGTCTCCGACCCAAAGTAGAGCTGACAGCCCGCCCGCCGAGAG 2146
DB 362 GAGTGTCCAGAGGTCTCCGACCCAAAGTAGAGCTGACAGCCCGCCCGCCGAGAG 421
QY 2147 CCCCACCCCGGGCCCGCCCGCCCGAGAGCTTAAAGCGCGCGCGCTTGGCGAGAGCCAC 2206
DB 422 CCCCACCCCGGGCCCGCCCGCCCGAGAGCTTAAAGCGCGCGCGCTTGGCGAGAGCCAC 481
QY 2207 TGGCAAGCAGAGTGTGCGCGCGCGCTTGGAGATTGACTGTCAGAGCTCGCCGAGCTGTCGA 2266
DB 482 TGGCAAGCAGAGTGTGCGCGCGCGCTTGGAGATTGACTGTCAGAGCTCGCCGAGCTGTCGA 541
QY 2267 CGCG 2270
DB 542 CGCG 545
RESULT 6
ABL3892
ID ABL3892 standard; DNA; 5283 BP.
XX
XX ABL3892;
AC
XX 26-MAR-2002 (first entry)
XX
XX Human immune system associated gene SBQ ID NO: 1865.
DB
XX Human; immune system disease; cytosine methylation; antiaesthetic;
XX antiarteriosclerotic; antianemic; cytosolic; noctropic;
XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX antineuritic; antiaortic; antidiabetic; antipsoriatic;
XX antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
XX ds.
XX
XX Homo sapiens.
OS
XX MO20020928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP007537.
XX
XX 30-JUN-2000; 2000DB-01032529.
XX
XX 01-SEP-2000; 2000DB-01043826.
XX
XX (EPIDG-) BPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2002-130909/17.
XX
XX Claim 1; SEQ ID NO 1865; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention
SQ
Query Match 16.0%; Score 364.2; DB 6; Length 5283;
Best Local Similarity 77.4%; Pred. No. 1.8e-61;

Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

QY 1668 CGAAGAGCGCGCGCTGTAAACCAATCCAGACGAGCGCGGTGCGAGGCCCGCCAGTCCCGC 1727

DB 2 CGAATACCGCGCGCTGTAAATTAATCAATACGAGGTGCGAGCGGTGTTAGTTTGT 61

QY 1728 CCTGACGAGAGCGCGCGCTGCTGCTGAGAGAGGTGAGTTTCCAGCGGTAGG 1787

DB 62 TTTGTAGAGAGTTAGTCGCGCTTCTGTAAGAGGTGAGTTTGTAGCGTA-GG 120

QY 1788 GAGGCTGCGCATTAAGAGAGAGTCACTTAAGACAGCGCCCGCTGAGCGCTTGTAG 1847

DB 121 GGGTTGGGTTATTAAGAGAGAGTATTAAGTACGTTAG--TGACGTTGTAG 178

QY 1848 AAACCTCTCTGCGTGGAGAGCAAGGTGTGTACTGTGACAAAGCTTGTTCGCGCT 1907

DB 179 AAATCGTTTGGTGGAGAGTAAAGGTGTGTGTGATTAAGATTTGTTTGGCGCT 238

QY 1908 CAGTCTTGCATCTCAAGAGAGTGGCGCGCGAGAGTGTGAGCAGAGCGCGGAG 1967

DB 239 TAGTTTGTATTTTATTAAGAGTTGGCGCTTCAAGAGTGTGAGTAAAGCGCGGAG 298

QY 1968 TGGCAAGGAGTGAACCATCTCGGAGAGCAAGAGTAAACCGGTGATGAGACGACGGA 2027

DB 299 TGTAAAGGAGTGAATTTTCGGGGAAGCAAGAGTAAACCGGTGATGAGACGGA 358

QY 2028 AACGGAGTGAAGAAATCATAGAGAAACCTTACGCGCGCGTCCCGCGAAAGCG 2087

DB 359 AACGGAGTGAAGAAATCATAGAGAAATTTTACGCGCGCGTCCCGCGAAAGCG 418

QY 2088 GCTGCTCCAGAGGTCCGACCCCAAGTAGAGTGGAGCGCGCGCGCGCGCGCGCAAGC 2147

DB 419 GTTGTTTAGAGTTTCTGATTTTAAGTAGAGTTGTAGTTTGTTCGTTTGTAGGT 478

QY 2148 CCCACCCCGCGCGCGCGCGAGGCTTAAGCGCGCGCGCGCTGCGCGAGCCCACT 2207

DB 479 TTTATTTTGGGTTTCTGTTTGAAGTTAAGTCGCTGCTTGGCGGAGTTTATTT 538

QY 2208 GCGAAGCCAGCTGCGCGCGCTTGGAGTTGATCTGCAAGCTGCGCGCGCTGCTGAG 2267

DB 539 GCGAAGTTAGTTGCGCGCGCTTGGAGTTGATCTTACGTTGCTGCTGCTGAGC 598

QY 2268 GCG 2270

DB 599 GCG 601

RESULT 7
ABL3893/c
ID ABL3893 standard; DNA; 5283 BP.

XX ABL3893;
AC
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1866.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiasthmatic; antiasthmatic; antiasthmatic; antiasthmatic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antirheumatic; antidiabetic; antipsoriatic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW de.
XX
XX Homo sapiens.
OS
XX WO200200928-A2.
XX
XX 03-JAN-2002.
PD
XX 02-JUL-2001; 2001WO-EP007537.
PF

XX 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
XX (EPID-) EPIDEMIOLOGY AG.
XX
XX Olek A, Piepenbrock C, Berlin K,
DR WPI, 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
XX Claim 1; SEQ ID NO 1866; 32pp + Sequence listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 5283 BP; 1342 A; 136 C; 1475 G; 2330 T; 0 U; 0 Other;
Query Match 13.8%; Score 312.4; DB 6; Length 5283;
Best Local Similarity 72.0%; Pred. No. 2.5e-51;
Matches 435; Conservative 0; Mismatches 166; Indels 3; Gaps 2;

QY 1667 CCGAAGAGCGCGCGCTGTAAACCAATCCAGACGAGCGCGTCCGAGGCCCGCACTCCG 1726

DB 5283 CCGAAGAGCGCGCGCTGTAAACCAATCCAGACGAGCGCGTCCGAGGCCCGCACTCCG 5224

QY 1727 CCTGACGAGAGCGCGCGCTGCTGCTGAGAGAGGTGAGTTTCCAGCGTAG 1786

DB 5223 CCTGACGAGAGCGCGCGCTGCTGCTGAGAGAGGTGAGTTTCCAGCGTAG-A 5165

QY 1787 GAGGCTGAGCGCATTAAGAGAGAGTGCATTAAGACAGCGCGCGCTGAGCGCTTTA 1846

DB 5164 AAACCTTAACCGCATTAAGAGAGAGTGCATTAAGACAGCGCGCGCTGAGCGCTTTA 5107

QY 1847 GAACCGTCTGCTGCTGAGAGAGAGTGTGATCTGCAAGACTTGTTCGCGG 1906

DB 5106 AAACCGTCTGCTGAGAGAGAGTGTGATCTGCAAGACTTGTTCGCGG 5047

QY 1907 TCAGTCTTGCATCTCAAGAGAGTGGCGCGCGAGAGTGTGAGCGAGCGGGA 1966

DB 5046 TCAATCTTGCATCTCAAGAGAGTGGCGCGCGAGAGTGTGAGCGAGCGGGA 4987

QY 1967 GTGGCAAGAGAGTGCATCTGAGAGAGAGTGCATTAAGCGCGGTGATGAGCGCAG 2026

DB 4986 ATTAACCAAGAGAGTGCATCTGAGAGAGAGTGCATTAAGCGCGGTGATGAGCGCAG 4927

QY 2027 AAACGAGAGTGAAGAAATCATGAGAGAGAGTGCATTAAGCGCGGTGATGAGCGCAG 2086

DB 4926 AAACGAGAGTGAAGAAATCATGAGAGAGAGTGCATTAAGCGCGGTGATGAGCGCAG 4867

QY 2087 GCGTCTTCAAGAGTGTGCGAGAGAGTGCATTAAGCGCGGTGATGAGCGCAG 2146

DB 4866 GACTACTTCAAGAGTGTGCGAGAGAGTGCATTAAGCGCGGTGATGAGCGCAG 4807

QY 2147 CCGAAGCGCGCGCGCGCGCGAGGCTTAAGCGCGCGCGCGCTGAGCGAGCGCAG 2206

DB 4806 CCGAAGCGCGCGCGCGCGCGAGGCTTAAGCGCGCGCGCGCTGAGCGAGCGCAG 4747

QY 2207 TGGAGAGCGAGTGTGCGCGCGCGCTTGGAGTTGATGTCACAGCTGCGCGCGCTGCGA 2266

DB 4746 TACGAAACCGCACTGAGCGCGCTTAAATTAATTAATTAATTAATTAATTAATTAATTA 4687

QY 2267 CCGC 2270

Db 4686 CGCG 4683

RESULT 8

ADL13819 ID ADL13819 standard; DNA; 41150 BP.

XX ADL13819;

XX

DT 06-MAY-2004 (first entry)

XX

DE Osteoarthritis-associated polymorphic nucleotide #351.

XX

KM ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;

KM joint space narrowing; osteophyte development; joint pain;

KM osteoarthritis; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PN W02003054166-A2.

XX

PD 03-JUL-2003.

XX

PF 19-DEC-2002; 2002WO-US041225.

XX

PR 20-DEC-2001; 2001US-0342603P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Jones KA, Schaffer A;

XX

XX WPI; 2003-559141/52.

XX

PT Determining susceptibility of an individual to joint space narrowing,

PT osteophyte development and/or joint pain comprises identifying whether

PT the individual has at least one polymorphism in a polymucleotide encoding

PT a protein.

XX

PS Disclosure; SEQ ID NO 351; 297bp; English.

XX

XX The invention relates to a method of determining susceptibility of an

CC individual to joint space narrowing and/or osteophyte development and/or

CC joint pain comprising identifying whether the individual has at least one

CC polymorphism in a polymucleotide encoding at least one of the protein

CC listed in the specification. The methods, composition and agent are

CC useful for modulating the susceptibility of an individual to joint space

CC narrowing and/or osteophyte development and/or joint pain that is

CC associated with a disease, preferably osteoarthritis. The cell line and

CC the non-human animal are useful for screening for an agent for diagnosing

CC an individual having susceptibility to joint space narrowing and/or

CC osteophyte development and/or joint pain. This sequence corresponds to

CC the polymucleotide encoding a protein listed in the specification. (Note:

CC The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences).

XX

XX

XX Sequence 41150 BP; 10143 A; 11252 C; 10866 G; 8889 T; 0 U; 0 Other;

XX

Query Match 8.3%; Score 188.4; DB 10; Length 41150;

Best Local Similarity 63.7%; Pred. NO. 7.1e-27;

Matches 354; Conservative 0; Mismatches 191; Indels 11; Gaps 4;

QY 5 GATCTGCCGCTCAGCTCCCAAGTGTGGATTGACGCGTGAAGCACTTCACTGG 64

DB 32914 GATCTGCCGCTCAGCTCCCAAGTGTGGATTGACGCGTGAAGCACTTCACTGG 32973

QY 65 CTACAAAGTTTCAAAATCATTTA---TCTAGTACCCATACATTTCTCCAGTTTGCCACA 121

DB 32974 CCGTGTGTTTATTAACCTAAACAGATTTAGAGTGTCTTTTAAATCATTTATTA 33033

QY 122 GGAATCTTATGACTTGGACGAGGCTCTAAATTCAGAGGGTGCAGCGTTGTATGTCTTA 181

DB 33034 TGAAGACTATCAACATACAGAAAAAGTTGACCATTCATATACCAACCACTAGATTCAAC 33093

QY 182 TAGAATTGCTCAGATCTGCCCCCACCCTGAAAAGAT---TTAAGAGATTTCTTGAGGCC 238

DB 33094 TATTGTAGCTTAATCTACCAATCTTCTTTCTAAACATTTAAAAATTAATTGCAGACC 33153

QY 239 AGGCACAGTGTGCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGACTGC 298

DB 33154 GGGCACAGTGTGCTCAGGTCTAATATCTTACCTTAGCATTGGAGAGCAAGAGTGAATGCACGC 33213

QY 299 TTGAGCCAGAGATTTGAGAGAGCCTGTGACCAACAGAGGAGCCTGTCTCAAAAGAA 358

DB 33214 TTGAGTTCAAGAGATTCAAGACAGCCTGGGCAATATAGTAGAGACCGTCTTCAAAAAA 33273

QY 359 TAAATAAATTAGCAGAGCTTAGTGTGCTCATCCCTGTGTGCTCCAGCTACTAGAGAGCAGA 418

DB 33274 TACAAAGCTTAGCCGCGGACATGTGTGGACAGCGCTGTAAATCCAGACTACTTGGGGAGCTGA 33333

QY 419 AGTAGA---CTGCTTGTCCCAAGAGGTCAAGACTGACAGTGAAGCCAGCCACC 474

DB 33334 GGTGGAGAGATCACTTGAAGCCAGAGAGTGAAGGCTGCAGTGAAGTCAATGCCA-C 33392

QY 475 TGCAATCCAGCCTGGGCAACAAAAGACCTGTCTCAAAAATAGTTAAATTAATA 534

DB 33393 TGTACTTCAGCCTGGGGTGAACAAAGTGAAGACTGTCTCAAAAATTAATAATTAATTG 33452

QY 535 ATATATAAATAATAGTTT 550

DB 33453 CAACATCCACATATT 33468

RESULT 9

ADN48556/c

ID ADN48556 standard; DNA; 44348 BP.

XX

AC ADN48556;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human Notch3 genomic DNA #2.

XX

KM Human; Notch3; gene; ds; antisense oligonucleotide;

KM phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;

KM 5-methylcytosine; hyperproliferative disorder; cancer; cytostatic.

XX

OS Homo sapiens.

XX

PN US2004102390-A1.

XX

PD 27-MAY-2004.

XX

PF 21-NOV-2002; 2002US-00301832.

XX

PR 21-NOV-2002; 2002US-00301832.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Freier SM, Dobie KM;

XX

XX WPI; 2004-399720/37.

DR GENBANK; NM_000435.

XX

PT New compound, particularly oligonucleotides targeted to a nucleic acid

PT encoding Notch3, useful for treating diseases associated with Notch3,

PT e.g. hyperproliferative disorders.

XX

XX Example 15; SEQ ID NO 11; 74bp; English.

XX

XX The invention relates to a compound targeted to a nucleic acid molecule

CC encoding the human Notch3 polypeptide. The compound is an antisense

CC oligonucleotide that specifically hybridizes with the nucleic acid and

CC inhibits expression of the polypeptide. The antisense oligonucleotide

CC comprises at least one modified internucleoside linkage i.e. a

CC phosphorothioate linkage, at least one modified sugar moiety, preferably

CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
CC comprising a 5-methylcytosine. The antisense compounds are useful for
CC modulating the expression of the human Notch3 polypeptide and in
CC preparation of a composition for treating hyperproliferative disorders,
CC e.g. cancer. This sequence represents genomic DNA encoding the human
CC Notch3 polypeptide of the invention.

XX Sequence 44348 BP; 9445 A; 11931 C; 12348 G; 10624 T; 0 U; 0 Other;

Query Match 8.3%; Score 188.4; DB 12; Length 44348;

Best Local Similarity 63.7%; Pred. No. 7.2e-27;

Matches 354; Conservative 0; Mismatches 191; Indels 11; Gaps 4;

```
Oy 5 GATCGCCCGGCTGCGCCGCTGCGGATTTGAGAGGCGTACGACCTGCG 64
Db 12725 GATCGCTGCTGCTGCGCTGCGGATTTGAGAGGCGTACGACCTGCG 12666
Oy 65 CTACAGTTTTCATTAATCATTTA---TCTAGTACCATACATTCCTCCAGTTTGTCCACA 121
Db 12665 CCGTGTGTTTATTAACCTTAAACAGTATTTAGTAGGCGCTTTTATATCATTTATTA 12606
Oy 122 GGACATCTTATGACTTGGAGCAAGCTGCTAAATTCAGAGGCTGCGAGCTTTGTATGCTTA 181
Db 12605 TGAGAACTATCAAAACATACAGAAAGTTGACCAATTCATATACCCACACTAGATTCAAC 12546
Oy 182 TAGATGTGCTAGATCTGCGCCCGCTGAAAGAT---TTAAGAGATTTCTTAGGCC 238
Db 12545 TATGTGTAGCTTAATCTACCAATCTTCTTTCTTAAACATTTAAATTAATTTGACAGACC 12486
Oy 239 AGGCACAGTGGCTCACCTGTAATTCAGTACTGTAGAGTCCGAGGTCAAGAGACTGC 298
Db 12485 GGGCACAATGGCTCAGCTATTAATCTAGACCTTTGGAGGCCAAGGTGATGATGGC 12486
Oy 299 TTGAGCCAGAGGTTCAAGAGAGCTTGAACAACAGGAGAGCTGTCACTACAAAGAA 358
Db 12425 TTGATTTAAGAGTTCAAGAGAGCTTGGGCAATATAGAGACCCGCTCTACAAAGAA 12366
Oy 359 TAAATTAATTTAGCCAGGCTTATGAGCTATCCCTGTGGTCCGAGTACTAGGAGAGCGAGA 418
Db 12365 TACAAAGCTTACCGGAGTGTGGCGACGCTGTAAATCCAGCTACTTGGGAGACTGA 12306
Oy 419 AGTAGA---CTGCTTGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCACC 474
Db 12305 GGTGGAGAGATCACTTGAAGCCAGAGAGTCAAGGCTGCAAGTGAAGTGAATATGCCA-C 12247
Oy 475 TGCATTCCAGCTGCGGCAACAAAGAGACCTGTCTCAAAAATTAAGTTAAATTAATA 534
Db 12246 TGTACTCCAGCTGCGGTGACAAAGTAGAGCTGTCTCAAAAATTAATAATTAATTG 12187
Oy 535 ATTAATTAATAATGTTT 550
Db 12186 CAATATCCACATATT 12171
```

RESULT 10

AA529967/C
ID AA529967 standard; DNA; 11172 BP.

XX AA529967;

DT 21-NOV-2001 (first entry)

XX Human lung antigen genomic DNA #37.

XX Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiatic; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virocidic; fungicide; cancer;
KW ophthalmological; veterinary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; db;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;

KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-infertility; food additive.

OS Homo sapiens.

XX WO200155303-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001301.

```
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 14-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218299P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 16-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.
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PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241825P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
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PR 05-DEC-2000; 2000US-0256719P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.

PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-457723/49.
XX
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT respiratory disorders related to the lung including lung cancers and also
PT for testing and detection e.g. diagnosis.
XX
PS Claim 1, SEQ ID NO 231; 507bp; English.
XX
XX
CC Sequences AA829931-AA830164 represent genomic DNA molecules, which encode
CC the lung antigen polypeptides of the invention. Lung antigen polypeptides
CC and their associated polymucleotides are useful in the diagnosis,
CC treatment and prevention of various types of disorders in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by detecting the presence or
CC absence of a mutation in a lung antigen polymucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischaemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma and pleurisy. The polypeptides can
CC also be used to aid wound healing, to prevent skin aging due to sunburn,
CC to maintain organs before transplantation, to regenerate tissues and in
CC chemocaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 7.64; Score 172.8; DB 5; Length 11172;
Best Local Similarity 58.54; Pred. No. 6.1e-24;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

QY 1 AACGATTCGCCGCTCAGCTCCCAAAGTCTGGATTGAGGCCACTGCAC 60
DB 8630 AAGTGATCCGCTGCTTGGCTCCCAAAGTCTAGATTACAGGATGATCCGCAC 8571

QY 61 CTGGCTACAGTTTCAAAATATATATAGTACCAATTCCTCCAGTTTGTCCAC 120
DB 8570 CTGGCTCCCTTAAAGATCTAACATTAATCCAGGCTCAACAAACATGAAGACAAA 8511

QY 121 AGACATCTTATGACTTGAACAAGCTGCTAAATCCAAAGGTCAGCGTTGTATGCT 180
DB 8510 AGGACTAATTAATTAAGTATATAGTTAATTAAGTTTCTGTGTATCTAATGAAGAGCTT 8451

QY 181 ATAGGATTCCTCAGATTCGCCCCACCTGAAAGAAATTTAAGAAATTTCTTAGAGCCAG 240
DB 8450 TCCCTCAGACAAAGATGATTAATTTGGGTTTTCTTTTAAGATGAGGAGCACTGCCAG 8391

QY 241 GCACAGTGGCTACACCTGTAAATTCAGTCTGTGAGAGGCCAGAGCTGAGCTT 300
DB 8390 GCACAGTGGCTCACACCTGTAAATTCAGCACTTTGGAGGCGAGGAGTGGAGCACT 8331

QY 301 GAGGCCAGAGTTCAAGAGCCTGTGACAACACAGAGAGA-CCTGTACTACAAAGAT 359
DB 8330 GAGGTACAGAGTTCAACACAGCTGTGCAATTAATTAAGTAAACCCCATCTTAAATTAAT 8271

QY 360 AATTAATTAAGCAGGCTTAATGAGCTATCCCTGTGTCCAGTACTTAGAGAGCCGAA 419
DB 8270 ACAAATTAATTAAGCAGGCGCGGTGCGTACCTGTATCTCCAGTACTTACAGAGGCTGAG 8211

QY 420 GTAGGACTGCTTTGCCAGAGAGTCA-AGAATGAGAGTACAGACCCAGCCACTGCA 478
DB 8210 ACAAATTAATTAAGCAGGAGGAGGAGGTTACAGTGAAGCTTAATTTGACCACTGCAC 8151

Oy 479 TTCCAGCTGGGCAACAAAAAGACCCGTCTCAAAAAATAGTAATAATAATAA 538
Db 8150 TCCAGCTTAGGTGGGACAGAGTGGAGCTCTTCTCAAAAAA 8091
Oy 539 TAAAAATAGTTAAACCTTAAACACATCTTTT 574
Db 8090 AAAAAAGTAGGAGCATGACTTATTATTATTCT 8055

RESULT 11
ADB33304/C
ID ADB33304 standard; DNA; 11172 BP.
XX AC ADB33304;
XX DT 04-DEC-2003 (first entry)
XX DE Human novel lung related polypeptide DNA SEQ ID NO 231.
XX KW gene therapy; lung antigen; neoplasia; acute myelogenous leukaemia;
KW adenocarcinoma; respiratory disorder; chronic rhinitis; sinusitis;
KW immunodeficiency; X-linked agammaglobulinaemia;
KW X-linked infantile agammaglobulinaemia; inflammatory disorder;
KW adrenailitis; alveolitis; immune complex disease; serum sickness;
KW polyarteritis nodosa; bleeding disorder; thrombocytopenia;
KW Von Willebrand's disease; acquired platelet dysfunction; kidney failure;
KW multiple myeloma; macrophage related disorder; Gaucher's disease;
KW Netman-Pick disease; tumour; colon cancer; pancreatic cancer;
KW renal disorder; nephritis; bone disorder; Albers-Schönberg disease;
KW bowleg; muscle disorder; Becker's muscular dystrophy;
KW Duchenne's muscular dystrophy; nervous disorder; ischemic lesion;
KW traumatic lesion; endocrine disorder; Cushing's syndrome;
KW corticosteroid deficiency; gastrointestinal disorder; dysphagia;
KW gastric reflux; human; ds.
XX OS Homo sapiens.
XX PN US2003054368-A1.
XX PD 20-MAR-2003.
XX PF 22-FEB-2002; 2002US-00079854.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
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PR 28-JUN-2000; 2000US-0214886P.
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PR 07-JUN-2000; 2000US-0209467P.
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PR 17-NOV-2000; 2000US-0249227P.
PR 17-NOV-2000; 2000US-0249228P.
PR 17-NOV-2000; 2000US-0249229P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 06-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0255678P.

(HUMA-) HUMAN GENOME SCT INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides,
useful for preventing, diagnosing and/or treating nervous system cancers
and metastases.

Disclosure: SEQ ID NO 11706; 1701bp + Sequence Listing; English.

The invention relates to novel genes (ABAI1004-ABR21534) and proteins
(ABAI478-ABR18001) useful for preventing, treating or ameliorating
medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification.
The nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC / (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcc_sequences

XX Sequence 25525 BP; 6205 A; 6343 C; 6691 G; 6286 T; 0 U; 0 Other;

Query Match 7.4%; Score 168.4; DB 5; Length 25525;

Best Local Similarity 62.1%; Pred. No. 5.3e-23;

Matches 334; Conservative 0; Mismatches 196; Indels 8; Gaps 4;

QY 1 AACGATCTGCCCGCCTGAGCTCCCAAGTGTGGATTGACAGCGTGAACCTTCAC 60
DB AACTGACCTGCGCACTCAGCTCCAAAGTGTGGATTGACAGCGTGAACCTTCAC 6852
QY 61 CTGGCTACAACTTTCAAAATATCATTTATGTAACCATTCCTCCAGTTGTCCAC 120
DB CCATCTCTAGGAGATTGTGATTCATTAATTAATTAATTAATTAATTAATTAATTA 6792
QY 121 AGGACATCTTATGACTTGAAGCAAGTGTGTAATAATTCAGAGGTGAGGTTGATGCT 180
DB 6791 CAGCCCACTTATGACATGACATGCAAAATTAAGTGTGATTAAGATTAAGGATGCGG 6732
QY 181 ATAGATTTCTCAATCT--GCCGCCACCTGAAAGAAATTAAGAAATTTCTTGAAGC 237
DB 6731 GAAAGACTTCTTGTCTCTGCGCAAGGCTGCTTACGTTAAGTAATGAATCTCCGAC 6672
QY 238 CAGGACAGTGGCTCACACCTGTATTTCCAGTACTGTGAGAGTCCGAGTCAAGAGCTG 297
DB 6671 CAGGAGTGGCTCACACCTGTATTCACACCTTGGAGGCGCAAGTGTGAGATCA 6612
QY 298 CTTGAGGCGAGAGTTCAGAGCCTGAGCAACACAGGAGACCTGTCACTACAAAGA 357
DB 6611 CTTGAGTGGGAGTTTGAACACAGCTGACCTGACATGAGAAACCCATCTCTATTA 6552
QY 358 ATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 417
DB 6551 AACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 6492
QY 418 A--AGTGAATCTGTTTCCCAAGAGTCAAGACTGAGTGAAGTGAAGCCAGCC 474
DB 6491 AGGCGAGGAATCTGTTAATCTGAAGAGCGGAGGTGAGTGAAGCCAGATCGACCA-C 6433
QY 475 TGCAATTCAGGCTGGGCAACAA-AAAGAGCCCTGTCTCAAAAAATTAATTAATTA 531
DB 6432 TGCACTCGAGCTGGGCAACAAAGAAATCTGTCTCAAAAAATTAATTAATTA 6375

RESULT 13
ADQ19501/c
ID ADQ19501 standard; DNA; 135005 BP.

XX AC ADQ19501;

XX XX 26-AUG-2004 (first entry)

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

XX KM ds.

XX OS Homo sapiens.

XX XX WO2004048938-A2.

PD 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

PR (PROT-) PROTEIN DESIGN LABS INC.

PA Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441206/41.

XX Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample

PT and comparing the gene expression, also useful in treating soft tissue

PS sarcoma.

XX Example 2; SEQ ID NO 2320; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cyostatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC DNA of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX Sequence 135005 BP; 32951 A; 33605 C; 32661 G; 35788 T; 0 U; 0 Other;

Query Match 7.4%; Score 167.2; DB 12; Length 135005;

Best Local Similarity 80.3%; Pred. No. 1.3e-22;

Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

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DB 8440 GGGTGAAGACAGTGGCTCACACCTGTATTTCCAGTACTGTGAGAGTGGAGAG 84781

QY 295 CTGCTGAGGCGAGAGTTCAGAGCCTGAGCAACACAGGAGAG--CCTGTCACTAC 352
DB 84780 TTGCTTGAAGGCGAGAGTTCAGAGCTATCTCTGGCAACATATGAGAGCCCTGTCTAC 84721

QY 353 AAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 412
DB 84720 AAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 84661

QY 413 GGCGAGATGAGACTGCTTG--TCCAGAGAGTCAAGACTGAGTGAAGCCAGCC 471
DB 84660 GGCTGAGATGAGATTTGTTAGCTTCAGAGAGTCAAGCGGCGAGTGAAGTGAAGTCC 84601

QY 472 ACCTGATTCAGGCTGGGCAACAAAAGAGCCCTGTCTCAAAAAATTA 521
DB 84600 A-CTGTACTCAACCTGGGCAACAGAGAGCCCTGTCTCAAAAAATTA 84552

RESULT 14
ADA02666
ID ADA02666 standard; DNA; 52242 BP.

XX AC ADA02666;

XX XX 06-NOV-2003 (first entry)

DE Human MDM2 carcinoma associated gene, SEQ ID NO:1184.

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast;

XX prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening;

XX KM gene; ds.

XX Homo sapiens.
OS
XX WO2003057146-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041414.
XX
XX 26-DEC-2001; 2001US-00035832.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX WPI; 2003-587068/55.
XX
XX New recombinant nucleic acid encoding carcinoma associated protein,
XX useful for preparing compositions for treating carcinomas.
XX
XX Claim 1; SEQ ID NO 1184; 245bp; English.
XX
XX The invention relates to recombinant carcinoma associated (CA) nucleic
XX acid sequences from mouse and human (ADA01482-ADA03094), and to
XX recombinant carcinoma associated proteins (CAP) encoded by them. The
XX invention also encompasses expression vectors and host cells comprising a
XX CA nucleic acid, a polypeptide (especially an antibody) that specifically
XX binds to the protein, and a biochip comprising CA nucleic acid or
XX fragments thereof. The sequences of the invention were identified using
XX oncogenic retroviruses, which insert into the genome of the host organism
XX at random. Many of these do not carry transduced host oncogenes or
XX pathogenic trans-acting viral genes meaning that cancer incidence is a
XX direct consequence of the effects of proviral integration into host
XX protooncogenes. The CA nucleic acid sequences can be used to diagnose
XX carcinoma (especially breast cancer, prostate cancer, lymphoma or
XX leukemia) or a propensity to carcinoma by determination of the sequence
XX of a CA gene, or by determination of CA gene expression in particular
XX tissues. CA nucleic acids, proteins and antibodies are also useful as
XX therapeutic agents and in screening and evaluating drug candidates. The
XX present sequence represents a specifically claimed human CA nucleic acid
XX sequence of the invention. Note: The complete sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 52242 BP; 14384 A; 10354 C; 10997 G; 16487 T; 0 U; 20 Other;
SQ
Query Match 7.3%; Score 166.6; DB 9; Length 52242;
Best Local Similarity 62.9%; Pred. No. 1.4e-22;
Matches 344; Conservative 0; Mismatches 189; Indels 14; Gaps 5;
QY 5 GATGTCGCCGCTCAGCTCCCAAGTGTGGATTTGAGGCGGTGAGCCACTCCTCCTGG 64
DB 5228 GATGTCGCTGTCTTGGCTCCCAAGTGTGGATTTGAGGCGGTGAGCCACTCCTGG 5287
QY 65 CTACAGTTTCAAAATACATTATCTAGTACCCATACATTTCTCCAGTTTGTCCACAGA 124
DB 5288 CCGGATTTTGGCTTTAAATACATTAATCACTATTCAGTTCAGATTTTGAAGAAGATMAAGA 5347
QY 125 CATCTTAAGACTTGTAGCA-----ACCTGCTAAATAATCAAGGGTGCAGCGTTTGTATGTC 179
DB 5348 ATTGAACACTCTTCTGTATTTTATAGTGTCTCAATAATTTGTGTAATCTCAGCATTTCTA 5407
QY 180 TATAGAGTTGTCTAGATCTGCCCC--ACCTGGAAGAATTTAAGAAATTTCTTGAAG 236
DB 5408 AACAGGTTTCTGACCTAAATCTTTAGTTTACACATGCTTTAAAGATTAAGTTTGG 5467
QY 237 CCAGCAGAGTGGTCCACACCTGTAATCCAGTACTGTGAGAGTCCGAGGTGAGGAGCT 296
DB 5468 CCAGCAGAGTGGTCCACACCTGTAATCCAGTACTGTGAGAGTCCGAGGTGAGGAGCT 5527
QY 297 GCTTGAAGCAGAGATTCAAGAGCCTGAGCAACACAGGAGAG-CCTGTCACTTACAA 355

DB 5528 ACCTGAGCCAGAGATTGAGACCCAGCTGGCCCAATAGTAATCCCTCTCTACTAA 5587
QY 356 GAATTAATAATTAAGCCAGCTTGTAGTGGCTCATCCCTGTGGTCCAGTACTAGGAGGC 415
DB 5588 AATATCAAAATATGAGCCGGGTATGTGGCACAACTGTATTCCTCAGTACTCGGAGGC 5647
QY 416 AGAAGTAGA-----CTGCTTGTCCAGAGAGTCAAGACTGAGCTGAGACCCAGCC 471
DB 5648 TGAGCAGAGAAATCACTTGAACCCAGAGAGTGAAGGCTGAATGAGCTGAGATCTGCC 5707
QY 472 ACCTGATTTCCAGCTGGGCAAAAGAGACCTGTCTCAAAAAATAGTTAAATAA 531
DB 5708 A-CTGCACTCCAACTGGTGAAGAGTGAAGTGAAGTCTCCCTCAAAAAAGAA 5766
QY 532 TAAATTA 538
DB 5767 AGACAAA 5773
RESULT 15
ADB72404
ID ADB72404 standard; DNA; 52242 BP.
AC ADB72404;
XX 04-DEC-2003 (first entry)
DT
XX Human MDN2 gene.
DE
XX human; ds; cytosstatic; gene therapy; vaccine; carcinoma; lymphomas;
XX cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX
XX Homo sapiens.
XX
XX WO2003008583-A2.
XX
XX 30-JAN-2003.
XX
XX 26-DEC-2001; 2001WO-US051291.
XX
XX 02-MAR-2001; 2001US-00798586.
XX
XX 23-OCT-2001; 2001US-00004113.
XX
XX 08-NOV-2001; 2001US-00052482.
XX
XX 30-NOV-2001; 2001US-00997722.
XX
XX 20-DEC-2001; 2001US-00034650.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW, Engelhard EK;
XX
XX WPI; 2003-239337/23.
XX
XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
XX cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
XX Claim 1; SEQ ID NO 232; 2304bp; English.
XX
XX The invention relates to a novel recombinant nucleic acid comprising a
XX nucleotide sequence selected from any of the 660 sequences fully defined
XX in the specification. A polynucleotide of the invention has cytosstatic
XX activity, and may have a use in gene therapy, or in a vaccine. The
XX recombinant nucleic acids and polypeptides are useful for treating
XX carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
XX sarcomas. The present sequence represents a human gene of the invention.
SQ
Query Match 7.3%; Score 166.6; DB 10; Length 52242;
Best Local Similarity 62.9%; Pred. No. 1.4e-22;
Matches 344; Conservative 0; Mismatches 189; Indels 14; Gaps 5;
QY 5 GATGTCGCCGCTCAGCTCCCAAGTGTGGATTTGAGGCGGTGAGCCACTCCTCCTGG 64

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Db 5228 GATCTGCTGCTCTTGGCTCCCAAGTACTGGGATTACAGGCGTGAGCCACTGCGTCGG 5287
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QY 180 TATAGATTTGCTCAGATCTGCCCC--ACCTGAAAAGATTTAAGAAATTTCTTGAGG 236
Db 5408 AACCGGTTCTGAGCTAAATCTGTGTAGTTTCACCATGCTTTAAAGATTAGTTGTGG 5467
QY 237 CCAAGCACAGTGTCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACT 296
Db 5468 CCAAGCACAGTGTCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACT 5527
QY 297 GCTTGAGGCCAGAGATTCAAGAGCAGCTTGACAAACAAGGAGA-CCTGTCACTACAAA 355
Db 5528 ACCTGAGGCCAGAGATTCAAGAGCAGCTTGACAAACAAGTGAATCCCGTCTTACTAA 5587
QY 356 GAATTAATTAATTAGCCAGGCTTAGTGTCTATCCCTGTGTGTCCTCAGTACTAGGAGGC 415
Db 5588 AAATTAACAAAATTAGCCGAGTATGTGCAACAAGCTTGTATCCAGCTACTCGGAGAGC 5647
QY 416 AGAAGTAGGA----CTGCTTGTCCAGAGAGGTCAAGACTGAGAGTGAAGCCAGCC 471
Db 5648 TGAAGCAGAGAAATCATCTTGAAACCCAGAGAGGTGAGAGCTGCATGAGCTGAGATCGTGC 5707
QY 472 ACCTGCATTCAGGCTTGAGGCAACAAAAGAGACCTGTGTCTCAAAAAAATAAGTTAATPAA 531
Db 5708 A-CTGCACTCCAACTGGGTGACAGAGTGAGACTCCGCTCAAAAAAAGAAAAAGAA 5766
QY 532 TAAATPAA 538
Db 5767 AGACAAA 5773
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Search completed: December 21, 2005, 18:03:52
Job time : 1260 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2005, 17:43:12 ; Search time 1635 seconds
(without alignments)
11481.032 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1_2270
Perfect score: 2270
Sequence: 1 aacggatctgcgcgcacg.....cgcccgctcgcgcgcg 2270

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries

Database : Published Applications NA Main:

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2: /cgn2_6/ptodata/1/pubphn/US08_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846.8	37.3	9314	US-10-197-019-1	Sequence 1, Appl1
2	550.6	24.3	562	US-09-925-065A-566754	Sequence 566754,
3	531.6	23.4	554	US-09-925-065A-177131	Sequence 177131,
4	447.4	19.7	1161	US-10-265-689-27	Sequence 27, Appl
5	364.2	16.0	5283	US-10-311-455-1865	Sequence 1865, Ap
6	312.4	13.8	5283	US-10-311-455-1866	Sequence 1866, Ap
7	188.4	8.3	44348	US-10-301-832-11	Sequence 11, Appl
8	175	7.7	160556	US-09-764-878-231	Sequence 6827, Ap
9	172.8	7.6	11172	US-10-719-993-6827	Sequence 231, App
10	172.8	7.6	11172	US-09-925-065A-770821	Sequence 770821,
11	168	7.4	563	US-10-723-860-2320	Sequence 2320, Ap
12	167.2	7.4	135005	US-10-756-149-1719	Sequence 1719, Ap
13	166.8	7.3	3030	US-10-027-632-115210	Sequence 115210,
14	166.8	7.3	3030	US-10-027-632-115211	Sequence 115211,
15	166.8	7.3	3030	US-10-027-632-115210	Sequence 115210,
16	166.8	7.3	3030	US-10-027-632-115211	Sequence 115211,
17	166.8	7.3	3030	US-10-027-632-115211	Sequence 115211,
18	166.8	7.3	52242	US-10-052-483-172	Sequence 172, App
19	166	7.3	1614	US-09-925-065A-551304	Sequence 551304,
20	165.6	7.3	1187	US-09-925-065A-71295	Sequence 71295, A
21	165.6	7.3	1187	US-09-925-065A-71295	Sequence 71295, A
22	164	7.2	1369	US-10-027-632-86881	Sequence 86881, A
23	164	7.2	1369	US-10-027-632-178961	Sequence 178961,

c 24	164	7.2	1369	6	US-10-027-632-86881	Sequence 86881, A
c 25	164	7.2	1369	6	US-10-027-632-178961	Sequence 178961,
c 26	164	7.2	1369	6	US-10-043-715-1	Sequence 1, Appl1
c 27	163.4	7.2	558	4	US-09-925-065A-822292	Sequence 822292,
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c 32	161.8	7.1	109906	7	US-10-235-182A-31	Sequence 31, Appl
c 33	161.4	7.1	383432	9	US-10-737-082-34	Sequence 34, Appl
c 34	161.4	7.1	383432	9	US-10-765-790-34	Sequence 34, Appl
c 35	161.2	7.1	56737	3	US-09-782-378A-17	Sequence 17, Appl
c 36	160.8	7.1	60815	5	US-10-087-192-52	Sequence 52, Appl
c 37	160.6	7.1	599	4	US-09-925-065A-875725	Sequence 875725,
c 38	160.6	7.1	599	4	US-09-925-065A-905153	Sequence 905153,
c 39	160.6	7.1	7739	3	US-09-764-877-3189	Sequence 3189, Ap
c 40	160.6	7.1	7739	6	US-10-242-515-3189	Sequence 3189, Ap
c 41	160.6	7.1	8133	7	US-10-380-124-10	Sequence 10, Appl
c 42	160.4	7.1	87467	7	US-10-741-601-5634	Sequence 5634, Ap
c 43	160.4	7.1	87467	8	US-10-741-600-17624	Sequence 17624, A
c 44	160.4	7.1	136436	9	US-10-756-149-3773	Sequence 3773, Ap
c 45	160.2	7.1	492	5	US-10-027-632-84916	Sequence 84916, A

ALIGNMENTS

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RESULT 1
US-10-197-019-1
Sequence 1, Application US/10197019
Publication No. US20030207284A1
GENERAL INFORMATION:
APPLICANT: Chew, Anne
APPLICANT: Denton, R. Rex
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Nandabalan, Krishnan
APPLICANT: Parks, Katie E.
TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
FILE REFERENCE: MMH-0042US
CURRENT APPLICATION NUMBER: US/10/197, 019
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02485
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 9314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1283)..(1283)
OTHER INFORMATION: P81: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (1714)..(1714)
OTHER INFORMATION: P82: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2051)..(2051)
OTHER INFORMATION: P83: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (214)..(2124)
OTHER INFORMATION: P84: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2287)..(2287)
OTHER INFORMATION: P85: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (2408)..(2408)
OTHER INFORMATION: P86: polymorphic base adenine or guanine

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66 NAME/KEY: allele
67 LOCATION: (8677)..(8677)
68 OTHER INFORMATION: PS23: polymorphic base thymine or adenine
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Query Match	37.3%	Score 846.8;	DB 6;	Length 9314;
Best Local Similarity	98.9%	Pred. No. 2a-204;		
Matches 874; Conservative	0;	Mismatches 7;	Indels 3;	Gaps 2

QY	1387	GGTCATCTCTGTAAGCGCTTTTCTGATCCAGAGGCTGGAACAGGAGCTGAGCTGAGGCGC	1446
Db	1	GGTCATCTCTCTGAGCGCTTTTCTCATCTCCAGAGCTGAACAGGAGCTGAGCTGAGGCGC	60
QY	1447	GCTCTGCTCTTGTCATCGTGCAGGAGGCGCGGCGCGTTTGCTGTCTGTGTGTAGAGACGTGAG	1506
Db	61	GCTCTGCTCTTGTCATCGTGCAGGAGGAGCGCGGCGCGTTTGCTGTCTGTGTGTAGAGACGTGAG	120
QY	1507	GTCAACGTGTGGGTGTCTCCGCGCCGCGCGGAGGCGCTTTAATGTCTCCGTGTCCCTTAAACGCGCAG	1566
Db	121	GTCAACGTGTGGGTGTCTCCGCGCCGCGCGGAGGCTTTAATGTCTCCGTGTCCCTTAAACGCGCAG	180
QY	1567	GCCGCTCCACCGAGGAGGAGAAAGCGCGAACCCGACGCCAGGCCAACGCGCTGTGTGCGATTG	1626
Db	181	GCGCTCCACCGAGGAGGAGAAAGCGCGAACCCGACGCCAGGCCAACGCGCTGTGTGCGATTG	240
QY	1627	CCGGGCGCACTGTGTCTGTGCAAGTTCTGATTTGGTTCTTCCCCCGACAAACGCGGCGCGCTGTGA	1686
Db	241	CCGGGCGCACTGTGTCTGTGCAAGTTCTGATTTGGTTCTTCCCCCGACAAACGCGGCGCGCTGTGA	300
QY	1687	ACCAATCGACAGCGAGGCGCGGTGCGAGAGGCCCGCCAGTCCGCGCCCTGCAGAGACCGACGCGC	1746
Db	301	ACCAATCGACAGCGAGGCGCGGTGCGAGAGGCCCGCCAGTCCGCGCCCTGCAGAGACCGACGCGC	360
QY	1747	CGCTCGCTCCGAGAGGAGGTGTGATTTGCTCCAGCGTGAAGGAGGCGCTGAGGCCCATTAATAAGA	1806
Db	361	CGCTCGCTCCGAGAGGAGGTGTGATTTGCTCCAGCGTGAAGGAGGCGCTGAGGCCCATTAATAAGA	419
QY	1807	GGAAGTGCACTTAAGACACAGGCGCCCGCGCTGACGCTTGTTAGAAACCGTCTCGGTGAGAA	1866
Db	420	GGAAGTGCACTTAAGACACAGGCGCCCGCTGACGCTTGTTAGAAACCGTCTCGGTGAGAA	477
QY	1867	GGCAAGAGGTGTGTGACTGTGACAAAGACTTGTCTTGTGCGCGGTCACTCTTGCCATCTTCACA	1926
Db	478	GGCAAGAGGTGTGTGACTGTGACAAAGACTTGTCTTGTGCGCGGTCACTCTTGCCATCTTCACA	537
QY	1927	GAGTTTGGCGGCCCCGAGAGAGTGTGAAGGACAGAGCGCGGAGGTGTGCAAGGAGTGAACATC	1986
Db	538	GAGTTTGGCGGCCCCGAGAGAGTGTGAAGGACAGAGCGCGGAGGTGTGCAAGGAGTGAACATC	597
QY	1987	TCGGGGAACGAAAGAGTAAACGCGCGTGTATGTGAGCGCACCGGAAACGAGAGTGTGAAAGTGC	2046
Db	598	TCGGGGAACGAAAGAGTAAACGCGCGTGTATGTGAGCGCACCGGAAACGAGAGTGTGAAAGTGC	657
QY	2047	ATGAGAGAGAACCTTAAGCGCGGAGCGGTCTCCCGCGGAAAGCGGCGCTGTCTCAAGGCTCTCCG	2106
Db	658	ATGAGAGAGAACCTTAAGCGCGGAGCGGTCTCCCGCGGAAAGCGGCGCTGTCTCAAGGCTCTCCG	717
QY	2107	ACCCAAGTAGAGGTGTGAGAGGCGCGGCGCCGCGACAGGCGCCCAACCCCGAGGCGCCGCGC	2166
Db	718	ACCCAAGTAGAGGTGTGAGAGGCGCGGCGCCGCGACAGGCGCCCAACCCCGAGGCGCCGCGC	777
QY	2167	CCGAGGCTTAAGCGCGCGCGCGCTGCGCGAGGCCCTCACTGCGAAGCCCAAGCTTGCGCGC	2226
Db	778	CCGAGGCTTAAGCGCGCGCGCGCTGCGCGAGGCCCTCACTGCGAAGCCCAAGCTTGCGCGC	837
QY	2227	GCGTTTGGATTGACTGTGTCAACGCTTCGCGCGCGCTGTGTCCGACGCG	2270
Db	838	GCGTTTGGATTGACTGTGTCAACGCTTCGCGCGCGCTGTGTCCGACGCG	891

RESULT 2
 US-09-925-065A-566754
 ; Sequence 566754, Application US/09925065A
 ; Publication No. US20050228172A9
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Wang, David G.
 ;
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.115
 ; CURRENT APPLICATION NUMBER: US/09/925, 065A
 ; CURRENT FILING DATE: 2001-08-08


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? PRIOR APPLICATION NUMBER: US 60/243,096
? PRIOR FILING DATE: 2000-10-24
? PRIOR APPLICATION NUMBER: US 60/252,147
? PRIOR FILING DATE: 2000-11-20
? PRIOR APPLICATION NUMBER: US 60/250,092
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/261,766
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/289,846
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: fastseq for windows Version 4.0
? SEQ ID NO 566754
? LENGTH: 562
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-925-065A-566754

```

Query Match %	24.3%	Score 550.6	DB 4	Length 562
Best Local Similarity	99.6%	Pred. No. 1.4e-129		
Matches 561, Conservative	1	Mismatches 0	Indels 1	Gaps 1

OY		905	TTCCTCCTTCCCTTTCTTCTGCTCTTTCGTCTTGCTCTTCCCTCTCTCTCTGATTT	964
Dd		1	TTTTCTTCTTCTCTTCTTCTTCTTGTCTTGTCTTCTTCTCTCTCTCTCTCTT	60
OY		965	CTTTCCTCTCTTCTTCTTCTTCTCAATGGACAAGATCTCTCATGGACAAATAATC	102
Dd		61	CTTTCCTCTCTTCTTCTTCTTCTTAATGGCAAAGATCTCTCATGGACAATAATATC	120
OY		1025	TGCCTTAGCTTCTGTTTCCAGCGTGCCTCTGTGCGAAGACATGCGCTCGGCGTCTTCT	108
Dd		121	TGCCTTAGCTTCTGTTTCCAGCGTGCCTCTGTGCGAAGACATGCGCTCGG- GTGTTTCT	179
OY		1085	TTCCGCTTAATATTATCCAGGCCCATCCCAGCTGTGTCCTCCCTCACGTGTTCCCTGGACGT	1144
Dd		180	TTCCGCTTAATATTATCCAGGCCCATCCCAGCTGTGTCCTCCCTCACGTGTTCCCTGGACGT	239
OY		1145	CCCTTCTGCTGTGTA AAA CACA TATGCGCGCGCGGCTGACACAGGCTGTAA GTGTGAATA	1204
Dd		240	CCCTTCTGCTGTGTA AAA CACA TATGCGCGCGCGGCTGACACAGGCTGTAA GTGTGAATA	299
OY		1205	TCAGGAAGATGACTGAAGCTCTTTGGGACTCCGTTTCTCATTTGTA AATGGA GGTAA T	126
Dd		300	TCAGGAAGATGACTGAAGCTCTTTGGGACTCCGTTTCTCATTTGTA AATGGA GGTAA T	359
OY		1285	ACCAGCCCTTCTTCACTCCCCCAAGGACGCTGTTGTCCCGGCGAGA GGSGCCCA TTGTT	1332
Dd		360	ACCAGCCCTTCTTCACTCCCCCAAGGACGCTGTTGTGTCCCGGCGAGA GGSGCCCA TTGTT	419
OY		1325	GGCTGTTCACGCATCA GTTACCCCA CAGACGGGCTAGCCCA TTAAA AGGCGAACAGGC	1384
Dd		420	GGCTGTTCACGCRTCA GTTACCCCA CAGAGGGGCTAGCCCA TTAAA AGGCGAACAGGC	479
OY		1385	CCGGTCCATCTCTGACGCGCTTTTCTCATCCAGGGCTGGA CAGGCA GCTGSCCTTGAGCC	1444
Dd		480	CCGGTCCATCTCTGACGCGCTTTTCTCATCCAGGGCTGGA CAGGCA GCTGSCCTTGAGCC	539
OY		1445	CGGCTCTGCTTGTCA CGTCGGG	1467
Dd		540	CGGCTCTGCTTGTCA CGTCGGG	562

```

RESULT 3
US-09-925-065A-177131/C
; Sequence 177131, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108627.135
; CURRENT APPLICATION NUMBER: US/09/925.065A

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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177131
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-177131

```

Query Match 23.4%; Score 531.6; DB 4; Length 554;
Best Local Similarity 99.5%; Pred. No. 9.8e-125;
Matches 553; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY	1131	TGTTCCCTGGAGGACCCCTTCGTCGCGGTGAAGAAACAATATGGCGCGGCTGTACACAGGGTG	1190
Db	554	TGTTCCCTGGAGGACCCCTTCGTCGCGGTGAAGAAACAATATGGCGCGGCTGTACACAGGGTG	495
QY	1191	TAAGTGTGTGAATATCAGAGAAAGATGACTGAAACGTCCTTGGGACTCCGTTTCCATTTGTA	1250
Db	494	TAAGTGTGTGAATATCAGAGAAAGATGACTGAAACGTCCTTGGGACTCCGTTTCCATTTGTA	435
QY	1251	AAATGAGAGTTAATATCACAGCCTTCTTTACTCCCAACGCAAGTGTTTGTCCGGCCAG	1310
Db	434	AAATGAGAGTTAATATCACAGCCTTCTTTACTCCCAACGCAAGTGTTTGTCCGGCCAG	375
QY	1311	AGGGCCCAATGTGTGGCGTTCAAGCATCAGTTAACCACAGAGACGGGTGACGCAATTA	1370
Db	374	AGGG-CCAAATGTGTGGCGTTCAAGCATCAGTTAACCACAGAGACGGGTGACGCAATTA	316
QY	1371	AAGCGAACAACAGGCCCGGTCCATCTCCTGACGCGCTTTTCTTCATCCAGGGCTGACAGCG	1430
Db	315	AAGCGAACAACAGGCCCGGTCCATCTCCTGACGCGCTTTTCTTCATCCAGGGCTGACAGCG	256
QY	1431	AGCTGGCCTGGGCCCGGCTCTGCTTGTCACTGTGCGGGGGCCGGCCGTTTGTCTGTG	1490
Db	255	AGCTGGCCTGGGG-CCGGCTCTGCTTGTCACTGTGCGGGGGCCGGCCCGTTTGTCTGTGTG	197
QY	1491	TGTGTAGGAGAGGTAGGTCAACGTCGAGGAGTCGCCGCCCGCGGGGCTTTAGTGTCCCT	1550
Db	196	TGTGTAGGAGAGGTAGGTCAACGTCGAGGAGTCGCCGCCCGCGGGGCTTTAGTGTCCCT	137
QY	1551	GATCCCTTAAACGCAGAGCCGCTCCACCGGGGGAGAAAGCGCGAAACCCACGCCAGCCCAA	1610
Db	136	GATCCCTTAAACGCAGAGCCGCTCCACCGGGGGAGAAAGCGCGAAACCCACGCCAGCCCAA	77
QY	1611	CGGCTGTTGTGGTTGCCGGGCCAATCTGTGTGCAAGTCTGATTTGTTCTTCCCCGA	1670
Db	76	CGGCTGTTGTGGTTGCCGGGCCAATCTGTGTGCAAGTCTGATTTGTTCTTCCCCGA	17
QY	1671	CAACGCGGCGGCTGTA	1686
Db	16	CAACGCGGCGGCTGTA	1

RESULT 4
US-10-265-689-27
Sequence 27, Application US/10265689
Publication No. US2003011975A1
GENERAL INFORMATION:
APPLICANT: STRUTT, RICHARD S.
APPLICANT: COLLINS, SHEILA A.
APPLICANT: WARDEN, CRAIG H.
APPLICANT: SELDIN, MICHAEL F.

```

; APPLICANT: RICOUIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: "n" bases may be a, t, c, g, modified or unknown
US-10-265-689-27

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Query Match          19.7%; Score 447.4; DB 6; Length 1161;
Best Local Similarity 94.9%; Pred. No. 3.9e-103;
Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;

QY 1733 AGAGGCCAGCCGCGCTGCTCGCAGAGAGGAGTGTGTTGCTCCAGCGT--AGGGGGG 1790
DB 2  ANGAACACACCGGCGGTTCGTTCCGAGAGGTTGTTAGTTTCCAGAGGTTAAAGGGGG 61
QY 1791 CTGGGCCCATTAAGAGAGAGTGC-ACCTTAAGACACGCGCCCGCTGACGCTTTGTAA 1849
DB 62  CTGGGCCCATTAAGAGAGAGTGC-ACCTTAAGACACGCGCCCGCTGACGCTTTGTAA 121
QY 1850 ACCGCTCT--GGCTGGGAAGGCAAGAGGTGTGATCTGACAAAGCTTTCT--GGCGGT 1907
DB 122  ACTCTTCGGGTGTGGAAAGGCAAGAGGTGTGATCTGACAAAGTGTCTTCTGGCGGT 181
QY 1908 CAGTCTTGCATCTCTCACAAGAGTGTGCGGCCCGAGAGAGTGTGAGGACAGAGCGGGAG 1967
DB 182  CAGTCTTGCATCTCTCACAAGAGTGTGCGGCCCGAGAGAGTGTGAGGACAGAGCGGGAG 241
QY 1968 TGGCAAGGAGTGTACATCTCGGGGAACGAAGAGTAAACCGGTGATGGACGACGG- 2026
DB 242  TGGCAAGGAGTGTACATCTCGGGGAACGAAGAGTAAACCGGTGATGGACGACGCA 301
QY 2027 AAACGGAGGTGAGAAAGTCAATGAGAGAACCTTAGCGGGGGCGTCCCGCGGAAAGGC 2086
DB 302  AAACGGAGGTGAGAAAGTCAATGAGAGAACCTTAGCGGGGGCGTCCCGCGGAAAGGC 361
QY 2087 GACTGTCTCAGAGTCTCCGCAACCAAGTGAAGAGTGCAGAGCCCGCCCGCCGACAG 2146
DB 362  GACTGTCTCAGAGTCTCCGCAACCAAGTGAAGAGTGCAGAGCCCGCCCGCCGACAG 421
QY 2147 CCCCACCCCGGGGCCCGCCCGGAGGCTTAAAGCGCGCGCGCTGCGGAGGCCAC 2206
DB 422  CCCCACCCCGGGGCCCGCCCGGAGGCTTAAAGCGCGCGCGCTGCGGAGGCCAC 481
QY 2207 TGGCAAGCCAGCTGCGGCGCGCTTGGATTGACTGTCCAGCGCTCGCCGGCTGTCCGA 2266
DB 482  TGGCAAGCCAGCTGCGGCGCGCTTGGATTGACTGTCCAGCGCTCGCCGGCTGTCCGA 541
QY 2267 GCGG 2270
DB 542  GCGG 545

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RESULT 5
US-10-311-455-1865
; Sequence 1865, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander

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; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1865
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1865

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Query Match          16.0%; Score 364.2; DB 6; Length 5283;
Best Local Similarity 77.4%; Pred. No. 1.3e-81;
Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

QY 1668 GCACACGCGCGGCTGTAACATCGACAGACGAGCGGTCGCGAGCCCACTCCGC 1727
DB 2  CGATACGCGCGGCTGTAATTAATCATACGAGTCGATCGGAGGTTTATGTTTCGT 61
QY 1728 CTGCAAGAGCCAGCGCGCTGCTCGCAGAGAGGTGTGATTTGCCAGCGTAAAGG 1787
DB 62  TTGTAGAGATGTAGTCGCGGCTGCTGTAAGAGGCGGTGATTTGTTAGGTA-GG 120
QY 1788 GGGGTGGCCCATTAAGAGAGAGTGCATTAAGACACGCGCCCGCTGACGCTGTAG 1847
DB 121  GGGGTGGCTTATTAAGAGAGAGTGTATTAAGATACGCTTAAAG--TGAAGCTGTAG 178
QY 1848 AAACCGTCTGTGCTGAGAGCAAGAGTGTGATCTGACAAGACTTGTTCGCGGT 1907
DB 179  AAATCGTTTGTGTTGGAGAGTAAAGAGTGTGATTTGAATTAAGATTTGTTGGCGGT 238
QY 1908 CAGTCTTGCATCTCTCACAAGAGTGTGCGGCCCGAGAGAGTGTGAGCAAGCGGGAG 1967
DB 239  TAGTTTGTATTATTTTATAGAGTGTGCGGTTCAAGAGAGTGTGAGTAGAGCGGGAG 298
QY 1968 TGGCAAGGAGTGCATCTCGGGGAACGAAGAGTAAACCGGTGATGGACGACGGA 2027
DB 299  TGGTAAGGAGTGTATTTTCGGGGAAAGAAAGAGTAAACCGGTGATGGACGTAACGGA 358
QY 2028 AACGGAGTGAAGAAAGTCAATGAGAGAACCTTAGCGGGGGCGTCCCGCGAAGAGCG 2087
DB 359  AACGGAGTGAAGAAAGTCAATGAGAGAAATTTAGGCGGGGGCGTTCGCGAAGAGCG 418
QY 2088 GCTGTCTCAGAGTCTCCGCAACCAAGTGAAGCTGCAAGCGCGGCCCGCCCGACAGC 2147
DB 419  GTTGTTTAGGTTTGTGTTTGAATTAAGTGAAGTGTGTAAGTTCGTTTCGTTGAGGT 478
QY 2148 CCCCACCCCGGGGCCCGCCCGGAGGCTTAAAGCGCGCGCGCTGCGGAGGCCACT 2207
DB 479  TTTATTTTGGGTTCGTTTTCGAGGTTTAAAGTCGCGTGTGTTGCGGAGGTTTATTT 538
QY 2208 GCGAAGCCAGCTGCGCGCTTGGATTGACTGTCCAGCGTCCGCGGCTGTCCGAC 2267
DB 539  GCGAAGTTTACGTCGCGCGTTTGGATTGATTGTTTACGTTTCGTTCCGTTCCGTTGAC 598
QY 2268 GCG 2270
DB 599  GCG 601

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RESULT 6
US-10-311-455-1866/c

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; Sequence 1866, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; NUMBER OF SEQ ID NOS: 09-01
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1866

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```

Query Match      13.8%; Score 312.4; DB 6; Length 5283;
Best Local Similarity 72.0%; Pred. No. 2e-68;
Matches 435; Conservative 0; Mismatches 166; Indels 3; Gaps 2;

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QY 1667 CCGACACGCGGCGCTGTAACCAATCGACGAGCGCGGCTGCGAGGCCCGATCCG 1726
DB 5283 CCGACACGCGGCGCTGTAACCAATCGACGAGCGCGGCTGCGAGGCCCGATCCG 5224
QY 1727 CCTGCGAGGCGCGCGCGCTGCTGCGAGGCGGTGAGTTTCCCGAGGTAG 1786
DB 5223 CCTGCGAGGCGCGCGCGCTGCTGCGAGGCGGTGAGTTTCCCGAGGTAG 5165
QY 1787 GGGGCTGGGCGCTTAAAGAGAGTGCATTAAAGACGCGCGCGCTGAGCGCTTTTA 1846
DB 5164 AAAATTAACCATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5107
QY 1847 GAAACGCTGCTGCGGAGGCGAGGCGGTGCTGACCTGAGCAAGCTTTGTTGCGG 1906
DB 5106 AAAACGCTGCTGCGGAGGCGAGGCGGTGCTGACCTGAGCAAGCTTTGTTGCGG 5047
QY 1907 TCACTCTTGCATCTCTCAAGAGGTTGCGCGCGCGAGAGGTGTAGGCGAGCGGGA 1966
DB 5046 TCACTCTTGCATCTCTCAAGAGGTTGCGCGCGCGAGAGGTGTAGGCGAGCGGGA 4987
QY 1967 GTGGCAGGAGTGCATCTTGGGGAACGAAAGGTAAACCGGTGATGGAGCGACGG 2026
DB 4986 ATAAATTAACCATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4927
QY 2027 AAAACGAGTGAAGAGTCAATGAGAGAACCTTGGCGGCGGCGCGCGGCGGAGG 2086
DB 4926 AAAACGAGTGAAGAGTCAATGAGAGAACCTTGGCGGCGGCGCGGCGGAGG 4867
QY 2087 GCGTCTCAGGCTGCGCGACCAAGTGAAGTGTGCGAGCGCGCGCGCGCGCGAG 2146
DB 4866 GACTACTCAAAATCTCCGCGACCAAAATTAACCAAAATTAACCAAAATTAACCAAA 4807
QY 2147 CCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 2206
DB 4806 CCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 4747
QY 2207 TCGCAGGCGCGAGCTGCGCGCTTGGAGTGTGATCTGACGCTGCGCGCGCTGCG 2266
DB 4746 TACGAAACCACTACGCGCGCTTAAATTAATCACTACGCTGCGCGCGCTGCG 4687
QY 2267 CCGG 2270
DB 4686 CCGG 4683

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RESULT 7
US-10-301-832-11/c
; Sequence 11, Application US/10301832
; Publication No. US20040102390A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF NOTCH3 EXPRESSION
; FILE REFERENCE: RFS-0414
; CURRENT APPLICATION NUMBER: US/10/301,832
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 155
; SEQ ID NO 11
; LENGTH: 44348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-301-832-11

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```

Query Match      8.3%; Score 188.4; DB 7; Length 44348;
Best Local Similarity 63.7%; Pred. No. 2.2e-36;
Matches 354; Conservative 0; Mismatches 191; Indels 11; Gaps 4;

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QY 5 GATCTGCGCGCGCTGAGCGCTCCCAAGTGTGGAGTTGAGGCGTGAGCCACTCG 64
DB 12725 GATCTGCGCGCGCTGAGCGCTCCCAAGTGTGGAGTTGAGGCGTGAGCCACTCG 12666
QY 65 CTACAGTTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 121
DB 12665 CTGTTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 12606
QY 122 GACATCTTAATGACTTGAAGAGCTGTAATAATCAAGGTCAGCGCTTGTATGCTA 181
DB 12605 TGAGAACTATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12546
QY 182 TAGATTTGCTGATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 238
DB 12545 TAGATTTGCTGATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12486
QY 239 AGGACAGTGTGCTCAACCTGTAATTCAGTACTGTGAGAGTCCAGGTCAGAGACTGC 298
DB 12485 AGGACAGTGTGCTCAACCTGTAATTCAGTACTGTGAGAGTCCAGGTCAGAGACTGC 12426
QY 299 TTGAGCGCAGGAGTTCAAGAGCAGCTTGGAACAACAGGAGAGCTGTCACTAACA 358
DB 12425 TTGAGCGCAGGAGTTCAAGAGCAGCTTGGAACAACAGGAGAGCTGTCACTAACA 12366
QY 359 TAAATTAATTAAGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
DB 12365 TAAATTAATTAAGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12306
QY 419 AGTAGA-----CTGCTTGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGC 474
DB 12305 GGTGGAGAGTCACTTGAAGCCAGAGAGTCAAGAGTGAAGTGAAGTGAAGTGAAG 12247
QY 475 TGCAATTCAGCTTGGGCAACAAAGAGACCTGTCTCAAAATTAATTAATTAATTA 534
DB 12246 TGCAATTCAGCTTGGGCAACAAAGAGACCTGTCTCAAAATTAATTAATTAATTA 12187
QY 535 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 550
DB 12186 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12171

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RESULT 8
US-10-719-993-6827/c
; Sequence 6827, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARILLI, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```

FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719.993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 6827
LENGTH: 160556
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(160556)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6827

Query Match 7.7%; Score 175; DB 8; Length 160556;
Best Local Similarity 67.7%; Pred. No. 1e-32;
Matches 258; Conservative 2; Mismatches 117; Indels 4; Gaps 1;

Qy 216 ATTAAAGAAATTTCTTGAAGCCAGGACAGTGGCTCAGCTGTAAATTCAGTACTGTG 275
Db 30112 ATTCAAAATTAATATCTCAAGCCGGGTGCAATGCTCAATGCTTAATCTTGAACATTTG 30053
Qy 276 AGAGTCGAGGTCAAGAGACTGCTTGAAGCCAGAGATTCAAGAGAGCTGAGCAACA 335
Db 30052 GGAAGCCCAAGGACAGGTGATTACGTGAGTCAAGAGATTCAAGAGAGCTGAGCAACA 29993
Qy 336 GGGAGACCTGTCTACTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 395
Db 29992 GTGACACTGTCTACTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 29933
Qy 396 GTCCAGCTACTGAAGGAGGAGAGAGTGA-----CTGCTTGTCCAGAGAGTCAAGACTG 451
Db 29932 GTCCAGCTACTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 29873
Qy 452 CAGTGAAGTGAAGCCAGCCAGCTGTCAATTCAGCTGTGGGCAACAAAGAGAGAGCTGTCT 511
Db 29872 CAGTGAAGTGAAGTGAAGCCAGCCAGCTGTGGGCAACAGAGAGAGAGAGCTGTCT 29813
Qy 512 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 571
Db 29812 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 29753
Qy 572 TTCAAGAGAGACTCTTAAG 592
Db 29752 TGACAAAAATGTCTTAAG 29732

RESULT 9
US-09-764-878-231/c
Sequence 231, Application US/09764878
Patent No. US20020090615A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
PRIORITY FILING DATE: 2001-01-17
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 231
LENGTH: 11172
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-878-231

Query Match 7.6%; Score 172.8; DB 3; Length 11172;
Best Local Similarity 58.5%; Pred. No. 1e-32;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;
Qy 1 AACGATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGCAAGCGTGAAGCAACTTAC 60

Db 8630 AAGGATCCCGCTGCGCTTGGCCTCCCAAGTGTGAGATTACAGAGCATGAGCTACCCGAC 8571
Qy 61 CTGGCTCAAGTTTTCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db 8570 CTGGCTCCCGCTTAAAGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 8511
Qy 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATTCAGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 8510 AGGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8451
Qy 181 ATAGGATGCTCAGATCTGCCCGCCAGCTGAAAGATTTAAGAAATTTCTTGAAGCCAG 240
Db 8450 TCCCTCAGACAAAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8391
Qy 241 GCACAGTGGCTCAGACCTGTAAATTCAGTACTGTGAGAGTCCGAGTCAAGGAGCTGCT 300
Db 8390 GCACAGTGGCTCAGACCTGTAAATTCAGTACTGTGAGAGGAGGAGGAGGAGGAGGAGCT 8331
Qy 301 GAGGCCAGAGTTCAAGAGAGGCTGTGACACACAGGAGAG-CCTGTCACTACAAGAAAT 359
Db 8330 GAGGTCAAGAGTTCAAGAGAGGCTGTGACCAATTAATTAATTAATTAATTAATTAATTA 8271
Qy 360 AATTAATTAAGCCAGGCTTATGAGTCTATCCTGTGTCCAGTACTTGAAGAGGAGGAG 419
Db 8270 ACAAATTAAGCCAGGCGGTGTGTGCTTACACTGTATCTCCAGTACTTGAAGAGGAGCT 8211
Qy 420 GTAGACTGTGTGCTCCAGAGGAGTCA-AGAATGAGAGTGAAGTCAAGCCAGGAGCTGCA 478
Db 8210 ACAGAAATTTGCTGAACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8151
Qy 479 TTCCAGCTGTGGCAACAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 538
Db 8150 TCCAGCTTATGAGTGTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 8091
Qy 539 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 574
Db 8090 AAAAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8055

RESULT 10
US-10-079-854-231/c
Sequence 231, Application US/10079854
Publication No. US20030054368A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121C1
CURRENT APPLICATION NUMBER: US/10/079,854
PRIORITY FILING DATE: 2002-02-22
Prior application removed - See File Wrapper or PAM
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 231
LENGTH: 11172
TYPE: DNA
ORGANISM: Homo sapiens
US-10-079-854-231

Query Match 7.6%; Score 172.8; DB 5; Length 11172;
Best Local Similarity 58.5%; Pred. No. 1e-32;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

Qy 1 AACGATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGCAAGCGGAGGAGCACTTAC 60
Db 8630 AAGTATCCCGCTGCTTGGCTCCCAAGTGTGAGATTACAGGAGGAGGAGGAGGAGGAG 8571
Qy 61 CTGGCTCAAGTTTTCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db 8570 CTGGCTCCCGCTTAAAGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 8511
Qy 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATTCAGAGGAGGAGGAGGAGGAGGAGGAG 180

Db 8510 AGGACTAATTAATAGATATATTAATTAATTAATTTCTGTGTGTAATGAGACGCTT 8451
Qy 181 ATAGATTGCTCAGATCTGCCCCCAGCCCTGAAAGAAATTTAGAAATTTCTTGAGCCAG 240
Db 8450 TCCCTCAGACAAAGATGATTAATTTGGGTTTTCTTTTAAAGTGGAGCTGCGCAG 8391
Qy 241 GCACAGTGGCTCAGACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGAGACTGCTT 300
Db 8390 GCACAGTGGCTCAGACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGAGACTGCTT 8331
Qy 301 GAGGCCAGAGTTCAGAGCAGCTGTGACCAACAGAGGAGA-CCTGTCACTAACAAAGAT 359
Db 8330 GAGGTCAAGAGTTCAGAGCAGCTGTGACCAATATGTATAAACCCCATCTTACTTAAAT 8271
Qy 360 AATTAATTAAGCCGCTTAACTGTGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGCAGAA 419
Db 8270 ACAAATTAATTAAGCCGCTGCGGTGCGTACCTGTATGTCACAGTACTAGAGGAGCTGAG 8211
Qy 420 GTAGGACTGCTTGTCCAGAGAGTCA-AGACTGAGTGTGAGACCCAGCAGCTGCA 478
Db 8210 ACAAATTAATTAAGCCGCTGCGGTGCGTACCTGTATGTCACAGTACTAGAGGAGCTGAG 8151
Qy 479 TTCAGCTGTGCGCAAAAGAGAGCCTGTCTCAAAATTAATTAATTAATTAATTAATTA 538
Db 8150 TCCAGCTGTGCGTGTGAGCAGAGTGTGAGTCTATCTCAAAAAAATTAATTAATTAATTA 8091
Qy 539 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 574
Db 8090 AAAAAAGATGAGGAGCCATGACTTATTAATTAATTTGT 8055

RESULT 11

US-09-925-065A-770821/c
; Sequence 770821, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: US/09/925, 065A
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770821
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-770821

Query Match 7.4%; Score 168; DB 4; Length 563;
Best Local Similarity 74.6%; Pred. No. 4,1e-32;
Matches 252; Conservative 0; Mismatches 80; Indels 6; Gaps 3;

Qy 218 TTAAGAGATTTCTTGAAGCCAGGACAGTGTGCTCAGACCTGTATTTCCAGTACTGTGAG 277
Db 493 TTCAAGATATCTTGAAGCCAGGACAGTGTGCTCAGACCTGTATTTCCAGTACTGTGAG 434
Qy 278 AGTCCAGGTGAGAGTGTGCTTGAAGCCAGGACAGTGTGCTCAGACCTGTGAGAGCAGG 337
Db 433 AGTCAAGGTGAGTGTGCTTGAAGCCAGGACAGTGTGCTCAGACCTGTGAGAGCAGG 374
Qy 338 GAGACCTGTCACTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 397

Db 373 GAAACCTGTCTATTAATAAATACAAAAATTAAGCTGKGCATGTGTGAGCAGTCCGTAT 314
Qy 398 CCCAGCTACTAGGAGGACAGAGTGAAGTCTGTT-----CCGAGAGTCAAGACTGCA 453
Db 313 CCCAGCTACTAGGAGGCTGTGAGGAGAGTGAAGTCTGTTAAACCCGAGGAGGAGTGTCA 254
Qy 454 GTGAGTGAAGCCAGGACCTGCACTTCCAGCTGTGAGGACAAAGAGAGCCTGTCTC- 512
Db 253 GTGAGTGAAGTGTGCGCA-TTGACCAACAGCTGTGAGTGTGAGAGAGAGTGTCTCA 195
Qy 513 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 550
Db 194 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 157

RESULT 12

US-10-723-860-2320/c
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nabeela
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882, 0193, NPUS01
; CURRENT FILING DATE: US/10/723, 860
; PRIOR APPLICATION NUMBER: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

Query Match 7.4%; Score 167.2; DB 8; Length 135005;
Best Local Similarity 80.3%; Pred. No. 9.3e-33;
Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

Qy 235 GGCAGGACAGTGTGCTCAGACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGGAG 294
Db 84840 GGCAGGACAGTGTGCTCAGACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGGAG 84781
Qy 295 CTGCTGAGGCGCAGAGTTCAGAGCAGCTGTGACCAACAGGAGGAG--CCTGTCACTAC 352
Db 84780 TTGCTTGAAGGCGCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAG 84721
Qy 353 AAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412
Db 84720 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 84661
Qy 413 GGCAGAGTGAAGTCTGTTG-TCCAGAGGTTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 471
Db 84660 GGCAGAGTGAAGTCTGTTG-TCCAGAGGTTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 84601
Qy 472 ACTGATTCAGGCTGCGGCAACAAAGAGAGCCTGTCTCAAAAAATTA 521
Db 84600 A-CTGTACTCAACCTGTGCGGCAACAGAGAGCCTGTCTCAAAAAATTA 84552

RESULT 13

US-10-756-149-1719/c
; Sequence 1719, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nabeela
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1719
LENGTH: 135005
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-756-149-1719

Query Match 7.4%; Score 167.2; DB 9; Length 135005;
Best Local Similarity 80.3%; Pred. No. 9.3e-31;
Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

Qy 235 GGCCAGGACAGTGGCTCAGACCTGTATATCCAGTACTGTGAGAGTCCGAGGTACAGAGA 294
Db 84840 GGCTGACACAGTGGCTCAGCTCTGTATATCTCAGACTTTGGAGGCGAGGTAGAGAGA 84781
Qy 295 CTGCTTGAAGCCAGAGTTCAGAGCAGCCTTGACCAACACAGGAGA--CCTGTCACTAC 352
Db 84780 TTGCTTGAAGGCGAGAGTTCAAGACTATCTGGGCAACATAGTGAACCCCTGTCTTAC 84721
Qy 353 AAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 412
Db 84720 AAAAAATGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 84661
Qy 413 GCGAAGATAGAGTCTGCTTG--TCCAGAGAGGTCAAGACTGAGTGAAGTCCAGACC 471
Db 84660 GGCTGAGTATGAGTTGCTTGAAGTCAAGAGGTCCAGGCGGAGTGAAGTGAACAGTCC 84601
Qy 472 ACTGCATTCCAGCTGGGCAACAAAAGAGACCTGTCTCAAAAATAA 521
Db 84600 A-CTGTACTCCAACTGGGCAACAGAACAGACCTGTCTCAAAAAA 84552

RESULT 14
US-10-027-632-115210/c
Sequence 115210, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 115210
LENGTH: 3030
TYPE: DNA
ORGANISM: Human
US-10-027-632-115210

Query Match 7.3%; Score 166.8; DB 5; Length 3030;
Best Local Similarity 61.8%; Pred. No. 1.9e-31;
Matches 336; Conservative 0; Mismatches 197; Indels 11; Gaps 4;

Qy 1 AACGATCTGCCCGCTCAGCTCCCAAGAGTGTGAGATTGACAGGCTGAGCCACTTAC 60
Db 2458 AAGGATCTTCTGGCTCAGCTCAGCAAAATGCTGAGATTACAGAGTGTGATCAGAC 2399
Qy 61 CTGCTTCAAGTTTCAAAATATATTATCTAGTACCAATTCATTCAGTTTGTCCAC 120
Db 2398 CTGCCCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2339
Qy 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATCCAGAGGTGAGAGCTTTGATGTCT 180
Db 2338 GACAAAGCCACATGATGATCTTCAAGTTTATTAAGTTTATATGTAATTTCTTAATGT 2279
Qy 181 ATAGGATGCTCAGATGTGCCCACTGAA-----AGATTTAAGAAATTTCTTGA 234
Db 2278 AAGAAATGAATACAGATCTCTGAGCTGATTTTCAATTAATTAATTAATTAATTAATTA 2219
Qy 235 GGCCAGGACAGTGGCTCAGACCTGTATATCCAGTACTGTGAGAGTCCGAGGTACAGAGA 294
Db 2218 GGCTGACACAGTGGCTCAGCTCTGTATATTCAGACTTTAAGAGGCGAAGGTGAGAGA 2159
Qy 295 CTGCTTGAAGCCAGAGTTCAGAGCAGCCTTGACCAACACAGGAGAC--TGTCACTA 351
Db 2158 TGGTTGGGCGCAGAGTTTGAACACAGCCTTGAGCAACCTTAGTAGAGCCCGTTTCA 2099
Qy 352 CAAAGAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 411
Db 2098 AAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2039
Qy 412 AGGAGAAATGAAGTCTGCTTG--TCCAGAGAGTCAAGACTGAGTGAAGTCCAGCCAGC 470
Db 2038 AGGAGAGTGAATTCATCTGAGGCCAGAGTTTGAAGCTGAGAGTGAATGATCTGT 1979
Qy 471 CACCTGATTCCAGCTGGGCAACAAAAGAGACCTGTCTCAAAAATAATTAATTA 530
Db 1978 CA-CTGACTCCAGCTGGGCAACAGAGTGAATTCCTGTCTCAAAAAAAGGTCTTA 1920
Qy 531 ATAA 534
Db 1919 AAAA 1916

RESULT 15
US-10-027-632-115211/c
Sequence 115211, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 115211
LENGTH: 3030
TYPE: DNA
ORGANISM: Human
US-10-027-632-115211

Query Match 7.3%; Score 166.8; DB 5; Length 3030;
 Best Local Similarity 61.8%; Pred No. 1.9e-31;
 Matches 336; Conservative 0; Mismatches 197; Indels 11; Gaps 4;

QY	1	AACGATCTGCCCGCTCAGCCCTCCCAAAGTGTGGATTGCAAGGCTGAGGCACTTCAC	60
DB	2458	AAGCATCTTCCTGCTCAGCTTACCAAAATGCTGAGTTACAGGTGTAATCACAGCAC	2399
QY	61	CTGGCTACAGTTTCAAAATATCTTATCTAGTACCATATCTCCAGTTTGTCCAC	120
DB	2398	CTGGCCCTTAATTAATCTTTTGAATTATGTTTCTTGAAGTACCTCTTTCTAA	2339
QY	121	AGGACATCTTATGATTTGAGCAAGCTGCTAAATCAAGGGTGCAAGGTTTGTATCT	180
DB	2338	GACAAAGCCACATGATCTTCAGTTTATTAAGTTTATATATGTAATCTTTATATGT	2279
QY	181	ATAGATTGCTCAGATCTGCCCCCACTGAA-----AGATTTAAGAAATTTCTTGA	234
DB	2278	AAAGAAATGATATGATTTCTTGAGCTTGATTTTCCATATCATATTAAGCTTGA	2219
QY	235	GGCCAGGCAAGTGGCTCACACTGTAAATTCAGTATGTGAGAGTCCGAGGTCAAGGA	294
DB	2218	GGCTAGGCAAGTGGCTCATGCTTGTAAATTCAGCACTTTAGAGGCCAAGGTGGAAGA	2159
QY	295	CTGCTTAGGCGCAGGATTCAAGAGCAGCTGGAACAACAAGGAGACC---TGTCACTA	351
DB	2158	TGTTTGGGGCCAGAGTTTGAGACCAAGCTGGCAACTGATGAGACCCCGTTCCACA	2099
QY	352	CAAGAATTAATTAATTAAGCCAGGCTTAGTGGCTCATCCCTGTGCTCCAGCTACTAGGG	411
DB	2098	AAATTTTATTAATTAAGTGGGATGAGTGAATGCTGTGCTCACTACTTGGG	2039
QY	412	AGGCAGAGTGAAGTCTGTG-TCCGAGAGGTCAAGACTGCACTGAGCTGAGACCCAGC	470
DB	2038	AGGCAGAGTGAATCACTTGAGCCCAAGATTGAGGCTGCATGAGCTATGATCGTGT	1979
QY	471	CACCTGCAATTCAGGCTGGGCAAAAGAGACCCCTGCTCAAAAAATTAAGTTAAATA	530
DB	1978	CA-CTGCACTCCAGCCTGGGCAACAGTAAAGATCCTGTCTCAAAAAAAGGTCTTA	1920
QY	531	ATAA 534	
DB	1919	AAAA 1916	

Search completed: December 21, 2005, 23:57:45
 Job time : 1640 secs

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	8, Appl
06, App	
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3361, A	
3362, A	
3402, A	
3461, A	
75, App	
3359, A	
1, Appl	
3461, A	
, Appl1	
33278, A	
33262, A	
33231, A	
33365, A	
33244, A	
44, Appl	
3422, A	
339, A	
3318, A	
33318, A	
3476, A	
3198, A	
2, Appl	
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aps	3,
GGCTC	252
GGCTC	1348
GAGT	312
GAGT	1400
TGAC	371
TGAC	1466
GGCTT	431
GGTTG	1522
GGCTT	487
GGCTT	158
TATAG	547

Db 1588 GGGTGAAGGAGGAGGATCTCTCAATAATAATAATAATAATAATAATAATAATA 1647
Qy 548 TTTAAACCTTAA 559
Db 1648 TTTAATCGCCAA 1659

RESULT 2

US-11-121-086-58
Sequence 58, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 58
LENGTH: 180654
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-58

Query Match 7.3%; Score 165.2; DB 7; Length 180654;
Best Local Similarity 70.7%; Pred. No. 4.7e-20;
Matches 263; Conservative 0; Mismatches 103; Indels 6; Gaps 3;

Qy 193 AGATCTGCCCCACCCCTGAAGAATTAAAGAATTCTTGAGGCGCAGCAAGTGCTC 252
Db 161439 ATATTGTCTCTTGCAAACTCATGTGAAATTTAATCCCAAGCCGCGCACAAGTGCTC 161498
Qy 253 ACACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGCGCAGAGT 312
Db 161499 ACGCTGTAAATCCAGCATTTTGGAGAGCCGAGGCGGAGATCACTGAGGTCAAGAGT 161558
Qy 313 TCAAGAGCAGCTTGAGCAACACAGGAGAG-CCTGTCACTCAAAAGATTAATAATTAGC 371
Db 161559 TCAAGAGCAGCTTGAGCAACAGTGGAAACCCCATCTCTCAAAAATACAAAATTAGC 161618
Qy 372 CAGGCTTAAAGTCTCATCCTGTGTGCTCCAGTACTAGGAGGAGAGTGAAGTGAAGTCTT 431
Db 161619 CGGGCTGTGTGACACACCCCTGTGATCCAGTACTCGAAAGCTGAGGCGAGAGAGTTG 161678
Qy 432 GT---CCAGAGAGTCAAGACTGAGTGAAGCTGAGCCAGCCACTGCAATTCAGGCT 487
Db 161679 CTGAGCCTGGAGGAGCAGAGTTCAGTGAAGCCAGATCGTGCCA-CTGCACTCGAGCT 161737
Qy 488 GGGCAACAAAAGAGACCTCTGTCTCAAAAATAAGTTAAATTAATTAATAATAATAATAG 547
Db 161738 GGGTGAACAAAGCAGATTTCTGTCTCAATAATAATAATAATAATAATAATAATAA 161797
Qy 548 TTTAAACCTTAA 559
Db 161798 TTTAATCGCCAA 161809

RESULT 3

US-10-995-561-13237/c
Sequence 13237, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13237
LENGTH: 87672
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-13237

Query Match 7.1%; Score 160.4; DB 6; Length 87672;
Best Local Similarity 70.6%; Pred. No. 2.9e-19;
Matches 243; Conservative 0; Mismatches 96; Indels 5; Gaps 2;

Qy 225 AATTCTTGAAGCCAGGACAGAGTGGCTACACCTGTAATTCAGTACTGTGAGAGTCCGA 284
Db 36715 AAGACCTTCGGCTGGGACAGATGGCTCAAGCCTGTAAATCCAGCACTTTGGAGGCGAA 36656
Qy 285 GGTCAAGAGACTGTTTGAAGCCAGAGATTCAAGAGCAGCTTGACAAACAGAGGAGACT 344
Db 36655 AGTGGTGGATCACTTGAAGTCAAGAGTTTCAAGACCACTTGGCCAAACAGCGAAACCC 36596
Qy 345 GTCACTCAAAAGATTAATAATTAGCAGGCTTAAAGTCAATCCCTGTGTCCAGCT 404
Db 36595 ATTCTACTAAAAACAAAAATTAGCAGGAGGAGTGTGACACAGCTGTAGTCCAGCT 36536
Qy 405 ACTAGGAGCAGCAAGTGAAGTGTCTGT-----CCAGAGAGTCAAGACTGCAAGTGAAGT 460
Db 36535 ACTGGAGAGCTGAGGAGAGAGATTCCTTGAACCCAGAGTGTGAGAGTTCCAGTGAAGT 36476
Qy 461 GAGACCCAGCCACTGCATTCAGGCTGGGCAACAAAAGAGCCTGTCTCAAAAATA 520
Db 36475 GAGATGTGCGCA-CTGTACTCCAGCCCTGGCGACAGAGCAAGTCCATCTCAAAAAAT 36417
Qy 521 AGTTAAATTAATAATAATAATAATAATAAGTTTAAACCTTAACACA 564
Db 36416 AAATTAATAATAATAATAATAATAAGACCTTCTTCTTAAGGTCA 36373

RESULT 4

US-11-112-908-56
Sequence 56, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PatentIn version 3.3
SEQ ID NO 56
LENGTH: 150468
TYPE: DNA
ORGANISM: Homo sapiens
US-11-112-908-56

Query Match 7.0%; Score 159.8; DB 7; Length 150468;
Best Local Similarity 75.4%; Pred. No. 3.9e-19;
Matches 239; Conservative 0; Mismatches 72; Indels 6; Gaps 3;

Qy 235 GGGCAGGACAGTGGCTCAACCTGTAAATTCAGTACTGTGAGAGTCCAGAGTCAAGGA 294
Db 9823 GGGCAGGACAGTGGCTCAACCTGTAAATTCAGTACTGTGAGAGTCCAGAGTGGAGGA 9882

us-09-869-098a-1_copy_1_2270.rnpbn

```

Sequence 55,Application US/11112908
Publication No. US2005026059A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIORITY APPLICATION NUMBER: US 60/564,758
PRIORITY FILING DATE: 2004-04-23
PRIORITY APPLICATION NUMBER: US 60/575,978
PRIORITY FILING DATE: 2004-06-01
PRIORITY APPLICATION NUMBER: US 60/631,702
PRIORITY FILING DATE: 2004-11-30
PRIORITY APPLICATION NUMBER: US 60/633,826
PRIORITY FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PatentIn version 3.3

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55

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	Query Match	Best Local Similarity	7.0%;	Score 159.8;	DB 7;	Length 193789;
	Matches 233;	Conservative	0;	Mismatches 72;	Indels	Gaps 3;
QY	235	GGCACGACACAGTGGCTCAACCTGTAATTCAGTACTGTGAGAGTCGAGGTCAGAGGA				294
Db	60008	GGCCAGGCACAGTGGCTCAACGCTGTGATCCAGACACTTTGGAGAGCCAAAGTGGGTGGA				60067
QY	295	CTGCTTGAGGCCAGAGGTTCAAGAGAGGCTTGGAACAACAGAGGAGA-CCGTCTCACTACA				353
Db	60068	TCACTTTAAGTCCAGAGTCCGAGACCAAGCTCTACCAACATGGTGAATCCCAATCTCTACT				60127
QY	354	AAGAAATAAATAATTGAGCAGGCTTGATGGCTCATCTCCCTGTGGTCCAGACTACTAGGAG				413
Db	60128	AAAAAATACAAAATTGACCAAGCGGTGGTGGCGCATGCTGTAAATCCAGACTACTGGGAG				60187

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60188 ACTGACCGTAGGAGATCTCTGAAACCAGGAGGTCGACGTGACGTGAGATTCGG 60247

[illegible]

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00: 520 AATTAAATTTAAATTTAA 546
DD 60248 CCA-C1GCA11C1CA1CC1GCGCAACGACGCGAC1C1G1C1C1AAAAAA1AA1AA1AA1AA 80350
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50307 TAAATTAATTAATTAAGA 50323

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RESULT 7
US-10-995-561-13262

Sequence 13262, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

FILE REFERENCE: CL001559

:
 : CURRENT APPLICATION NUMBER: 05/10/995,561
 :
 : CURRENT FILING DATE: 2004-11-24
 :
 : ATTENDED OR CTO TO VOC OFFIC

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; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12263

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; ORGANISM: Homo sapiens
;
; FEATURE:

```

NAME/KEY: misc_feature
 LOCATION: (11...141121)
 OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
 US-10-995-561-13262

Query Match 7.0%; Score 159; DB 6; Length 141121;
 Best Local Similarity 71.4%; Pred. No. 5.3e-19;

Matches 252; Conservative 0; Mismatches 95; Indels 6; Gaps 3;

QY 191 TCAGATCTGCCCCCACTGTAAGATTTTAAAGATTTCTTGAAGGCAAGGACAGTGGC 250
 DB 10586 TGAGACCTCTGCTCTTCAAAAAATTAATAATTAATAATGAAGGCCAGTTAGTGGC 10645
 QY 251 TCACACCTGTAATTCAGATCTGTGAAGTCCGAGGCTGAGAGCTCTGAGGCCAGA 310
 DB 10646 TCACACCTGTAATCTAGTACTTTGGAGGCTGAGGAGTGGATGCTGAGCTCAGGA 10705
 QY 311 GTTCAAGACGCTTGACCAACACAGGAGG-CTGTCACTCAAAAGATTAATAATTA 369
 DB 10706 GTTCAAGACGCTTGAGCAACATGTTGAAACCCCATCTTATTAATACTCAAAAAATTA 10765
 QY 370 GCCAGGCTTAGTGTGCTCATCCCTGTGCTCCAGCTACTAGGAGGCAAGATAGA---- 425
 DB 10766 GCCAGGATGTGTGACGCTGTAGTCCAGCTACTCAGAGGCTGAAAGTGGAGAT 10825
 QY 426 CTGCTTGTCCAGAGGTTCAAGACTGCAGTGAGTGAAGCCAGCCACTGCAATTCCAGC 485
 DB 10826 CGCTGGAATCAGAGGTTGAGGTTGCAGTGAGCTGAGATCAGGCCA-CTACACTCCAGC 10884
 QY 486 CTGGGCAACAAAAGACCTCTCTCAAAAAATTAAGTTAATAATTAATAATA 538
 DB 10885 ATGGGCAACAGATGAGACTGTCTCTCAATAATAATAATAATAATAATA 10937

RESULT 8

US-11-121-086-30/c

Sequence 30, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138, 6000-00000

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3

SEQ ID NO 30

LENGTH: 158692

TYPE: DNA

ORGANISM: Homo sapiens

US-11-121-086-30

Query Match 7.0%; Score 158.6; DB 7; Length 158692;
 Best Local Similarity 74.9%; Pred. No. 6.3e-19;

Matches 239; Conservative 0; Mismatches 74; Indels 6; Gaps 3;

QY 233 GAGGCCAGGCACTGTGCTCACCTGTATTTCCAGTACTGTGAGAGTCCAGGTCAGAG 292
 DB 155468 GAGGCCAGGCACTGTGCTCACCTGTATTTCCAGGCACTTTGGAGGCAAGGTTAGGCG 155209
 QY 293 GACTGCTTGAAGGAGAGTTCAGAGAGGCTGAGCAACAGAGGAGA-CCTGTCACTA 351
 DB 155208 GACTGCTTGAAGGAGAGTTCAGAGAGGCTGAGCAACAGGAGAGAGGAGAGGAGG 155149
 QY 352 CAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 411
 DB 155148 CAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 155089
 QY 412 AGGCAAGTGAAGTGTGTGT-----CCAGAGGTCAAGCTGCAAGTGAAGTGAAGCC 467

DB 155088 AGGCTGAGGTGGAGAGCTGCTTGAAGCCAGAGGCTGCAAGTGAAGTGAATCG 155029
 QY 468 AGCCACCTGATTCAGAGCTGGGCAACAAAAGAGCCCTGTCTCAAAAAATTAATTA 527
 DB 155028 CACC-CCTGCACTCCAGCTGATGATGACATTTGACACACTGCTCTCAAAAAA 154970
 QY 528 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 546
 DB 154969 AAAAAAAGAAAAGAAAA 154951

RESULT 9

US-11-112-908-45

Sequence 45, Application US/11112908

Publication No. US20050260659A1

GENERAL INFORMATION:

APPLICANT: Hattie, Cole

APPLICANT: David, Lisa M.

TITLE OF INVENTION: Breast Cancer Biomarkers

FILE REFERENCE: 04-164-US

CURRENT FILING DATE: 2005-04-22

PRIOR APPLICATION NUMBER: US 60/564,758

PRIOR FILING DATE: 2004-04-23

PRIOR APPLICATION NUMBER: US 60/575,978

PRIOR FILING DATE: 2004-06-01

PRIOR APPLICATION NUMBER: US 60/631,702

PRIOR FILING DATE: 2004-11-30

PRIOR APPLICATION NUMBER: US 60/633,826

PRIOR FILING DATE: 2004-12-07

NUMBER OF SEQ ID NOS: 511

SOFTWARE: PatentIn version 3.3

SEQ ID NO 45

LENGTH: 182314

TYPE: DNA

ORGANISM: Homo sapiens

US-11-112-908-45

Query Match 7.0%; Score 158.2; DB 7; Length 182314;
 Best Local Similarity 69.7%; Pred. No. 7.5e-19;

Matches 260; Conservative 0; Mismatches 103; Indels 10; Gaps 3;

QY 227 TTCTTGAAGCCAGGCAAGTGTCTCACCTGTATTTCCAGTACTGTGAGAGTCCAGG 286
 DB 20121 TTCTTGAAGCCAGGCAAGTGTCTCACCTGTATTTCCAGGCACTTTGGAGAGTGAAG 20180
 QY 287 TCAGAGAGCTGCTTGAAGCCAGGAGTTCAGAGAGGCTGAGCAACAGAGGAGAC---- 342
 DB 20181 TCAGAGAGCTGCTTGAAGCCAGGAGTTCAGAGAGGCTGAGCAACAGAGGAGACCTTG 20240
 QY 343 -CTGTCACTCAAAAGATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 401
 DB 20241 TCTCTCAAAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 20300
 QY 402 GCTACTAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 457
 DB 20301 GCTACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20360
 QY 458 GCTGAGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 517
 DB 20361 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20419
 QY 518 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 577
 DB 20420 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 20479
 QY 578 AGAGAGCTTTTA 590
 DB 20480 TGAGAGAGCTTGA 20492

RESULT 10
 US-11-121-086-72/c

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Sequence 72, Application US/11121086
Publication No. US2005026459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 72
LENGTH: 162173
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-72

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Query Match	6.9%;	Score 157.4;	DB 7;	Length.162173;
Best Local Similarity	69.6%;	Pred. No. 1e-18;		
Matches 243;	Conservative 0;	Mismatches 101;	Indels 5;	Gaps 2;

OY	217	TTTAAGAGAATTCCTTGGAGCCGAGGCACAGTGCGCTCAACACTGTAAATTCCAGAACCTGTGA	276
Db	100622	TATAAATAATAGTAGAGTGGCTGGGSCATGGGGGCTCACACTGTAAATCCACGACACTTTGG	100563
OY	277	GAGTCGAGGTCAGAGNACTGCTGTGAGGCCACGAGGTTCAAAGCAGCCTGGACAACAGC	336
Db	100562	GAGGCCAAGGCGGGGACAGATCACCTGAGGTCAGGAGTTCAAAGACCAACTGGCCAAACTAG	100503
OY	337	GGAGACTGTCTCACTACAAAGAAATAAATAATTAGCAGGCTTAGTGGCTTCATCCCTGTGG	396
Db	100502	TGAANAACGTCTCTACTAAAAATACAAAATTATAGCCGACATGTGGCGCATCTGTAA	100443
OY	397	TCCCAGCTACTAGGAGGAGGACAAAGTAGAGCTGTTGT-----CCCAAGAGTCAAAGACTGC	452
Db	100442	TCCCAGCTACTTAGGAGGCGTGAATGCGAGAAATTGTTGNAACCCAGAGGTGACACTTAC	100383
OY	453	AGTAGCTGAGACCACGACCGTCATTCOCAGCTGGGCAACAAAAGAGACCCCTGTCTC	512
Db	100382	AGTAGGCCCAAGATTGTGCCA-CTGCAATTCTAGCTGGGCGAATAGACTGAGACTCCCGTTGC	100324
OY	513	AAAAAATAAGTTAAATTAATAATAATAAATAATAGTTAAACCCCTAATC	561
Db	100323	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATGAGATAGCTTCTTGAAAC	100275

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RESULT 11
US-11-159-597-20/c
; Sequence 20, Application US/11159597
; Publication No. US20050255559A1
; GENERAL INFORMATION:
; APPLICANT: Uebele, Victor N.
; APPLICANT: Swanson, Richard J.
; APPLICANT: Liu, Yuan
; APPLICANT: Lagutka, Armando
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM SENSITIVE POTASSIUM
; TITLE OF INVENTION: CHANNEL
; FILE REFERENCE: 20499P
; CURRENT APPLICATION NUMBER: US/11/159,597
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/031,691
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/19585
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/144,764
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48000
; TYPE: DNA
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(48000)
; OTHER INFORMATION: n = A,T,C or G
US-11-159-597-20..

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Query Match	6.9%	Score 157.2;	DB 7;	Length 48000;
Best Local Similarity	67.3%	Pred. No. 9.5e-19;		
Matches 253; Conservative	0;	Mismatches 118;	Indels 5;	Gaps 2;

[illegible]

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RESULT 12
US-11-121-086-49
; Sequence 49, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11,121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 159146
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-49

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	Query Match	Best Local Similarity	Score	DB 7	length
Matches	274	Conservative	6.94	69.24	159146
				0	1.1e-18
				Mismatches	113
				Indels	9
				Gaps	4
Qy	211	AAABAATTAGAGAAATTTCTTGAGGCGACAGCGTGCACACCTGTAATTCACAGA	270		
Db	104462	AATTATTTTCAGATTTAAAGTTGAGCGCGGCTCAGTGGCTCACCTGTATTCACAGA	104521		
Qy	271	CTGTGAGAGTCCGAGGCTCAGAGGACTGCTTTGAGGCGACAGATTCMAAGACGCTTGGACA	330		
Db	104522	CTTGTGTAGACCGGAGGTGGGACAGATCACCTTAGAGTTCAGAGATTCAGAGACCTGGGCA	104581		

QY 331 ACA-CAGGAGAGCTGTCTACTACAAAGATAATTAATTAGCCAGGCTTGTGCTCATC 389
| | | | |
Db 104582 ACATGATGAAACCCCGTCTCTACTATAAAATACAAAATATACAGGCAATGTGGCGACA 104641
| | | | |
QY 390 CCGTGGCCAGCTACTAGGAGGAGGAGTAAGA----CTGCTGTGCCAGAGAGTCA 445
| | | | |
Db 104642 CCGTAATCCAGCTACTCTGTAGGCTAGGCGAGAGATCTTTAAACCAAGAGGTGG 104701
| | | | |
QY 446 AGACTGAGTGAAGTGAAGCCAGCCAGCTGCTATCCAGCTGGGCAACAAAAGAGACC 505
| | | | |
Db 104702 AGGTTGAGTGAAGCAAGATGGCGCA-CTGCACCCCGCTGGGCAACAAAGTAGACT 104760
| | | | |
QY 506 CTGTCTCAAAAATAATAGTTAATAA---TAAATATAAATAATGTTTAAACCTTAACA 562
| | | | |
Db 104761 CTGTCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 104820
| | | | |
QY 563 CATCTCTTTTCAAGAGACTCTTAAAGACTTC 598
| | | | |
Db 104821 CAGCTAACCTTCCAGAGAACTTCTGCCAGAAATTC 104856
| | | | |

RESULT 13

US-11-121-086-13
; Sequence 13, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138, 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 191797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-13

Query Match 6.9%; Score 156.8; DB 7; Length 191797;
Best Local Similarity 70.4%; Pred. No. 1.3e-18;
Matches 259; Conservative 0; Mismatches 92; Indels 17; Gaps 3;

QY 211 AAAGATTAAAGAAATTTCTTGAAGCCAGGCAAGTGGCTCAACCTGTAATTCAGTA 270
| | | | |
Db 127850 AAGTAAGTAAGAAAGAAAGTTTAAGGCTGGGCTGATGGCTCAAGCTGTAAATCCAGCA 127909
| | | | |
QY 271 CTGTGAGAGTCCAGAGTGAAGAGCTGCTTGAAGCCAGAGTTCAAGAGACCTGAGCA 330
| | | | |
Db 127910 CTTTGGGAGGCTGAGATGGGTGAATPACTTGAAGATGAAGAGTTCAAGCCAGCTGGCCA 127969
| | | | |
QY 331 ACAAGGAGAGCTGTCTACTACAAAGATAAATA-----AATTAGCCAGGCTT 378
| | | | |
Db 127970 ACATGGTGAATCTGTCTCTACTATAAATAAATAAATAAATAAATAAATAAATAAATA 128029
| | | | |
QY 379 AGTGGCTATCCCGTGGTGGCTCCAGCTACTAGGAGGAGGAGTGAAGG-----CTGCTTCTC 434
| | | | |
Db 128030 GGTGGTTACACCTGTAAATCCAGCTACCCGGAGGCTGAAGGTGAAGAAATCAAGTTGAAC 128089
| | | | |
QY 435 CCAAGAGTCAAGACTGAGAGTGAAGCTGAGACCCAGCCAGCTGCAATTCAGGCTGGGCAAC 494
| | | | |
Db 128090 CCAAGAGTGAAGGTTGAGTGAAGCTGAGATCAAGCCA-CTGCACCTCAAGCTGGGCAAC 128148
| | | | |
QY 495 AAAAAGAGACCTGTCTCAAAAATAATAGTTAATAATTAATTAATTAATTAATTAATTAAT 554
| | | | |
Db 128149 AAGGTGAACCTCAATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 128208
| | | | |
QY 555 CCTAACA 562
| | | | |
Db 128209 TCTTATCA 128216
| | | | |

RESULT 14

US-11-121-086-9/c
; Sequence 9, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138, 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 196200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-9

Query Match 6.9%; Score 156; DB 7; Length 196200;
Best Local Similarity 70.4%; Pred. No. 1.8e-18;
Matches 252; Conservative 0; Mismatches 100; Indels 6; Gaps 3;

QY 212 AAGAATTAAAGAAATTTCTTGAAGCCAGGCAAGTGGCTCAACCTGTAATTCAGTAC 271
| | | | |
Db 53744 ATGATTTAAATAAATTAACCTGAGGAGCCAGACATGTGGCTCAATGCTGTAAATCCAGCAC 53685
| | | | |
QY 272 TGTGAGAGTCCAGAGTGAAGAGCTGCTTGAAGCCAGAGTTCAAGAGACCTGAGCAA 331
| | | | |
Db 53684 TTGGAGAGCTGAGTGGGCGATCACTTGAAGTCAAGAGTTCAAGCCAGCTGGCCAA 53625
| | | | |
QY 332 CACAGGAGAG-CTGTCTACTACAAAGATAAATAATTAATTAATTAATTAATTAATTAATTA 390
| | | | |
Db 53624 CATGTGAACCCCTGTCTCTAATAAATAATCAAAATAATCAAGACATGGTGGCGCATGC 53565
| | | | |
QY 391 CTGTGTCCAGCTACTAGGAGGAGAGTAAGA-----CTGCTGTCCAGAGAGTCAA 446
| | | | |
Db 53564 CTAGAGTCCAGCTACTTGGAGGCTGAGGAGAGTAATGCTTGAACCCCGAGAGTGAA 53505
| | | | |
QY 447 GACTGAGTGAAGTGAAGCCAGCCAGCTGCAATTCAGAGCTGGGCAACAAAAGAGACC 506
| | | | |
Db 53504 GTTGCAGTGAAGCAGAGATTGTGCA-ATGCACTCCAGCTGGGCAACAGAGTGAAGCTC 53446
| | | | |
QY 507 TGTCTCAAAAATAATAGTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 564
| | | | |
Db 53445 CATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 53388
| | | | |

RESULT 15

US-11-121-086-10/c
; Sequence 10, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138, 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 199321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-10

Query Match 6.9%; Score 156; DB 7; Length 199321;
 Best Local Similarity 70.4%; Pred. No. 1.8e-18;
 Matches 252; Conservative 0; Mismatches 100; Indels 6; Gaps 3;

QY	212	AAGATTAAAGAAATTTCTTGAGGCCAGGCAAGTGGCTCAACCTGTAAATTCAGTAC	271
Db	177161	ATGATTTAAATAAATACTGAGGGGCCAGACATGGTCTCATGCTGTAAATCCAGCNC	177102
QY	272	TGTGAGACTCCGAGGTCAGAGACTGCTTGAGGCCAGAGTTCAAGAGCAGCTTGGACNA	331
Db	177101	TTTGGAGGCTGAGGTGGGCGGATCATTGAGGTCAGAGTTCAAGACCAAGCTTGGCCNA	177042
QY	332	CACAGGGAGA-CCTGTCACTACAAAGAAATTAATTAGCCAGGCTTAGTGGTCATCC	390
Db	177041	CATGCTGAACCTCTCTCTACTAATAATACAAAATATATCCAGGCATGTTGGCCATGC	176982
QY	391	CTGTGTTCCAGCTACTAGGAGGAGAGTNGA----CTGCTTGTCCAGAGGTCA	446
Db	176981	CTAGAGTCCAGCTACTTGGGAGGCTGAGGAGAGAAATGGCTGACCCCGGAGGTGA	176922
QY	447	GACTGCATGTGAGCTGAGACCCAGCCACTGTCATTCAGCTTGGGCACAAAAAGAGACC	506
Db	176921	GATTGCACTGAGCAGAGATGTGCCA-ATGCATCCAGCTTGGGCAAGAGTGAAGCTC	176863
QY	507	TGTCTCAAAAATAAGTTAAATTAATAATAATAATAATAATAATAATAATAATAATA	564
Db	176862	CATCTCAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	176805

Search completed: December 22, 2005, 00:03:08
 Job time : 315 secs

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185 GATTGCTCAGATCTGCCCCACCCTGAAGAATTAAAGAAATTCTTGAGGCCAGGCAC 244

Dh 27868 GATTGCTCAGATCTGCCCCCACTCTGAAAGATTCTTGAAGGCGAC 27927
Qy 245 AGTGGCTCACAAGCTGTAATTCAGATCTGTAGAGTCCGAGGTCAAGAGCTGCTTGAAG 304
Db 27928 AGTGGCTCACAAGCTGTAATTCAGATCTGTAGAGTCCGAGGTCAAGAGCTGCTTGAAG 27987
Qy 305 CCAGAGATTCAAGAGCAGCTTGAACAACAAGAGAGCTGTCACTAACAAGAAATA 364
Db 27988 CCAGAGATTCAAGAGCAGCTTGAACAACAAGAGAGCTGTCACTAACAAGAAATA 28047
Qy 365 AATTAGCCAGGCTTATGAGTCTCATCCCTGAGTCCAGCTACTAGGAGGAGAAATAG 424
Db 28048 AATTAGCCAGGCTTATGAGTCTCATCCCTGAGTCCAGCTACTAGGAGGAGAAATAG 28107
Qy 425 ACTGCTTCTCCAGAGGCTCAAGACTGTAGAGTGAAGCCAGCCACTGCAATCCAG 484
Db 28108 ACTGCTTCTCCAGAGGCTCAAGACTGTAGAGTGAAGCCAGCCACTGCAATCCAG 28167
Qy 485 CCTGGGCAACAAAAGAGACCTGTCTCAAAAATAAGTTAATTAATTAATTAATA 544
Db 28168 CCTGGGCAACAAAAGAGACCTGTCTCAAAAATAAGTTAATTAATTAATTAATA 28227
Qy 545 TAGTTTAAACCTTAAACATCTCTTTTCAAGAGACTTTCTTAAGACTTCATGCTG 604
Db 28228 TAGTTTAAACCTTAAACATCTCTTTTCAAGAGACTTTCTTAAGACTTCATGCTG 28287
Qy 605 GGTCTGTGTGATCTCACTTCCCTTTTCAAGCTCACTTTTAAACAGTCTCTTTTCC 664
Db 28288 GGTCTGTGTGATCTCACTTCCCTTTTCAAGCTCACTTTTAAACAGTCTCTTTTCC 28347
Qy 665 AAGATTAATAAGTATAGTTTCTGGAATCAGATTTCTTCTGTTTGAAGCAGGAG 724
Db 28348 AAGATTAATAAGTATAGTTTCTGGAATCAGATTTCTTCTGTTTGAAGCAGGAG 28407
Qy 725 GACAAATTTTGTCTGAGGCTTGTGATCTGTCTGTGTGCTGACGATCTCAAGC 784
Db 28408 GACAAATTTTGTCTGAGGCTTGTGATCTGTCTGTGTGCTGACGATCTCAAGC 28467
Qy 785 AAATTTGCGAGCCTCTCCGGAATGACAGCCAGACAGAGCTCAGCGAAAAGCTAGAG 844
Db 28468 AAATTTGCGAGCCTCTCCGGAATGACAGCCAGACAGAGCTCAGCGAAAAGCTAGAG 28527
Qy 845 ACCTGGCGAGGAGACTCAAGTGCACAAAAAACTTATCTTTTCTTTTCTTCTTTC 904
Db 28528 ACCTGGCGAGGAGACTCAAGTGCACAAAAAACTTATCTTTTCTTTTCTTCTTTC 28587
Qy 905 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 964
Db 28588 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 28647
Qy 965 CTTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1024
Db 28648 CTTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 28707
Qy 1025 TGCCTTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1084
Db 28708 TGCCTTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 28767
Qy 1085 TTCCGCTAATTAATCAAGGCGCAATCCAGCTCTGTGTCTTCTTCTTCTTCTTCTTCTT 1144
Db 28768 TTCCGCTAATTAATCAAGGCGCAATCCAGCTCTGTGTCTTCTTCTTCTTCTTCTTCTT 28827
Qy 1145 CCTCTCTGTGTGAAAACAATATGAGCGCGCTGACAGAGGTGAAGTGTGAATA 1204
Db 28828 CCTCTCTGTGTGAAAACAATATGAGCGCGCTGACAGAGGTGAAGTGTGAATA 28887
Qy 1205 TCAGGAAGATGATGAAGCTTTTGGACTCCGTTCTCAATGTAAATGAGGTAAAT 1264
Db 28888 TCAGGAAGATGATGAAGCTTTTGGACTCCGTTCTCAATGTAAATGAGGTAAAT 28947
Qy 1265 ACCAGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1324
Db 28948 ACCAGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 29007

Qy 1325 GGTGTTCAGCATCAAGTTACCCCAACAGACGAGTTCAGCCAAATTAAGCGAACAGGC 1384
Db 29008 GGTGTTCAGCATCAAGTTACCCCAACAGACGAGTTCAGCCAAATTAAGCGAACAGGC 29067
Qy 1385 CCGGTTCATCTTCTGACGCTTTTCTCATCTCCAGAGGTGTGAACAGGAGCTGTGGCC 1444
Db 29068 CCGGTTCATCTTCTGACGCTTTTCTCATCTCCAGAGGTGTGAACAGGAGCTGTGGCC 29127
Qy 1445 CCGCTGCTGTGTGACGTGCGAGGAGCGCGCGCTTGTCTGTGTGTGTAGAGGCTG 1504
Db 29128 CCGCTGCTGTGTGACGTGCGAGGAGCGCGCGCTTGTCTGTGTGTGTAGAGGCTG 29187
Qy 1505 AGGTCAAGTGTGTGTCTCCGCGCGCGCGCGCTTATAGTCTGTGTCTTAAAGCC 1564
Db 29188 AGGTCAAGTGTGTGTCTCCGCGCGCGCGCGCTTATAGTCTGTGTCTTAAAGCC 29247
Qy 1565 AGGCGCTTCAACGCGGAGAGAGCGCGAACCCCAAGCCGAGCCCAAGCTGTGTGTGT 1624
Db 29248 AGGCGCTTCAACGCGGAGAGAGCGCGAACCCCAAGCCGAGCCCAAGCTGTGTGTGT 29307
Qy 1625 TGCCTGGGCACTGTGTGTGAGTGTGATTTGTTCTTCTTCTTCTTCTTCTTCTTCTT 1684
Db 29308 TGCCTGGGCACTGTGTGTGAGTGTGATTTGTTCTTCTTCTTCTTCTTCTTCTTCTT 29367
Qy 1685 TAAACAATCGACAGCGAGCGCGGTGCGAGAGCCCAAGTCCCGCTTGTCAAGAGCCAG 1744
Db 29368 TAAACAATCGACAGCGAGCGCGGTGCGAGAGCCCAAGTCCCGCTTGTCAAGAGCCAG 29427
Qy 1745 CGGCTGTCTGTGAGAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1804
Db 29428 CGGCTGTCTGTGAGAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29487
Qy 1805 GAGGAATGTGACTTTAAGACAGCGCGCGCTGTGACGCTGTGTAGAAACGCTGTGTGT 1864
Db 29488 GAGGAATGTGACTTTAAGACAGCGCGCGCTGTGACGCTGTGTAGAAACGCTGTGTGT 29546
Qy 1865 AAGCAAGAGGTGTGTGACTGTGACAAAGCTTGTGTGTGTGTGTGTGTGTGTGTGT 1924
Db 29547 AAGCAAGAGGTGTGTGACTGTGACAAAGCTTGTGTGTGTGTGTGTGTGTGTGTGT 29606
Qy 1925 CAGAGTTTGGCGCGCGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1984
Db 29607 CAGAGTTTGGCGCGCGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29666
Qy 1985 TCTCGGGAACGAAGGATTAACGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2044
Db 29667 TCTCGGGAACGAAGGATTAACGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29726
Qy 2045 TCATGAGAGAACCTTGAAGCGGAGCGGTCTCCCGGAAAGCGAGCTGTCTCAAGGTCTCC 2104
Db 29727 TCATGAGAGAACCTTGAAGCGGAGCGGTCTCCCGGAAAGCGAGCTGTCTCAAGGTCTCC 29786
Qy 2105 GCACCAAGTGAAGCTGTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2164
Db 29787 GCACCAAGTGAAGCTGTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29846
Qy 2165 CCCCAGAGCTTAAAGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2224
Db 29847 CCCCAGAGCTTAAAGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29906
Qy 2225 GCGCTTGTGGAATGTGCTGTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2270
Db 29907 GCGCTTGTGGAATGTGCTGTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29952

RESULT 2
US-09-949-016-15281
; Sequence 15281, Appl: cation US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIORITY FILING DATE: 2000-04-14
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-03
PRIORITY FILING DATE: 2000-09-08
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15281
LENGTH: 11808
TYPE: DNA
ORGANISM: Human
US-09-949-016-15281

Query Match 89.1%; Score 2022.8; DB 3; Length 11808;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

233 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 292
1 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 60
293 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 352
61 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 120
353 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412
121 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
413 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 472
181 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 240
473 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 532
241 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 300
533 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 592
301 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
593 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 652
361 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 420
653 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 712
421 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 480
713 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 772
481 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 540
773 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 832
541 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 600
833 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 892
601 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
893 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 952
661 AAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
953 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1012
721 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 780

1013 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1072
781 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 840
1073 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1132
841 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 900
1133 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1192
901 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 960
1193 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1252
961 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1020
1253 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1312
1021 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1080
1313 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1372
1081 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1140
1373 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1432
1141 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1200
1433 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1492
1201 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1260
1493 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1552
1261 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1320
1553 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1612
1321 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1380
1613 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1672
1381 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1440
1673 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1732
1441 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1500
1733 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1792
1501 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1560
1793 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1852
1561 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1619
1853 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1912
1620 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1679
1913 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1972
1680 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1739
1973 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 2032
1740 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1799
2033 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 2092
1800 GAGGCGAGGCAAGTGGCTCAACCTGTATTCAGTACGTGTGAGAGTCCGAGGTGAG 1859

QY	2093	1860	QY	2153	QY	1920	QY	2213	QY	1980
CCAGAGGCTCCGACCCCAAGTAGAGGCTGCGAGGCGCCGAGCCCGCCCGAGAGCCAC	2153	TTCCAGAGGCTCTCCGACCCCAAGTAGAGGCTGCGAGGCGCCGAGCCCGCCCGAGAGCCAC	1919	CCCGAGGCCCGGCCCGAGGCTTAAAGCGCGCGCGCGCTGTGCGAGAGCCCACTGCGAA	2212	CCCGAGGCCCGGCCCGAGGCTTAAAGCGCGCGCGCGCTGTGCGAGAGCCCACTGCGAA	1979	GCCCAGCTCGCGCGCGCTTTGGATTGACTGTCCAGCGCTCGCCGAGCTGTCTCCAGCGCG	2037	GCCCAGCTCGCGCGCGCTTTGGATTGACTGTCCAGCGCTCGCCGAGCTGTCTCCAGCGCG

RESULT

```

US-08-846-012A-1
: Sequence 1, Application US/08846012A
: Patent No. 5807740
:
: GENERAL INFORMATION:
: APPLICANT: AMARAL, M. Catherine.
: APPLICANT: CHEN, Jin-Long
: TITLE OF INVENTION: Regulators of UCP2 Gene Expression
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/846,012A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: T97-003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 736 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
:
US-08-846-012A-1

```

Query Match	21.4%	Score 485;	DB 2;	Length 736;
Best Local Similarity	99.6%	Pred. No. 3.5e-100;		
Matches 507; Conservative	0;	Mismatches 0;	Indels 2;	Gaps 2;

1762 GGGTGGTAGTTTGCCAGCGTAGGGGGCTGGGCCATAAAGAGGAAGTGCACCTTAAG 1821

1 GGGTGGGTAGTTTGGCCACGCTAGGCGGCGCTGGGCCCATAAAGAGGAAGTCACCTTAG 60

1822 ACACGGCCCCGTGACGCTGTAGAAACCGTCTGCTGGGAAGCAAGAGTGTG 1881

61 ACAAGGCCCGCTGAGCG - TGTTAGAACCGTCTCGCTGGGAGGCAAGAGTGTGTG 119

1882 ACTGCAAGACTTGTTCGCGCGTCACTTCGCATCTCACAGAGTTGGCGCCG 1941

120 ACTGACAAAGACTTGTTCGTGGCGGTCACTTGCATCTCACAGAGTTGGCGGCCG 179

1942 AGAGGTGTAGGCGAGAGCGGGAGTGGCAAGGAGTGACATCTCGGGACGAGGA 2001

180 AGAGAGTGTGAGCGAGGCGGGAGTGGCAAGGAGTGCATCTTCGGGCAAGAGGA 239

QY	2002	GTAAACCGCGGATGATGGAGCGACCGAAACGGGAATGTGAGAAAGCATGAGAGAAACCTTA	2061
Db	240	GTAAACCGCGGATGATGGAGCGACCGAAACGGGAATGTGAGAAAGCATGAGAGAAACCTTA	299
QY	2062	GGCGGGGCGGTCCCGCGGAAAGCGCGCTGCTCGAGGATCTCGGACCCCAAGTAGAGACT	2121
Db	300	GGCGGGGCGGTCCCGCGGAAAGCGCGCTGCTCGAGGATCTCGGACCCCAAGTAGAGAG-T	358
QY	2122	GGCAGAGCCCGGACCCCGACCGGACCGCCCAAGGCGGAGCCCGGAGGCTTAAAGCG	2181
Db	359	GGCAGAGCCCGGACCCCGACCGGACCGCCCAAGGCGGAGCCCGGAGGCTTAAAGCG	418
QY	2182	CGCGCGCGCTGCGCGGAGCCCACTGCGAAGCCCAAGCTGCGCGCGCTTGGATTGACT	2241
Db	419	CGCGCGCGCTGCGCGGAGCCCACTGCGAAGCCCAAGCTGCGCGCGCTTGGATTGACT	478
QY	2242	GTCACGCTGCGCCCGGCTCGTCCGACGCG	2270
Db	479	GTCACGCTGCGCCCGGCTCGTCCGACGCG	507

RESULT 4

US-09-100-29/-1
Sequence 19, Application US/09100297
Patent No. 5849514
GENERAL INFORMATION:
APPLICANT: AMARAL, M. Catherine.
TITLE OF INVENTION: Regulators of UCP2 Gene Expression
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA

```

; ZIP: 94104
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,297

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;
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,012
;

```

! FILING DATE:
! ATTORNEY/AGENT INFORMATION:
!

! NAME: OSMAN, RICHARD A
! REGISTRATION NUMBER: 36,627
!

REFERENCE/DOCKET NUMBER: T97-003
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342

```

; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:

```

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; LENGTH: 736 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: double
; TOPOLOGY: linear
;

```

MOLECULE 1
US-09-100-297-1

Query Match	21.4%	Score 485	DB 2	Length 736
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Best Local Similarity 99.6%; Pred. No. 3.5e-100;
Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1762 GGGTGGGTAGTTTGGCCAGCGTAGGGGGGGCTGGGCCCATAAAGAGGAAGTGCACTTAAG 1821

Db 1 GGGTGGTAGTTTGCCAGCGTAGGGGGCTGGCCCATAAAAAGAGAGTGCATTAAg 60

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QY 1822 ACAGGCGCCGCTGAGCTTGTAGAAACGCTCTGAGTGGAGGAGAGAGTGTGTG 1881
DB 61 ACAGGCGCCGCTGAGCTTGTAGAAACGCTCTGAGTGGAGGAGAGAGTGTGTG 119
QY 1882 ACTGACAAAGATTGTTCTGCGCGTCACTCTTGCATCTTCAAGAGTTGCGGCGCG 1941
DB 120 ACTGACAAAGATTGTTCTGCGCGTCACTCTTGCATCTTCAAGAGTTGCGGCGCG 179
QY 1942 AGAGGTGTGAGGAGAGGCGGAGTGGCAAGGAGTGCATCTTCTGCGGAGCAAGA 2001
DB 180 AGAGGTGTGAGGAGAGGCGGAGTGGCAAGGAGTGCATCTTCTGCGGAGCAAGA 239
QY 2002 GTAAACGCGGTGATGGAGCGACGGAACGAGGAGTGAAGAAATGATGAGAGAGCTA 2061
DB 240 GTAAACGCGGTGATGGAGCGACGGAACGAGGAGTGAAGAAATGATGAGAGAGCTA 299
QY 2062 GCGCGGCGGTCTCCCGCGAAAGCGGCTGCTCCAGGCTCTCCGACCCCAAGTAAAGCT 2121
DB 300 GCGCGGCGGTCTCCCGCGAAAGCGGCTGCTCCAGGCTCTCCGACCCCAAGTAAAGCT 358
QY 2122 GCGAGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2181
DB 359 GCGAGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 418
QY 2182 GCGCGCGCGCTGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2241
DB 419 GCGCGCGCGCTGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 478
QY 2242 GTCCACGCTCGCGCGCGCTGCTCCAGCGCG 2270
DB 479 GTCCACGCTCGCGCGCGCGCTGCTCCAGCGCG 507

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RESULT 5
US-09-949-016-176561/c
Sequence 176561, Application US/09949016
Patent No. 6812339

```

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176561
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-176561

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Query Match 7.5%; Score 170.4; DB 3; Length 601;
Best Local Similarity 74.7%; Pred. No. 4.2e-29;
Matches 254; Conservative 0; Mismatches 81; Indels 5; Gaps 3;

```

QY 217 TTTAAGAGATTCTTGAAGCCAGGACAGTGGCTCACACCTGTAAATTCAGTACTGTGA 276
DB 600 TTTTAAATTAATTAATTCGCGGCGAGGCGAGTGGCTCACACCTGTAAATTCAGTACTGTGA 541
QY 277 GAGTCCGAGTCAAGAGAGTGTGAGGCGAGAGTGTCAAGGAGAGCTTGGCAACAG 336
DB 540 GAGGCGAGAGTGTGAGGCTCACCTGAGGCGAGAGTGTCAAGGAGAGCTTGGCAACAG 481
QY 337 GGAGA-CCTGTCACTAACAAGATTAATTAATTAAGGCTTAACTAGTGTCTCCCTGTG 395

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DB 480 CGAAACCCATCTCCAAATTAATAAATTAAGCCGCGGCGTCAAGGAGAGTGTGGA 421
QY 396 GTCCAGTACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 452
DB 420 ATCCAGTACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361
QY 453 AGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 512
DB 360 ATTGAGCTGATGATGATGCA-CTGCGTTCCAGGCTTGGGCAACAAAGGAGCTCATCTC 302
QY 513 AAAAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 552
DB 301 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 262

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RESULT 6
US-09-949-016-16780/c
Sequence 16780, Application US/09949016
Patent No. 6812339

```

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16780
LENGTH: 35493
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (35493)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16780

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Query Match 7.5%; Score 170.4; DB 3; Length 35493;
Best Local Similarity 74.7%; Pred. No. 1.8e-28;
Matches 254; Conservative 0; Mismatches 81; Indels 5; Gaps 3;

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QY 217 TTTAAGAGATTCTTGAAGCCAGGACAGTGGCTCACACCTGTAAATTCAGTACTGTGA 276
DB 12792 TTTTAAATTAATTAATTCGCGGCGAGGCGAGTGGCTCACACCTGTAAATTCAGTACTGTGA 12733
QY 277 GAGTCCGAGTCAAGAGAGTGTGAGGCGAGAGTGTCAAGGAGAGCTTGGCAACAG 336
DB 12732 GAGGCGAGAGTGTGAGGCTCACCTGAGGCGAGAGTGTCAAGGAGAGCTTGGCAACAG 12673
QY 337 GGAGA-CCTGTCACTAACAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 395
DB 12672 CGAAACCCATCTCCAAATTAATAAATTAAGCCGCGGCGTCAAGGAGAGTGTGGA 12613
QY 396 GTCCAGTACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 452
DB 12612 ATCCAGTACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12553
QY 453 AGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 512
DB 12552 ATTGAGCTGATGATGCA-CTGCGTTCCAGGCTTGGGCAACAAAGGAGCTCATCTC 12494
QY 513 AAAAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 552
DB 12493 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 12454

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RESULT 7
US-09-949-016-15382/c
; Sequence 15382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 15382
; LENGTH: 37292
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(37292)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15382

Query Match 7.4%; Score 168.4; DB 3; Length 37292;
Best Local Similarity 63.2%; Pred. No. 5.2e-26;
Matches 345; Conservative 0; Mismatches 186; Indels 15; Gaps 5;

QY 5 GATGTCGGCCGCTCAGCTCCCAAGTGTGAGATTGAGCGGTGAGCCCTCAGCTG 64
DB 31797 GATGTCGGCCGCTCAGCTCCCAAGTGTGAGATTGAGCGGTGAGCCCTCAGCTG 31738
QY 65 CTACAGTTTCAAAATATATTATAGTACCAATATCTCCAGTTGTCCACAGA 124
DB 31737 C-----CTTAGCACTGAGGGTTTCAATTCACAGTGTCCCATAGTTCTGGGGGGT 31685
QY 125 CATCTTATGACTTGAAGCAAGCTGCTAAATCCCAAGGTGAGCGTTGTATGTCTATAG 184
DB 31684 TGCCGTGAGGGCTGTCCACTGAGGAAAGATGTAGGAATGATC-TCAGTCCCTCTTC 31626
QY 185 GATTGCTCAGATGTGCCCCCACTGAAAGATTAAAGAAATTTCTTGAAGCCAGGAC 244
DB 31625 AAGTCCCTTCTATCTGTGCTTCCCTATTAAGCATTTCTACTAAG--TCTTCAGGCTGGGCGT 31568
QY 245 AGTGGCTCACACTGTAAATTCAGTACTGTGAGAGTCCGAGGTGAGAGACTGCTTGAAG 304
DB 31567 GGTGGCTCATGCTTAATATCCAGCAAGTTGGAGAGCTGAGGTGGAAGATTGCTTGAAGC 31508
QY 305 CCAGAGTTTCAAGAGCAAGCTGTGACACACAGAGAGACTGTCTACTACAAAGATTAATA 364
DB 31507 CTTGAGATTTCAGACCAAGCTGTGGCAACATTAAGACCTGTCTCTACAAAAATTTAAA 31448
QY 365 AATTAGCAGGCTTATAGTGTCTATCCCTGTGATCCAGACTACTAGGAGGAGAGTATAG 424
DB 31447 AATTAGCAGGCTTATAGTGTCTATCCCTGTGATCCAGACTACTAGGAGGAGTATAG 31388
QY 425 A-----TGCTTGTCCAGAGAGTCAAGCTGCAAGTGAAGCTGAGACCCAGCCACTGCA 480
DB 31387 AGGACCCGATTGAGCTGTGAGAGTGAAGCTGCAAGTGAAGCTGAGAGCTGAGAGTGG 31329
QY 481 CCAGCTGTGGGCAAAAGAGACCTGTCTCAAAATAATTAATTAATAATAATA 540
DB 31328 CCAGCTGTGGGCAAAAGAGACCTGTCTCAAAATAATTAATTAATAATAATAATA 31269
QY 541 AAAATA 546
DB 31268 AAAATA 31263

RESULT 8
US-09-949-016-16674/c
; Sequence 16674, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 16674
; LENGTH: 126237
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16674

Query Match 7.4%; Score 167.4; DB 3; Length 126237;
Best Local Similarity 70.1%; Pred. No. 1.4e-27;
Matches 253; Conservative 0; Mismatches 106; Indels 2; Gaps 2;

QY 178 TCTATAGAAATGCTCAGATGTGCCCCCACTGAAAGATTAAAGAAATTTCTTGAAGC 237
DB 21667 TCCCTTGAAGCAATCAGGGTGAACAGCTATTTATTCCTATTTAAAGTAACATAGGC 21608
QY 238 CAGGCAAGGGCTCACAAGCTGTAATTCAGTACTGTGAGAGCCGAGGTGAGAGCTG 297
DB 21607 CAGGTGAGGGCTCACAAGCTGTAATTCAGTACTGTGAGAGCCGAGGTGAGAGCTG 21548
QY 298 CTTGAGGCCAGAGTTCAAGAGCAAGCTGTGACACACAGAGAG-CTGTCTACTACAAAG 356
DB 21547 CATGAGCCCGGAGTTTGAACCAAGTCTGGGCAACACAGGAGACCCCATCTTACAAAC 21488
QY 357 AATTAATAATTAAGCAGGCTTATAGTGTCTATCCCTGTGTCTCCAGCTACTAGGAGGCA 416
DB 21487 AAACAAATAATTAAGCTGGGATGATGATGATGATGATGATGATGATGATGATGAT 21428
QY 417 GAATGAGACTGCTGTGCTCCAGAGGTCAAGCTGCAAGTGAAGCTGAGACCCAGCCACTG 476
DB 21427 GAGGCAAGACTGCTGTGAGCCCGAGGTCAAGACTGCTGAGCTGTGAGCTGTGAGCTG 21369
QY 477 CATTCAAGCTGTGGCAAAAGAGACCTGTCTCAAAATAATTAATTAATAATAAT 536
DB 21368 CACTACAGCTGTGGTGAACAGTGAAGACCTGTCTTGGAAAAAACAACAAACCCCAAC 21309
QY 537 A 537
DB 21308 A 21308

RESULT 9
US-09-949-016-16675/c
; Sequence 16675, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

```

: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 16675
: LENGTH: 126237
: TYPE: DNA
: ORGANISM: Human
: US-03-949-016-16675

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Query Match	7.4%	Score 167.4;	DB 3;	Length 126237;
Best Local Similarity	70.1%;	Pred. No. 1.4e-27;		
Matches 253; Conservative	0;	Mismatches 106;	Indels 2;	Gaps 2;

QY	178	TCATATAGAAATTGCTCAGATCTGGCCCCCAACCCCTGAAAGAAATTTAAGAGAAATTTCTTGAGGC	237
Db	21667	TCTCTTTGAAAGCATCAGGGGTGACCGAGTATTTTATTTCTCTATTTAAAGTAACATAGGC	21608
QY	238	CAGGCACAGTGGCTCAACCTGTAAATTCCAGTACTGTGAGAGTCCGAGGTCAAGAGACTG	297
Db	21607	CAGGTGACAGTGGCTCAACCTGTAAATCCAGCACTTTGGGAGGCCAAGGACAGAGATCA	21548
QY	298	CTTGAGGCCACGAGATTCAAGAGCAGCCTGGAACAACAAGGAGA-CTGTCACTACAAG	356
Db	21547	CATAGACCCCGGAGTTTGAGACCAAGTCTGGGCAACAAGGAGAACCCCATCTCTCAAAAC	21488
QY	357	AATTAATAAATTGAGCCAGGCTTTAGTGGTCATATCCCTGTGGTCCACACTACTAGGAGAGCA	416
Db	21487	AAACAAAATAATGAGCTGGGCAATGTATGCAATGCTGTGTCCCACTATGTGGGAGCT	21428
QY	417	GAACTAGAGACTGCTTGTCCAGAGAGGTCAAGACTGACAGTGAAGCTGAGACCCAGCCACTG	476
Db	21427	GAGCACAAGACTGCTTGAAGCCCGAGAGGTCAAGACTGCTGTAGCTGTGACACTGTGCCA-CTG	21369
QY	477	CATTCCAGCCTGGGCAACAAAAGAGACCTGTCTCAAAAAATTAAGTTAATAATAAT	536
Db	21368	CACATACAGCCTGGGTGACAGAGTGAAGACCTGTCTTGGAAAAAACAACAAAACCCAAAC	21309
QY	537	A 537	
Db	21308	A 21308	

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RESULT 10
US-09-949-016-14788
; Sequence 14788, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14788
; LENGTH: 16230
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14788

```

Query Match	7.4%;	Score 167;	DB 3;	Length 16230;
Best Local Similarity	73.6%;	Pred. No. 8e-28;		
Matches 254;	Conservative	0;	Mismatches 85;	Indels 6;
				Gaps 3

[illegible]

```

RESULT 11
US-09-949-016-12816
; Sequence 12816, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12816
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12816

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	Query Match	Best Local Match	Similarity	7.3%;	Score	165.2;	DB	3;	Length	99370;
	Matches	240;	Conservative	0;	Mismatches	83;	Indels	5;	Gaps	2;
QY	223	AGAATTTCTTGAGGCCAGGCAAGTGCTCAACCTGTAAATTCAGTACTGTGAAGATCC	282							
Db	66639	ATATTTTTCACAGGCCAGGTGACGTGGCTCCACACGTAAATTCACACATTTGGAGGCC	66698							
QY	283	GAGGTCCAGAGACTGTCTTGAGGCCAGAGATTCAGAGACGCTTGACACACAGGGAGA-	341							
Db	66699	AAGGTGGCAGAGATCACATAAGTCCAGGAGTTCAAGACAGCTCGACAAACATAGGCAAAAC	66758							
QY	342	CTGTGTACTTCAAAAGATTAATTAATTAATGACAGGCTTAAGTGGCTCATCCCTGTGGTCCCA	401							
Db	66759	CCGTCTCTCTCAATTAATAACAAAATTAATGACAGGCAATGGTGGTTATGCTGTGGTCCCA	66818							
QY	402	GCTACTAGGGAGGCGAGAAATGAGA-----CTGCTTGTGCCAGAGAGTCAAGACTGACAGTGA	457							
Db	66819	GCTACTAGGAGGGGTGAGGTGGGAGGATCACTTGAACCCAGGAGCAGAGGTTGACAGTGA	66878							
QY	458	GCTGAGACCCAGGCAACTGTGATTTCCAGCTGTGGGCAACAAAAGAGACCTGTGTCAAAAA	517							
Db	66879	GCTGAGATCATGCCCCATGTGACCTTGTAGCTGGGGGAACAGAGCAGACCCGTGTCTCAAAAA	66938							

Qy 518 ATAGTTAAATTAATAATAATAAAT 545
Db 66939 AAAAAAAAAAACCAACCCCAAAAT 66966

RESULT 12
US-09-949-016-17540
; Sequence 17540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540

Query Match 7.3%; Score 165.2; DB 3; Length 99370;
Best Local Similarity 73.2%; Pred. No. 4e-27;
Matches 240; Conservative 0; Mismatches 83; Indels 5; Gaps 2;

Qy 223 AGAATTTCTTGAAGCCGACGACAGTGGTTCACACTGTAATTCAGTACTGTGAAGTCC 282
Db 66639 ATATTGTGACAGGCGAGGTGTCAGTGGTCAAGTGAATTCAGACTTTGGAGAGCC 66698
Qy 283 GAGGTGAGAGGAGCTTGAAGCCAGGAGTCAAGAGAGCCCTGGAACAACAGAGGAGA- 341
Db 66699 AAGGTGAGAGGATCATATTAATTCAGAGTTCAGAGAGCCCTGGAACAACAGAGGAGA- 66758
Qy 342 CCTGTCACTACAAAGAAATTAATAATTAAGCCAGGCTTAAGTGGCTCATCTCCGTGGTCCA 401
Db 66759 CCTGTCTACAAATAATTAATAATTAAGCCAGGAGTGGCTTAAGTGGCTGGTCCA 66818
Qy 402 GCTACTAGGAGGCGAGAGTGA---CTGCTGTGTCCAGAGAGTCAAGACTGCAATGA 457
Db 66819 GCTACTAGGAGGCGTGAAGTGGAGATCACTGAACCCAGAGAGAGAGGTTGCAATGA 66878
Qy 458 GCTGAGAGCCAGCCAGCTGATTCAGGCTGGGCAACAAAGAGACCTGTCTCAAAA 517
Db 66879 GCTGAGATCATGCCACTGCTGAGCTGGGAAAGAGAGAGACCTGTCTCAAAA 66938
Qy 518 ATAGTTAAATTAATAATAATAAAT 545
Db 66939 AAAAAAAAAAACCAACCCCAAAAT 66966

RESULT 13
US-09-949-016-27232/c
; Sequence 27232, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 27232
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27232

Query Match 7.2%; Score 164.2; DB 3; Length 601;
Best Local Similarity 59.7%; Pred. No. 1e-27;
Matches 330; Conservative 1; Mismatches 214; Indels 8; Gaps 3;

Qy 6 ATTCGCGCGCTCAGCTTCCCAAGTGGTGGATTCAGAGCGGAGCCACTCAGCTGGC 65
Db 588 ATCTGCTGCTCAGCTCAGAGTGTGATTCAGAGCGGAGCCACTGTCAGGC 529
Qy 66 TACAAGT---TTCAAAATACATTTATCTAGTACCCATACATTCCTCAGTTGTCCAG 122
Db 528 CCTCATGACTTTTAAAAAACAATTAAAGAAATAGACTTGTGTAATAAGTAAATG 469
Qy 123 GACATCTTATGACTGAGCAAGCTGTAAATTCAGAGGTGACGCTTTGTAT 182
Db 468 GACAGAAATTTGAATTAATATATGATTCATTAATAGAAAGATATTTGAAATGTAT 409
Qy 183 AGAATGCTCAGATTCGCCCCCAGCTGAAAGAAATTTAAGAAATTTCTGAGCCAGC 242
Db 408 TCAAAATGATTTCTTACCCATATGAATTAATTTTAAATTAATTAATTTCTGCGCAGGC 349
Qy 243 ACAATGCTCAGACTGTATATTCAGTACTGTGAGAGTCCAGAGTCAAGTCTTGA 302
Db 348 ACGGTGCTATGCTGTATATTCAGACTTCGAGAGCGGAGAGGTAATCACTGA 289
Qy 303 GGCAGAGTTCAAGAGCAGCTTGAACAACAAGAGAGCTGTCACTACAAAGATPAA 362
Db 288 GGTCAAGAGTTCAAGACAGCTGATCAATCAACAAACCCATCTCTATAAAATAC 229
Qy 363 TAAATTAAGCAGCTTATGAGTCCATCCCTGTGTGCTCCAGCTAAGGAGGAGAGTA 422
Db 228 AAAATTAAGCGGAGTGTGAGTGTGATGTCTGTATCCAGCTTCTGAGGAGTGAAGCA 169
Qy 423 GGA---CTGCTGTCCCAAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCA-CCTGC 477
Db 168 GGAAGATCGCTTGAACCCGAGGAGCGAGGTTGCAAGTGAAGTGAAGTGAAGTGC 109
Qy 478 ATTCAGCTGAGCAACAAAGAGAGCCCTGTCTCAAAAATTAAGTTAAATTAATA 537
Db 108 ACTCAGCTGAGCAACAGCAAGAACTCATCTCAAAAAAAAAAAAAAAAAATTATTGA 49
Qy 538 ATAAATTAAGTT 550
Db 48 TTCTGAATTAATGT 36

RESULT 14
US-09-949-016-160756/c
; Sequence 160756, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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